

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 12:21:38 ; Search time 13284 Seconds
(without alignments)

10154.434 Million cell updates/sec

Title: US-09-927-112-1

Sequence: 1 tcgcgatctagaactagtgg.....ggtaacggyggcccaagcccg 4635

Scoring table: IDENTITY_NUC
Gapcod 10.0 Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REFERENCE
AUTHORS

1. Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Tribouley, C.M., Yue, H., Khan, F.A., Gandhi, A.R., Au-Young, J., Lal, P., Kearney, L., Elliott, V.S., Ding, L. and Thornton, M.


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VERSION  AX392826.1 GI:19700922
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REFERENCE
  1 Griffin,J.A., Paterson,C., Gandhi,A.R., Lu,Y., Yao,M.G.,
    Baughn,M.R., Wallis,N.K., Hafalia,A.J., Ding,L., Tribouley,C.M.,
    Das,D., Thomson,M. and Lal,P.
    Lipid metabolism enzymes
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4827 CCGGAGCGGCGGCGCAG 4886
3510 GTGAACACCGGAG 3569
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3570 GCAAGCAATTCGAG 3629
4947 GCAAGCAATTCGAG 5006
3630 CTGAGCCTCAAGCTATTCGAG 3689
5007 CTGAGCCTCAAGCTATTCGAG 5066
3690 AAGCAGAGTTCAG 3749
5067 AAGCAGAGTTCAG 5126
3750 GGCATTCGAG 3809
5127 GGCATTCGAG 5186
3810 CAGGAGAGATGAG 3869
5187 CAGGAGAGATGAG 5246
3870 ATGTTCTCGGCGGAG 3899
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RESULT 3

AK074149
 LOCUS AK074149 4411 bp mRNA linear PRI 15-FEB-2002
 DEFINITION Homo sapiens mRNA for FLJ00222 protein.
 ACCESSION AK074149
 VERSION AK074149.1 GI:18676645
 KEYWORDS fis (full insert sequence).
 SOURCE Homo sapiens adult spleen cDNA to mRNA, clone: FLJ00222.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.
 TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen
 JOURNAL Published Only in Database (2002)
 REFERENCE 2 (bases 1 to 4411)
 AUTHORS Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, URL: http://www.kazusa.or.jp/NEDO, Tel: 81-438-52-3913, Fax: 81-438-52-3914)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert and 5'- & 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES
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BASE COUNT 740 a 1528 c 1438 g 705 t
 ORIGIN

Query Match 54.5%; Score 2527.4; DB 9; Length 4411;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2542; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 2567 GATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2626
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QY 3167 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3226
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QY 3227 GAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3286
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QY 3287 CTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3346

AUTHORS Ohara, O.
 TITLE Direct Submission
 JOURNAL Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, Tel.: +81-438-52-3913,
 Fax: +81-438-52-3914)

FEATURES

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Location/Qualifiers
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BASE COUNT 1063 a 2450 c 2196 g 1237 t
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Query Match 33.2%; Score 1540.4; DB 9; Length 6946;
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 Matches 1552; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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RESULT 6
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 LOCUS AL139246 154736 bp DNA linear PRI 16-NOV-2001

DEFINITION	Human DNA sequence from clone RP3-395M20 on chromosome 1p36.11-36.33, complete sequence.
ACCESSION	AL139246
VERSION	AL139246.20
KEYWORDS	HTG.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 154736)
TITLE	Moore,M.
JOURNAL	Direct Submission
COMMENT	Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 17, 2001 this sequence version replaced g1:15912352. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGS/Chr1 RP3-395M20 is from the library RPCI-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2
FEATURES	<p>location/Qualifiers</p> <p>1..154736</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/chromosome="1"</p> <p>/map="p36.11-36.33"</p> <p>/clone="RP3-395M20"</p> <p>/clone_1lb="RPCI-3"</p> <p>76003</p> <p>/note="Tandem repeat. Forced join. Gap size estimated to be approximately 800bps by restriction digest data."</p> <p>125344..125387</p> <p>/note="Sequence from overlapping clone RP4-755G5 (AL589746). Assembly confirmed by restriction digest."</p>
BASE COUNT	29047 a 47325 c 48771 g 29593 t
ORIGIN	
Query Match	33.2% Score 1540.4; DB 9; Length 154736;
Best Local Similarity	99.9%; Pred. No. 3.2e-236;
Matches 1552; Conservative	0; Mismatches 1; Indels 1; Gaps 1;
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Db	56500	CATCCCATTTCCCACTCCTCTCTAGAGGACGGCTCCACGGGGTCCCTACTGGGAAGTTGATG	56559
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Db	56680	CCACTAGAAGGGGTGTCTCTTATGACTGAGAGGAGGACATACAGGAGCCGCTCCACAC	56739
Qy	4522	CACCTGTGCTCCAGACCCCTCGAACAGTTTCCTTCTGCCCCCAGCCAGGCTTGC	4581
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Qy	4582	CTCCGTAGTATGAACTGAGAGCGCGCGAGTGACAGGTAAAGGGGCCGAGCCCG	4635
Db	56799	CTCCGTAGTATGAACTGAGAGCGCGCGAGTGACAGGTAAAGGGGCCGAGCCCG	56852
RESULT 7			
AK096620			
LOCUS			
DEFINITION	AK096620	3283 bp	mRNA
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ACCESSION	AK096620		
VERSION	AK096620.1	GI:21756155	
KEYWORDS	oligo capping; f18 (full insert sequence).		
SOURCE	Homo sapiens fetal brain cDNA to mRNA, clone_11b:OCBBF2		
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ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
	Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,		
	Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,		
	Yamamoto,K., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,		
	Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,		
	Kikuchi,H., Kanda,K., Magatsuna,M., Murakawa,K., Kanohori,K.,		
	Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,		
	Sugano,S., Nagahari,K., Masuhio,Y., Negai,K. and Isogai,T.		
	NEDO human cDNA sequencing project		
	Unpublished		
	2 (bases 1 to 3283)		
TITLE	Isogai,T. and Yamamoto,J.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7		
AUTHORS	Kazusa-Kamatari, Kikazazu, Chiba 292-0812, Japan		
JOURNAL	(E-mail:genom@shri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)		
	NEDO human cDNA sequencing project supported by Ministry of		
	Economy, Trade and Industry of Japan, cDNA full insert sequencing:		
	Research Association for Biotechnology (RAB); cDNA library		
	construction: Helix Research Institute (HRI) (supported by Japan		
	Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,		
	HRI, and Biotechnology Center, National Institute of Technology and		
	Evaluation; clone selection for full insert sequencing: HRI and		
	RAB; annotation: HRI and RAB.		
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 ACCESSION BC019679.1 GI:18044627
 VERSION
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 SOURCE
 ORGANISM

Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 2480)

REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submissions
 JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarone, P.H., Garcia, A.M., Lu, X., Huiy, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRK Plate: 29 Row: n Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7662133.
Location/Qualifiers

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CDS

BASE COUNT 443 a 865 c 798 g 374 t
ORIGIN

Query Match 18.6%; Score 861; DB 9; Length 2480;
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Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GCCAGGGCGATTCAACCTCGAGGAGACCCCTCGCCGCGGACGCTCAAGAGCAGC 180
QY 2701 TGGTGTCCGATCATGAGTCGACGAGAGCTTCCCAAGCCGCGGACGCTCAAGAGCAGC 2760
Db 181 TGGTGTCCGATCATGAGTCGACGAGAGCTTCCCAAGCCGCGGACGCTCAAGAGCAGC 240
QY 2761 ACCGTGGAGATCATGAGACCCCTTTGTGAGAGTGAAGATCATTTGGCTCCCTGTGACT 2820
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QY 3361 CCGGAGCGGAGCGGCGGCGGAG 3381
Db 841 CCGGAGCGGAGCGGCGGCGGAG 861

RESULT 9
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
Zhu, Z.
Regulation of human phosphatidylinositol-specific phospholipase
c-like enzyme
Patent: WO 0226996-A 1 04-Apr-2002;

JOURNAL
Bayer Aktiengesellschaft (DE)

FEATURES
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BASE COUNT 1659 a 1214 c 1203 g 1475 t

Query Match 16.8%; Score 780; DB 6; Length 5551;
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 Matches 1255; Conservative 0; Mismatches 670; Indels 23; Gaps 5;

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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 1 (sites)
 Tanaka, A., Kocani, H., Nomura, N., and Ohara, O.
 Prediction of the coding sequences of unidentified human genes.
 XIV. The complete sequences of 100 new cDNA clones from brain which
 code for large proteins in vitro
 JOURNAL
 MEDLINE
 9937452
 2 (bases 1 to 5551)
 Ohara, O., Nagase, T., and Kikuno, R.
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology, Yata 1532-3, Kisarazu, Chiba
 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
 Fax:+81-438-52-3914)
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 BASE COUNT 1659 a 1214 c 1203 g 1475 t
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 Best Local Similarity 64.4%; Pred. No. 1e-114;
 Matches 1255; Conservative 0; Mismatches 670; Indels 23; Gaps 5;

Db 181 GAAGCTTCAAGAACTTCATGCGTAGTCCCTGCTGTACATATTATTAACCATTTGACACAT 240
 1389 CATGTGACCAAGGACATGAGCAGCGCTGAGCCACATCACTTCACTCCGTGCCAAC 1448
 Db 241 GAAGTACCAAGACATGATGACGCCCTCTGCAACTCACTACATTTGCTTCTCAACAT 300
 1449 ACCTACCTGTGGGTGACCAAGCTCATGCTCCAGTCAAGGCTGACATGATGCTGGGTC 1508
 Db 301 ACATACCTGATGAGACACAGCTCTTTTCAGTCCAAAGTGATGATGACCGGGTG 360
 1509 CTGACAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
 Db 361 CTGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 1569 ATTGTGACCAAGGCTGACCTGATCTGCAAGATCCCTCTTCAAGAAGCTCATTTGAAAC 1628
 Db 421 GTAGTACATCATGTTACATCTCTCACTTCAAAATTTCTTTCAAGATGTTGTGAGACC 480
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 1869 GAAGCGAGGTGTGATGAGGACAGTGTGATGATGATGATGATGATGATGATGATGATG 1925
 Db 721 GAAGGGAAGTGTGATGAGGACAGTGTGATGATGATGATGATGATGATGATGATGATG 780
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 Db 781 CTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
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 Db 841 GAGTCACTGTAAAGAACTCAAAATTCGATTAAGAAAGTCCGATGATGATGATGATG 900
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 Db 954 TCCAGATGTAAGAAAGTGAAGAAATCAATGACATGACATCCCTCATGACCACTTTGG 1013
 2165 CAGGCGAAGAGAGAGGCGACGACGATGAAGAGGCGGACGCTGAGGAGGAGATG- 2223
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 1074 CACACAGCAGATGCTGCGAAGAGGAGTGGCAGCTGTCAGATTTGGTGGCGAAGAA 1133
 Db 1134 AACATTAAGCTCTGCGGAGAACTCTGATTTGTTGTGTACACAACTCCGTGCGCC 1193
 2236 CCAAGATGATGATGAGGCGGCTGACGCTGCGAGGCTGTCTTCAAGCAAGCA 2395
 Db 1194 TCAAGACATTTG--TGATGACGAAACCAAGAAATGATTTATCTTATGATGAAACAG 1250
 2396 GGCCACCAAGATTTCTGAGCAGAAAGCGGCGCAGTCTTACGCTTCAACGACGAGCT 2455

Db	1251	AGCAGCATCAGGTTGTTTCAGCAAAAATCGAGCAGCTGATGATTATATATCAAAAGCAACT	1310
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Db	1311	CACAGGATTTTACCCCTCTGCTTACCGGATTGATTCAGTAACCTTCAACCTCTCCCTTA	1370
QY	2516	CTGGAAAGCCGGGCTGCCAAATGTGTGCGCTTGAATCAGTCAGTCAAGAGGAGCGGATGTGCGCA	2575
Db	1371	CTGGAAAGCGAGGCTGCCAGGCTAGTGGCACTGAAATTATCAATCTGAAGAGCAATAGATGCA	1430
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QY	2636	CATGTGCGCAGGCGGTGTTCAACCCCACTCGAGAGACCCCGCTGGCGGGAGCTCAAGAA	2695
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QY	2696	GCAGCTGTGCTCCGGATCATCATGTGGCCAGCAAGCTTCCCAAGCCGGCGCACTTCATGCT	2755
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QY	2816	GGACTGCAAGCAGGAGCAGACCCCGCTGTGAGCAGCAACGAGTTCAACCCCACTTGGA	2875
Db	1671	AGATTTGTTGTAAGATCAAAACCCGTGTGATGATGACAAATGATTTAAACCTGTGTGGGA	1730
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QY	2936	GGAACACATATCCCATCGGGCGTACTTCAATTTGGCCAGAGAGCCCTGAGCTTCAGACAT	2995
Db	1791	GGATCAACGATCCCATTTGAGCAGAGACTTTGTGTGCAAAAGAACTGTACCTTCAGCAGCTT	1850
QY	2996	GATTCACAGGCTTACAGCAGCTGTACTTAAGAGGATGAAAGAGGCTCCATCTTCTGTGCA	3055
Db	1851	AGTGCCTGGCTACCGGCATGTCTATTTTGGAAAGCATGACAGACATCATATTGTGTACA	1910
QY	3056	TGTGGCTGTCAAGTACATCAGCGGTAAAG	3083
Db	1911	CATAACCATCATGAATATCTATGGAAG	1938
RESULT 11			
LOCUS	AK022610		
DEFINITION	Homo sapiens cDNA FLJ12548 fis, clone NT2RM4000657, weakly similar to 1-3-PROSHAT1DYLINOSINOL 4,5-BIPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11).		
ACCESSION	AK022610		
VERSION	AK022610.1	GI:10434099	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens testis/carcinoma cell line:NT2 cDNA to mRNA, clone lib:NT2RM4 clone:NT2M4000657.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
TITLE	Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hirooka,S., Ishi,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negahari,K., Masuh,Y. and Kanehori,K.		
JOURNAL	NEDO human cDNA sequencing project		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1977)		
TITLE	Isogai,T. and Otsuki,T.		
JOURNAL	Direct Submission		
COMMENT	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,		

COMMENT	Genomics Laboratory: 1532-3 Yana, Kiharazu, Chiba 297-0812, Japan E-mail: genomics@nri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - 3' - end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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	/cell_type="teratocarcinoma"
	/clone_11b="NT2RM4"
	/note="Cloning vector: pME18SFL3-mRNA from uninduced NT2 neutonal precursor cells."
	474..1874
CDS	/note="unnamed protein product"
	/codon_start=1
	/protein_id="AB14129.1"
	/db_xref="GI:10434100"
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BASE COUNT	634 a 429 c 457 g 457 t
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Query Match	11.8%; Score 545.2; DB 9; Length 1977;
Best Local Similarity	61.5%; Pred. No. 3.3e-77;
Matches 987; Conservative	0; Mismatches 588; Indels 29; Gaps 6;
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1735	TCCTTGGGGAAGTGTGACTGCTGTATGATGAGCAGTGAAGATGCCACCACTCCCT 1794
61	TATTGGAGACAAATGTGACCTGTGATCTGTGATGTACGGGAGATGCAAGCAGCTTCAA 120
1795	CTCCACAGATGCTCAAGGGCAAGATCCCGTGAAGGGGAAAGAACTCCAGCCAAATCA 1854
121	GCCCTCAAGTTTGAABAGCAAAATTTCAAGTGAAGGGTGAAGATTTGCTTATACCTTG 180
1855	GCGAGATGCGAGAGAGCGAGGTGTCTGATGAGACAGTGTGATGAGATTGACATG 1914
181	GGGATGATGCAAGAGAGGGGAGATTTCAGATGAGCAGTGTGAGATGAATGAAGCG 240
1915	ACTGCAACTC---CTAATGGGATGATATCCAAATTCGAAACCGGTAGAAAACACTG 1971
241	AGTGAATTTAAGTCTCATATATATGTAATGGACCACTGAGCAATCAAGTGAATCTTTCA 300
1972	CTAAGAGAAATCGATTCCTCTCATCAAGAGATGGAAGATTCCGGGACTGTGAGAGACCCA 2031
301	TAAAGAAAAAATCTGAGATCACTTTAAAGATATCTCAATTCGAGATTAAGAAAGATCTG 360
2032	ACAATTTCTCGTCTCCACACTGTGCCCATTTGGAAGGCTGAGACGCAAGACAAAGCTG 2091
361	ATAATTTTCAAGTCCGGGCACT-----ACTGAAGCCACGATGTAAGGCTTTAAATGCA 413
2092	AAGAGACGTGAGTCTGG--GAGAGATCCGGGGCCAGACGAGCAATGGCCCGCTGTC 2150
414	CACCTGAAGCAGAGTCCAGATGTAAAGAAAGTGAAGAAATTCACATGGACGATCCCTTC 473
2151	GTGGAAAGCTTCTTCAGGCGCAAGAAAGAGGCGCAAGCTGTAAGAAAGCGGCGCAGCTG 2210


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Db 474 ATGACCACTTTGGAAAAATTAAGAAAACTACAAATATCGGTCTTAATCTTACAGTACT 533
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Db 534 GATGATGAGAAAGACACACAGCAGAGTACTGGCAAGAGGGGTGGCCAGCTGTACAGATTG 593
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QY 2322 AAGTCCGTGGCCACCCACACATAGAGATGAGGCGGCGCTCCAGCTGGCAGGTGTCTCC 2381
Db 654 AACTCGGTGGCGCTTCAGACATTTG---TGATGACGGAACACAGAAATGTGTATCA 710
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QY 2502 AACCCGACGCTTCTGTGAAGCGCGGCTGCCAAATGTGTGCTTGAATCACTACAGAG 2561
Db 831 AACCTCTCTCCCTACTGGAACGAGGCTGCCAGCTAGTGGCACTGAATTAATCAATCTGAA 890
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Db 891 GGAAGATATGAGCTTAACCGAGCCAAATTCAGGCAATTCAGCAATTTGTGCTATGTTC 950
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QY 3162 CGGCGCCGCGCGCGCTCTCTGTAAGCAGCGGATCTGTGCGCGCAGCGCGCGCGCG 3221
Db 1491 GTAC-----GGAAGGATCATTTGAGATGAATTTCTGTGAGCAGCAGAGTACGCGCCCA 1544
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RESULT 12
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LOCUS AX411650
DEFINITION Sequence 4 from Patent WO0226996.
ACCESSION AX411650
VERSION AX411650.1 GI:21444192
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1
Zhu,Z.
Regulation of human phosphatidylinositol-specific phospholipase
C-like enzyme
Patent: WO 0226996-A 4 04-APR-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1..646
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 168 a 161 c 136 g 181 t
ORIGIN

Query Match 7.1%; Score 328; DB 6; Length 646;
Best Local Similarity 71.2%; Pred. No. 1.7e-42;
Matches 433; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

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Db 516 CTTCTACACATACATCTGCTGTGAGACCAAGCTCTTCTGATCAAAAGTGAATGT 457
QY 1498 ATGCTTGGCTTCTGAGGCTGGCTGCGGTGCTGTGAGGTGAGTGTGAGATGAGCCCG 1557
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QY 1678 TCGAAACCACTGACATGATCCAGAGAGAAAGAAATGCGCCAGTATCTGAATGATCC 1737
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QY 1738 TTGGGAGAACCTGAGCCTGTGATCATGATGAGCAGTGAAGATGCGACACACTCCCTCTC 1797
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Db 156 CTCAAAGTTTGAAGGCAAAATTTCTAGTGAAGGTTAAGAAATGCTTATACACTTGGGG 97
QY 1858 AGATGCGAGAGAAAGCGAGGTGTGATGAGGACAGTGTGATGATGATGATGATGATG 1917
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QY 1918 GCAAGCTC 1925

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Db 36 GCAATTC 29

RESULT 13
LOCUS AK023083 3263 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens CDNA FLJ13021 fis, clone NT2RP3000742, weakly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (BC 3.1.4.11).

ACCESSION AK023083
VERSION AK023083.1 GI:10434839
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens telerocarcinoma cell line:NT2. CDNA to mRNA, clone 11b:NT2RP3 clone:NT2RP3000742.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
Isogai,T., Ota,T., Hayaashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishi,S., Kawai,Y., Saito,K., Yamamoto,J., Makamatsu,A., Nakamura,Y., Negahari,K., Masuko,Y. and Kanehori,K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3263)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genom@seihri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES
source location/Qualifiers
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/note="Cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."

BASE COUNT 829 a 820 c 888 g 726 t
ORIGIN

Query Match 7.0%; Score 323.4; DB 9; Length 3263;
Best Local Similarity 50.7%; Pred. No. 6,8e-42;
Matches 1013; Conservative 0; Mismatches 916; Indels 70; Gaps 7;

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Db 770 TCTGGAAGCTATGAG 829
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Db 830 TATGATGAGCTTCTCAGCTACCTGTGCTTAAGATGAGAGACCTTCAACCCAGCTG 889
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Db 1370 TGAAG 1429
QY 1925 CCTCAAG 1982
Db 1430 TGAAG 1489
QY 1983 -----CTGATTCCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2009
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QY 2010 -----ATTGGGACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
Db 1550 CCGAGCTTCAACATTCAG 1609
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QY 2123 GGCAG 2182
Db 1670 GGAAGTGAAG 1729
QY 2183 C-AAGCAAGTGAAG 2241
Db 1730 CAGAGTGAAG 1789
QY 2242 GAGGCGAG 2301
Db 1790 GAGTTATGAATGAGTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1849
QY 2302 CTGACTGTG-----TGAAGTCAACCAAGTCCGTGGCCACCCAGAGATGAGAGATG 2351
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QY 2352 GAGGCGGCTGAG 2410

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Db 1199 CGCTGCTGAGAGTGAAGTATATGAGGATGAGACTTAAGGGGAACTGTGTTTATACGGA 1258
Qy 1584 TACACTCTGACTTCAAGATCTCTTCAAAAGAGTCAATTGAACCATCAACAAATATGCC 1643
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Qy 1644 TTCAATCAAGATGATGATCCGATGATCTGTCCATGGAACCACTGACAGTGTCAATCCAG 1703
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Db 1379 CAGAGATGATAGACACACACTGATGATCTGGGAGAGAGCTCTGAGACACAC 1438
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Qy 1884 GATGAG 1889
Db 1559 GAAGAG 1564

RESULT 15
AX287194
LOCUS AX287194 2289 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 14 from Patent WO0168871.
ACCESSION AX287194
VERSION AX287194.1 GI:17049130
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Hu, Y., Nepomichy, B., Donoho, G., Hilbun, E., Turner, C.A., Abuhin, A.,
Friedrich, G., Zambrakowicz, B. and Sands, A.T.
Human phospholipases and polynucleotides encoding the same
JOURNAL Patent: WO 0168871-A 14 20-SEP-2001;
Lexicon Genetics Incorporated (US)
FEATURES
Location/Qualifiers
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BASE COUNT 568 a 588 c 623 g 510 t
ORIGIN

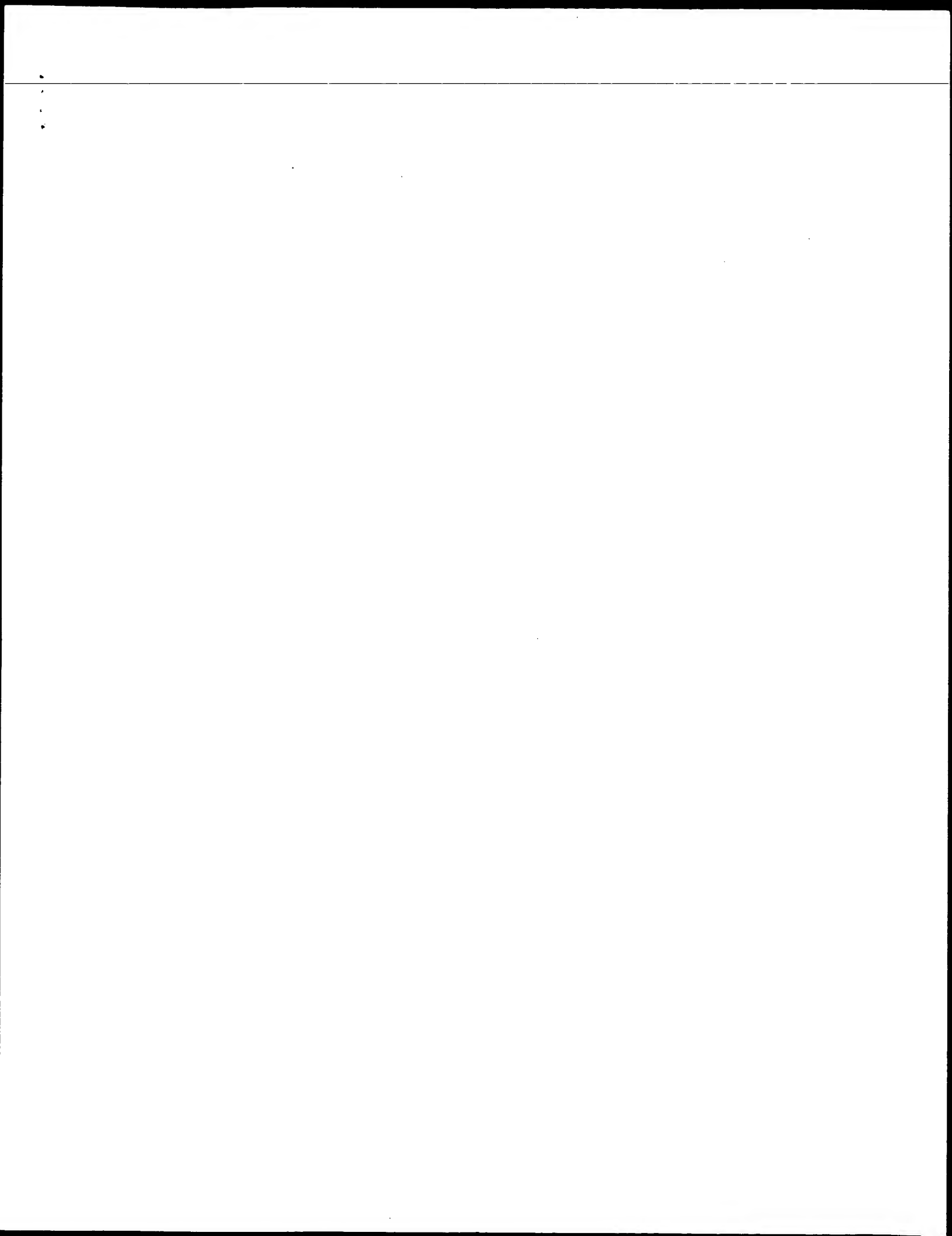
Query Match 6.7%; Score 308.6; DB 6; Length 2289;
Best Local Similarity 54.2%; Pred. No. 1.7e-39;
Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

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Db 289 GAGCCGCGCTCCACCTGAGACTTATGAGCCCAACAGTGTGAGAGGCGCCAGATATGATG 348
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Db 349 CGAGGAGCTCCAGCTGTGTGATCTTGTGTCACAGATGAGCCATCAAGAGCGCT---- 404
Qy 924 CGCACAGAGAGACAGTGGCTCAACAGACAGCTTCAAGAGCCGACAGAGCGGAGTGGC 983
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Db 457 AAGATGATTTTCAAGAAAGTTCAACGGTTATATGACCTTAATGATGTGAATGAGACCA 516
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Db 1354 CCTGAGTTGGAAGATCAGATTGGCGCTGGAGTCCCACTTGAGACTGAGCCTGAGCCC 1413
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 Db 1414 CAGGAGCAGAACCTTCAGATTAAAGACAAAAGAGAAATCCAGGCCATCTT 1466

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 Job time : 1360 secs



GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 12:21:39 ; Search time 1027 Seconds

(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3684.6	79.5	4237	24	Human lipid metabo
2	2838.4	61.2	6551	24	CDNA encoding huma
3	2161.4	46.6	2243	24	Human lipid metabo
4	1111.2	24.0	3433	24	Human lipid metabo
5	780	16.8	5551	23	DNA encoding novel
6	780	16.8	5551	23	Human PI-PLC-like
7	545.2	11.8	1977	22	Human cDNA sequenc
8	442.8	9.6	534	24	Human dltph polyinu
9	328	7.1	646	24	Human PI-PLC-like

10	323.4	7.0	3263	22	AAH16211	Human CDNA sequenc
11	308.6	6.7	2289	22	AAH17564	Novel human phosph
12	308.6	6.7	2289	22	AAH17564	Human phospholipase
13	308.6	6.7	2629	24	ABK10063	Human phospholipase
14	308.6	6.7	2709	22	AAH17567	Novel human phosph
15	307.6	6.6	1840	22	AAH19219	Human lipid metabo
16	306.6	6.6	2520	24	ABH60544	Human phospholipase
17	301.8	6.5	3425	22	AAH43471	Nucleotide sequenc
18	300.2	6.4	3544	22	AAH42603	Human phospholipase
19	297	6.4	2211	24	AAH34464	Gene #3294 used to
20	289.8	6.3	2627	24	ABH66796	DNA encoding novel
21	281.2	6.1	2158	23	ABK43682	Human polynucleoti
22	280.8	6.1	2104	22	AAH163875	Human novel polynu
23	276.8	6.0	3068	24	ABK94917	Human phospholipase
24	276.8	6.0	3068	24	ABK94917	Human phospholipase
25	276.2	6.0	2462	24	AAH23723	Human phospholipase
26	276.2	6.0	2540	24	AAH23722	Human lipid metabo
27	238.8	5.2	3594	24	ABH84695	DNA encoding inosi
28	202.4	4.4	5233	17	AAH15825	Human CDNA clone
29	198.4	4.3	817	22	AAH16851	Human nervous syst
30	195.4	4.2	567	22	AAH13565	CDNA encoding nove
31	195.4	4.2	567	22	AAH26989	Human polynucleoti
32	195.4	4.2	567	22	AAH3949	DNA encoding novel
33	195.4	4.2	567	22	ABK43964	Kidney cancer rela
34	194.2	4.2	4565	24	ABH68245	Kidney cancer rela
35	194.2	4.2	4565	24	ABH68245	Human breast cance
36	194.2	4.2	4565	24	ABH68865	Human breast cance
37	176.6	3.8	423	22	AAH15182	Phospholipase C-ga
38	176.6	3.8	3870	17	AAH12292	Phospholipase C-ga
39	176.4	3.8	3893	17	AAH12293	Human CDNA clone
40	174	3.8	863	23	AAH07553	Human CDNA sequenc
41	173	3.7	2416	22	AAH16555	Drosophila melanog
42	167.4	3.6	5370	23	ABH07877	Human CDNA differe
43	161	3.5	4519	24	ABH84127	Human CDNA differe
44	160	3.5	4242	24	ABH84021	Human CDNA differe

ALIGNMENTS

RESULT 1	ABH96005	standard; CDNA; 4237 BP.
ID	ABH96005	
XX	ABH96005;	
AC	04-MAR-2002	(first entry)
DT	04-MAR-2002	(first entry)
XX	Human lipid metabolism enzyme-5 (LME-5) CDNA.	
DE	Human lipid metabolism enzyme-5; cytosolic; neuroprotective;	
XX	immunopressive; anti-inflammatory; cardiovascular; gene therapy;	
KW	enzyme therapy; cancer; neurological disorder; autoimmune disorder;	
KW	inflammatory disorder; cardiovascular disorder; ss.	
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OS	Homo sapiens.	
XX		
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FT		/tag= a
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PD	15-NOV-2001.	
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XX	11-MAY-2001; 2001MO-US15210.	
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XX	11-MAY-2000; 2000US-203511P.	
XX	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	

XX (INCYTE GENOMICS INC.
 PA Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
 PI Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;
 PI Ding L, Thornton M;
 XX
 DR MPI: 2002-089794/12.
 DR P-PSDB; ABB08205.
 XX
 PT New lipid metabolism enzymes useful for diagnosing, treating and
 PT preventing cancer, neurological disorders, autoimmune/inflammatory
 PT disorders, and cardiovascular disorders
 XX
 PS Claim 5; Page 121-122; 122pp; English.
 XX
 CC The sequence encodes a novel human lipid metabolism enzyme (LME-5) of
 CC the invention. The invention relates to novel human LME's, and the
 CC polynucleotides which identify and encode them. The enzymes of the
 CC invention have cytosolic, neuroprotective, immunosuppressive,
 CC anti-inflammatory, and cardiovascular activity. The polypeptides and
 CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
 CC metabolism enzymes are useful in the diagnosis, treatment and prevention
 CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
 CC cardiovascular disorders, and in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
 CC for compounds that modulate the activity of LME. Polynucleotides encoding
 CC LME may be used for somatic or germline gene therapy, to detect and
 CC quantify gene expression in biopsied tissues in which expression of LME
 CC may be correlated with disease, to generate a transcript image of a
 CC tissue or cell type, to generate hybridization probes useful in mapping
 CC the naturally occurring genomic sequence, and for screening libraries of
 CC compounds in drug screening techniques. The polypeptide sequences may be
 CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
 CC primers derived from polynucleotide sequences encoding LME may be used to
 CC detect single nucleotide polymorphisms.
 CC
 XX Sequence 4237 BP; 816 A; 1327 C; 1370 G; 724 T; 0 other;
 XX
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 Query Match 79.5%; Score 3684.6; DB 24; Length 4237;
 Beel Local Similarity 94.6%; Pred. No. 0;
 Matches 3326; Conservative 0; Mismatches 4; Indels 219; Gaps 2;

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Db	687	AACGTGAACCTGCCCCCGGCACAGGGGTGAAGCATTTTCAGGGGTGCTGTCAATGCTCG	746
Qy	1067	-----	1066
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Qy	1647	ATCAAGATGATGATCCAGTATCTGTTCATGAAAACCACTGACATGATTCAGCAG	1706
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Qy	4107	GATTGAGGCCCCGACAGGCTGGGAGAACACAGCTGCTCTTGTCTGAGGAGTCTGGGAGCCCTGGG	4166
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Qy	4347	AGGTAGTGCAGCTCTGGGAGTCTCCTGAGGCCCTTGAGAGCGCTGTGAGAGCGCTGTGAGTGC	4406
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Qy	4407	TGCGTGAATGATTCCTTGAGGCCCTTGAGAGCGCTTGCCTGTGGGCTGAAGACATCCCACT	4466
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Db	4227	AGAGAGGAGG 4235	

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ID	ABK12390 standard; cDNA; 6551 BP.
AC	ABK12390;
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DT	05-JUN-2002 (first entry)
DE	cDNA encoding human lipid metabolism enzyme, LMM-6.
XX	
KW	human; lipid metabolism enzyme; LMM-6; immune system disorder;
KW	neurological disorder; developmental disorder; cancer; neotropic;
KW	cell proliferative disorder; immunomodulator; neuroprotective;
KW	cytostatic; gene; ss.
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XX	
FH	Key
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PN	WO200216597-A2.
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PD	28-FEB-2002.
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PF	22-AUG-2001; 2001WO-US26365.
XX	
PR	23-AUG-2000; 2000US-227429P.
PR	08-SEP-2000; 2000US-23170P.
PR	15-SEP-2000; 2000US-23312P.
PR	29-SEP-2000; 2000US-236885P.
PA	(INCY-) INCYTE GENOMICS INC.
PI	Giffin JA, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR,
PI	Mallia NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M,
PI	Lal P,
WI	WFI; 2002-280936/32.

DR P-PSDB : AAU77498 .
XX
XX New lipid metabolism enzymes, useful for diagnosing, treating or
PT preventing immune system disorders (e.g. Crohn's disease), neurological
PT disorders (e.g. Parkinson's disease), or cell proliferative disorders
PT (e.g. cancers) -
XX
XX
XX Claim 56; Page 120-122; 122pp; English.
PS
XX The present invention relates to the isolation of human lipid
CC metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the
CC polynucleotide sequences encoding them. The LMM polypeptides,
CC polynucleotides, agonists and antagonists are useful for diagnosing,
CC treating or preventing disorders associated with aberrant expression
CC of LMM, particularly immune system disorders (e.g. acquired
CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
CC Huntington's disease, dementia or Parkinson's disease), developmental
CC disorders (e.g. Down's syndrome) or cell proliferative disorders
CC (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,
CC myeloma or sarcoma). The present sequence encodes for human LMM-6.
XX
XQ Sequence 6551 BP; 1230 A; 2108 C; 2172 G; 1041 T; 0 other;

Query Match	61.2%;	Score 2838.4;	DB 24;	Length 6551;
Best Local Similarity	87.7%;	Pred. No. 0;		
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Db	2068	AACGTAACTGCTCCCGGAGAGGGTGAAGCAGATGTTCAAGGGTGGCTGTGTCATGCTCGG	2127
QY	1067	-----	1066

Db 2128 CTGGAGCAAGGAGAGCTGGCTCTCAGAGACAGGGCCCTGGTGGAGGTCGCAATTGGGG 2187
Qy 1067 -----GGAAGCGAGACAGGATGACCAACCAAGGAGCGTGGGTTTT 1106
Db 2188 ACCCAAGGCTTCATTTGACAGAAAGCGGACACGATGACACCAAGAGGACGGTGGGTTTT 2247
Qy 1107 GAAGAGTTCTGTGCTTTTCTTCAAGATGATGATCCAGCGCGGGAGCTTCACTGCTCATG 1166
Db 2248 GAAGAGTTCTGTGCTTTTCTTCAAGATGATGATCCAGCGCGGGAGCTTCACTGCTCATG 2307
Qy 1167 CTGACCTACAGCAACCAAGAGACCACTGATGCGGACGCTGAGCGCTTCTGCAAG 1226
Db 2308 CTGACCTACAGCAACCAAGAGACCACTGATGCGGACGCTGAGCGCTTCTGCAAG 2367
Qy 1227 GTGAGAGCAAGATGGCGGGGTGTGACCTCTGAGAGCTGCCAGACATCATCGACGATT 1286
Db 2368 GTGAGAGCAAGATGGCGGGGTGTGACCTCTGAGAGCTGCCAGACATCATCGACGATT 2427
Qy 1287 GAGCCATGCCCCAAGAAACAAAGATTAAGGGGCTGTGGGCAATGATGGCTTCACTCACTAC 1346
Db 2428 GAGCCATGCCCCAAGAAACAAAGATTAAGGGGCTGTGGGCAATGATGGCTTCACTCACTAC 2487
Qy 1347 ACCAGAGGCTCTGTGTGACATCTTCAACCTGAGACCAACCATGTGACACAGACATG 1406
Db 2488 ACCAGAGGCTCTGTGTGACATCTTCAACCTGAGACCAACCATGTGACACAGACATG 2547
Qy 1407 ACCGAGCGCTGAGCCACTATCTTCACTCTGCTCCCAACACCTACCTCTGTGGGTGAC 1466
Db 2548 ACCGAGCGCTGAGCCACTATCTTCACTCTGCTCCCAACACCTACCTCTGTGGGTGAC 2607
Qy 1467 CAGCTCATGCTCCAGTACCGGGTGGACATGATATGCTGGGCTGACGAGGTGGCTGGCCG 1526
Db 2608 CAGCTCATGCTCCAGTACCGGGTGGACATGATATGCTGGGCTGACGAGGTGGCTGGCCG 2667
Qy 1527 TGCGTGAAGGTGAGCTGCTGGATGGGCGGACGGGAGGCCATTTGACCAATGGCTAC 1586
Db 2668 TGCGTGAAGGTGAGCTGCTGGATGGGCGGACGGGAGGCCATTTGACCAATGGCTAC 2727
Qy 1587 ACTGTGACTTCAAGATCTCTTCAAGAGAGCTCATTTGAAACCATCAACAAATATGCTTC 1646
Db 2728 ACTGTGACTTCAAGATCTCTTCAAGAGAGCTCATTTGAAACCATCAACAAATATGCTTC 2787
Qy 1647 ATCAAGATGATGATACCGAGTATCTGTCCATGGAACCACTGAGTGCATCCAGAC 1706
Db 2788 ATCAAGATGATGATACCGAGTATCTGTCCATGGAACCACTGAGTGCATCCAGAC 2847
Qy 1707 AAGAAATGCGCCAGTATCTGATGACATCTTGGGGACAACTGGAAGCTGTATCATCAGTG 1766
Db 2848 AAGAAATGCGCCAGTATCTGATGACATCTTGGGGACAACTGGAAGCTGTATCATCAGTG 2907
Qy 1767 AGCAGTGAAGTGCACACCACTCCCTCTTCCACAGATGCTCAAGAGGAGCTGTG 1826
Db 2908 AGCAGTGAAGTGCACACCACTCCCTCTTCCACAGATGCTCAAGAGGAGCTGTG 2967
Qy 1827 AAGGGGAAGAGCTCCAGCAACATCAGGAGATGCGAGGAAGGAGAGTGTGAT 1886
Db 2968 AAGGGGAAGAGCTCCAGCAACATCAGGAGATGCGAGGAAGGAGAGTGTGAT 3027
Qy 1887 GAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1946
Db 3028 GAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087
Qy 1947 AATGCAAAAGCTGTGAAAAACCTGCTTAAGAGAACTGGAATTCCTCATCAAGAGTGTG 2006
Db 3088 AATGCAAAAGCTGTGAAAAACCTGCTTAAGAGAACTGGAATTCCTCATCAAGAGTGTG 3147
Qy 2007 AAGATTCGGGACCTGAGAGACCCCAACAACTTCTGCTCCACACTGTCCCATCTGGA 2066
Db 3148 AAGATTCGGGACCTGAGAGACCCCAACAACTTCTGCTCCACACTGTCCCATCTGGA 3207
Qy 2067 AAGCTCGACGCA----- 2080

Db 3208 AAGCTCGACGCAAGTGAAGAGCCAAAAAGTGAACCTCTGATGCGACAGGCCCCCCC 3267
Qy 2081 ----- 2080
Db 3268 GACAGCAAGCTGTGGGCCACAGGAGGCCCCGAAACGAGAGATGTCAAGCAGGCCCA 3327
Qy 2081 ----- 2080
Db 3328 GATCCAGCTGGGAGAGAGCGGAGAGCTGAGAGCTGTGTTGTGTGTGTGTGTGTGTGTGTGT 3387
Qy 2081 ----- 2080
Db 3388 CGAGTCTGTGTCTGATGAGACTCACTGCTCTTTTCCAGACAGTGTGGAGATCCAG 3447
Qy 2081 -----GAGCAAGGCTGAAGAGGACCTGAGATCTGGGAGAGATGCGGGGCCAGC 2129
Db 3448 GAGTGTGGAGAGAGCAAGCTGAAGAGAGAGCTGAGAGAGTGTGGGAGATGCGGGGCCAGC 3507
Qy 2130 AGACGCAATGGCCGCTGTGTGTGGAAAGCTTCTTCAGGCGCAAGAAAGAGGCGAGAG 2189
Db 3508 AGACGCAATGGCCGCTGTGTGTGGAAAGCTTCTTCAGGCGCAAGAAAGAGGCGAGAG 3567
Qy 2190 CTGAAGAGGCGGCGCAGGTTGAGAGGAGATGAGAGGTTGAGACTCCCGGAGGCGAG 2249
Db 3568 CTGAAGAGGCGGCGCAGGTTGAGAGGAGATGAGAGGTTGAGACTCCCGGAGGCGAG 3627
Qy 2250 AGCCGAGGCGGACCCGCGAGAGAGAACATGAAGCTGTCTCGGGCTCTTCTGACCTG 2309
Db 3628 AGCCGAGGCGGACCCGCGAGAGAGAACATGAAGCTGTCTCGGGCTCTTCTGACCTG 3687
Qy 2310 GTGAAGTACCAAGTCCGTGGCCACCCACGACATAGAGATGAGAGGCGGCTTCCAGCTGG 2369
Db 3688 GTGAAGTACCAAGTCCGTGGCCACCCACGACATAGAGATGAGAGGCGGCTTCCAGCTGG 3747
Qy 2370 CAGGTGTGCTCTTCAAGAGAGACCAAGGCGCACAGATTTCTGACAGAAACCGGCGAG 2429
Db 3748 CAGGTGTGCTCTTCAAGAGAGACCAAGGCGCACAGATTTCTGACAGAAACCGGCGAG 3807
Qy 2430 TACCTAAGCTTCAACAGAGAGAGCTTCCGCACTTACCTCTCTCTTCACTGTGTGAC 2489
Db 3808 TACCTAAGCTTCAACAGAGAGAGCTTCCGCACTTACCTCTCTCTTCACTGTGTGAC 3867
Qy 2490 TCCAGCACTTCAACCCGAGAGCTTCTGTGAAACGCGGCTGCGAAATGGTGGCCCTGAAAC 2549
Db 3868 TCCAGCACTTCAACCCGAGAGCTTCTGTGAAACGCGGCTGCGAAATGGTGGCCCTGAAAC 3927
Qy 2550 TACCAATCAGAGAGGAGAGTGTGACAGCTGAACGAGCCAAATTCAGGCGCAACGAGTGC 2609
Db 3928 TACCAATCAGAGAGGAGAGTGTGACAGCTGAACGAGCCAAATTCAGGCGCAACGAGTGC 3987
Qy 2610 TGGGCTAAGTACTCAAGCTGTGGTGCATGTGCCAGGGGCTTCAACCCCACTCGAG 2669
Db 3988 TGGGCTAAGTACTCAAGCTGTGGTGCATGTGCCAGGGGCTTCAACCCCACTCGAG 4047
Qy 2670 GACCCCTGCGGAGAGCTCAAGAAAGAGCTGTGTCTCCGATCACTGAGCAAGTGCAGAG 2729
Db 4048 GACCCCTGCGGAGAGCTCAAGAAAGAGCTGTGTCTCCGATCACTGAGCAAGTGCAGAG 4107
Qy 2730 CTTCGAAGCGCGGAGACTCAATGCTGGGAGACGCTGGGAGATCATGACCCCTTTGTG 2789
Db 4108 CTTCGAAGCGCGGAGACTCAATGCTGGGAGACGCTGGGAGATCATGACCCCTTTGTG 4167
Qy 2790 GAGGTGAAGTCAATTGGGCTCCCTGTGACTGACGAGAGAGAGCCGCGGTGTGAGC 4227
Db 4168 GAGGTGAAGTCAATTGGGCTCCCTGTGACTGACGAGAGAGAGCCGCGGTGTGAGC 4287
Qy 2850 GACAAAGGCTTCAACCCCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2909
Db 4228 GACAAAGGCTTCAACCCCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4287
Qy 2910 ATGCGCTGTGCTTCTCTGCTGTGGAGACAGATCCATCGGGGCTGACATTCATTTGCG 2969
Db 4288 ATGCGCTGTGCTTCTCTGCTGTGGAGACAGATCCATCGGGGCTGACATTCATTTGCG 4347

Db 61 GACCCATGCTGGGGGTGAGCTGAGGACAGGGGAGTGCGGTGAGAGAGGCTCCGGAGAGA 120
Qy 232 GGGCTGGGCAACACAGGCTGGGTGTGTGATGCTGCTGCGCCAGGCTTACACCCGAC 291
Db 121 GGGCTGGGCAACACAGGCTGGGTGTGTGATGCTGCTGCGCCAGGCTTACACCCGAC 180
Qy 292 AAGGAGACCGGGGGGCTGGGAGACAGAGACCTGACAGACGCTCTCTGCTCTG 351
Db 181 AAGGAGACCGGGGGGCTGGGAGACAGAGACCTGACAGACGCTCTCTGCTCTG 240
Qy 352 TGGACGGCCGGCCCGAGCTGTGATCCAGCCAGTCCAGCTTTCAGTTGCTGCCCCAC 411
Db 241 TGGACGGCCGGCCCGAGCTGTGATCCAGCCAGTCCAGCTTTCAGTTGCTGCCCCAC 300
Qy 412 CGACAGTCTCACTGCTCTCAATGATGCTCCCCGACAGCTGGGCCCCCTTCTGGCCAG 471
Db 301 CGACAGTCTCACTGCTCTCAATGATGCTCCCCGACAGCTGGGCCCCCTTCTGGCCAG 360
Qy 472 CTCTTCGGCTGAGGAGACCGAGGGCCGGATCCGGAGACAGTGGCTTTCTTGAGCGCA 531
Db 361 CTCTTCGGCTGAGGAGACCGAGGGCCGGATCCGGAGACAGTGGCTTTCTTGAGCGCA 420
Qy 532 ACATTCGCTGCTGTGAGACCGGTGCAATGGATGCAATGACAGGGGATGACAGTGTGA 591
Db 421 ACATTCGCTGCTGTGAGACCGGTGCAATGGATGCAATGACAGGGGATGACAGTGTGA 480
Qy 592 AGCTGCTGCGCTCCAAAGGCTGTGCTGCTTCTACCTGACAGACACCGCTCT 651
Db 481 AGCTGCTGCGCTCCAAAGGCTGTGCTGCTTCTACCTGACAGACACCGCTCT 540
Qy 652 GCATCCGCTGAGGCGCTCAACGAGAAAGAGGACCAAGATCTCCATGACCTCCATCC 711
Db 541 GCATCCGCTGAGGCGCTCAACGAGAAAGAGGACCAAGATCTCCATGACCTCCATCC 600
Qy 712 AGAGGTGAGTGAAGGGCGGCGAGTCCGAGGCTTTCAGCCCTTACCTGACGAGCTTCC 771
Db 601 AGAGGTGAGTGAAGGGCGGCGAGTCCGAGGCTTTCAGCCCTTACCTGACGAGCTTCC 660
Qy 772 ACCCCAACTGCTTTCAGATCTACACAGGCGACCGCGAGTGGCTGGAACCTGGCT 831
Db 661 ACCCCAACTGCTTTCAGATCTACACAGGCGACCGCGAGTGGCTGGAACCTGGCT 720
Qy 832 CCACAGAGGAGGAGTGGCGGCACTGGGTCACTGGCTTGGCTGCTGACCTGACCTGCGCA 891
Db 721 CCACAGAGGAGGAGTGGCGGCACTGGGTCACTGGGTCACTGGCTGCTGACCTGCGCA 780
Qy 892 TCAGCGAGAGGAGAGCTGTGCTGCGCGCAGCGCACAGGACCAAGTGGCTGAAGAGA 951
Db 781 TCAGCGAGAGGAGAGCTGTGCTGCGCGCAGCGCACAGGACCAAGTGGCTGAAGAGA 840
Qy 952 CGTTTGAAGAGGCGGAGAAAGGGGATGGCAGCTGAGCATTTGGAGGCTCTGAGC 1011
Db 841 CGTTTGAAGAGGCGGAGAAAGGGGATGGCAGCTGAGCATTTGGAGGCTCTGAGC 900
Qy 1012 TGCTGCAAGAGCTCAACGTGAACCTGCCCGGACAGAGGTGAACAGATGTTCAAGGAG 1071
Db 901 TGCTGCAAGAGCTCAACGTGAACCTGCCCGGACAGAGGTGAACAGATGTTCAAGGAG 960
Qy 1072 CGGACAGGATGACCAACAGAGAGAGCTGGGTTTGAAGATTTCTGTGCTTCAAGAGA 1131
Db 961 CGGACAGGATGACCAACAGAGAGAGCTGGGTTTGAAGATTTCTGTGCTTCAAGAGA 1020
Qy 1132 TGAATTCACCGCGCGGAGACCTTACCTGATGATGCTGATGCTGATGCTGATGCTGATG 1191
Db 1021 TGAATTCACCGCGCGGAGACCTTACCTGATGATGCTGATGCTGATGCTGATGCTGATG 1080
Qy 1192 ACCTGATGCTGCGCAGAGCTTCTGACAGTGAAGCAAGAGTGGCGGCTGTGA 1251
Db 1081 ACCTGATGCTGCGCAGAGCTTCTGACAGTGAAGCAAGAGTGGCGGCTGTGA 1140
Qy 1252 CCCTGAGAGCTGCGAGAGCATTCAGAGCTTTGAGCCATGGCCAGAAACAAAGAGTA 1311

Db 1141 CCCTGAGAGCTGCGAGAGCATTCAGAGCTTTGAGCCATGCCCAAGAAACAAAGATA 1200
Qy 1312 AGGGCTGCTGGGACATTGATGGCTTCAACAACTACACAGAGGCTGTGTGATCATCT 1371
Db 1201 AGGGCTGCTGGGACATTGATGGCTTCAACAACTACACAGAGGCTGTGTGATCATCT 1260
Qy 1372 TCAACCTTGAGCACCACCATGTGACACAGAGCATGACGCGCGCTGAGCCTACTTCA 1431
Db 1261 TCAACCTTGAGCACCACCATGTGACACAGAGCATGACGCGCGCTGAGCCTACTTCA 1320
Qy 1432 TCACCTGCTCCCAACACCTTACCTGAGGTGACAGCTCATGCTCCAGTACAGGGTGG 1491
Db 1321 TCACCTGCTCCCAACACCTTACCTGAGGTGACAGCTCATGCTCCAGTACAGGGTGG 1380
Qy 1492 ACATGTATGCTTGGGTCTGAGAGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1551
Db 1381 ACATGTATGCTTGGGTCTGAGAGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1552 GGGCGGAGGGAGCTCATTTGTGACCATGCTTACCTTGTACCTTCCAAAGTCTCTTCA 1611
Db 1441 GGGCGGAGGGAGCTCATTTGTGACCATGCTTACCTTGTACCTTCCAAAGTCTCTTCA 1500
Qy 1612 AAGAGTATGGAACCACTCAACAAATATGCTTCAATCAAGATGAGTACCAAGTATCC 1671
Db 1501 AAGAGTATGGAACCACTCAACAAATATGCTTCAATCAAGATGAGTACCAAGTATCC 1560
Qy 1672 TGTTCATGGAACCACTCAAGTGTATCATCAGAGAGAAATGGCCAGTATCTGACTG 1731
Db 1561 TGTTCATGGAACCACTCAAGTGTATCATCAGAGAGAAATGGCCAGTATCTGACTG 1620
Qy 1732 ACATCTTGGGAGCAAGCTGACCTGTATCATGATGAGAGTGAAGATGCCACACTCC 1791
Db 1621 ACATCTTGGGAGCAAGCTGACCTGTATCATGATGAGAGTGAAGATGCCACACTCC 1680
Qy 1792 CCTCTCCAGATGCTCAAGGGCAGATCTCGTGAAGGAGAAAGAGTCCAGCCACA 1851
Db 1681 CCTCTCCAGATGCTCAAGGGCAGATCTCGTGAAGGAGAAAGAGTCCAGCCACA 1740
Qy 1852 TCAGGAGAGATCGAGAGAGAGGAGGTGTGTGATGAGAGACATGCTGATGATGACG 1911
Db 1741 TCAGGAGAGATCGAGAGAGAGGAGGTGTGTGATGAGAGACATGCTGATGATGACG 1800
Qy 1912 ATGACTGCAAGCTCTCAATGGGAGTGCATCCAAATCGAAAGGTGTAGAAACATG 1971
Db 1801 ATGACTGCAAGCTCTCAATGGGAGTGCATCCAAATCGAAAGGTGTAGAAACATG 1860
Qy 1972 CTAAGAGAAATGGAATTCCTCATCAAAAGTGCAGAAATTCGAGATGTGAGACCTCA 2031
Db 1861 CTAAGAGAAATGGAATTCCTCATCAAAAGTGCAGAAATTCGAGATGTGAGACCTCA 1920
Qy 2032 ACAACTTCTCGGTCTTCACACTGTCTCCCATCTGAAAGCTGCGAGCGCAAGAGGCTG 2091
Db 1921 ACAACTTCTCGGTCTTCACACTGTCTCCCATCTGAAAGCTGCGAGCGCAAGAGGCTG 1980
Qy 2092 AAGAGAGCTGAGTCTGGGAGAGATCCGGGGCAGAGAGCGCAATGGCGGCTGCTG 2151
Db 1981 AAGAGAGCTGAGTCTGGGAGAGATCCGGGGCAGAGAGCGCAATGGCGGCTGCTG 2040
Qy 2152 TGGAGAGCTTCTCAGGCGCAGAAAGAGGAGGAGCTGAGAGAGGCGGCGAGCTGG 2211
Db 2041 TGGAGAGCTTCTCAGGCGCAGAAAGAGGAGGAGCTGAGAGAGGCGGCGAGCTGG 2100
Qy 2212 AAGAGGAGATGAGGATGAGACTCCCGGGAGGCCAGAGCCGAGGGGCGACCGGACGA 2271
Db 2101 AAGAGGAGATGAGGATGAGACTCCCGGGAGGCCAGAGCCGAGGGGCGACCGGACGA 2160
Qy 2272 AGA 2274
Db 2161 AGA 2163

RESULT 4
AB160537

ID ABL60537 standard; cDNA; 3433 BP.
 XX ABL60537;
 AC
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme (LME)-1 cDNA (clone id: 7472210CB1).
 XX
 KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective; gene;
 KW neoptotic; cerebroprotective; antiparkinsonian; antialzheimer's; vaccine;
 KW antileukemic; antimicrobial; anti-AIDS; cardiovascular; antiangiogenic;
 KW gene therapy; protein therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS /tag= a
 FT /product= "lipid metabolism enzyme"
 FT /note= "LME-1"
 XX
 PN W0200229036-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31302.
 XX
 PR 06-OCT-2000; 2000US-238388P.
 PR 13-OCT-2000; 2000US-240616P.
 PR 02-NOV-2000; 2000US-245719P.
 PR 08-NOV-2000; 2000US-247503P.
 PR 17-NOV-2000; 2000US-249503P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PI Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;
 PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;
 PI Lal PG, Tribouley CM;
 XX
 DR MPI: 2002-315862/35.
 DR P-PSDB; ABB08001.
 XX
 PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and
 PT Creutzfeld-Jakob disease -
 XX
 PS Claim 5; Page 121-122; 127pp; English.
 CC The invention relates to human lipid metabolism enzymes (LMEs) and
 CC encoding polynucleotides. The LMEs can be expressed by standard
 CC recombinant technology. The LME polypeptides, polynucleotides and
 CC modulators may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate LME expression such as cancer
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
 CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
 CC pectoris and mitral valve prolapse). The present sequence represents the
 CC human LME-1 encoding cDNA.
 XX
 SQ Sequence 3433 BP; 1042 A; 741 C; 842 G; 808 T; 0 other;
 Query Match 24.0%; Score 1111.2; DB 24; Length 3433;
 Best Local Similarity 65.5%; Pred. No. 4.4e-200;
 Matches 1711; Conservative 0; Mismatches 878; Indels 23; Gaps 5;

QY 605 CTCAGAGGCTCGTCCGCTTCTAATCTGAGCAGACCGCTCTGCAATCCGCTGAG 664
 Db 446 AACCAAGGCTTGTCCGCTCTTTTACCTGATGACACCGGACAGCTCCGATGGCG 505
 QY 665 GCCCTCAGCAAGAAACGAAAGGCGCAAGATCTCATGACTCCATCCAGAGAGTGA 724
 Db 506 ACCCTTAGAAGAGTGAAGGCAAAAATATCTATTGATTCATTAAAGTACTGA 565
 QY 725 GGGGCGGAGTCGAGAGTCTTCCAGCCCTACCTTGAAGGAGCTTCGACCCCACTGCTG 784
 Db 566 GGGCGGAGCTGAATATTTCCACAGACAGCTGAGGGGAATTTGACCCGAGCTGCTG 625
 QY 785 CTTACAGATCTTACCAAGGACCAACCGAGTGGCTGATCTTCCACAGACGGA 844
 Db 626 CTTACCAATTCATGACCAACCAATGAGTCCCTGAGCTCATCCACACCCCGA 685
 QY 845 GATGCGGCGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 904
 Db 686 GAGGCGGCGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
 QY 905 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 964
 Db 746 CTCCTTCCAAAAGGACAGAGACCCATGACCAATGGGTGAAGACACCTTGAAGAGC 805
 QY 965 CGACAAAGAGGGGATGCGACCTGAGCATTTGGGAGAGTCTGCACTGCTGCAAACT 1024
 Db 806 TGATTAAGATGTGTACGCGCTTGTGAATTTGAAGATATCATCAGCTGATGATTAAC 865
 QY 1025 CAAGTGAACTGCGCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1084
 Db 866 GAATGTATATGTGCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 925
 QY 1085 CCACCAAGGAGCTGCTGCTTGAAGATTTCTGCTTCTCAAGATGATGCCACCG 1144
 Db 926 GAATCAGAGAACTTTGACATTTGAGAGATTTGTTTTCATAAATGATGCTTTGAG 985
 QY 1145 CCGGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
 Db 986 ACGAGACCTTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1045
 QY 1205 CAGCTGCGAGGCTTCTGCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
 Db 1046 AGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105
 QY 1265 CCAGGATCATGAGCAGTTTGAAGCATGCTCCAGAAAACAGAGTAAAGGCTGCTG 1324
 Db 1106 TCTTGACATCATTAAGAAAGTTTGAAGTTTCAAGAAATTAAGTGAATAATGTTCT 1165
 QY 1325 CATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
 Db 1166 CATGAGGCTTCAAGACCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225
 QY 1385 CCAGCATGTCACAGAGACATGACGAGCGCTGAGCCACTTCTCATGACCTGCTG 1444
 Db 1226 CCATGAAGGTATCAAGACATGATGAGCCCTGCTGCACTTACTATGCTTCTCTCA 1285
 QY 1445 CAACACCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504
 Db 1286 CAATACATTAACCTGATGAGACAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1345
 QY 1505 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1564
 Db 1346 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405
 QY 1565 GCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
 Db 1406 GCCAGTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1465
 QY 1625 AATCATCAAAATATGCTTCTTCAAGATGATGATGATGATGATGATGATGATGAT 1684
 Db 1466 GACCATCAACAGATGCTTGTGTAAGATGATGATGATGATGATGATGATGATGAT 1525

QY 2106 T-CTGGGAGAGATCCGGGGCCAGCAGACGCAATGCGCCCTGTCGTGGAGCTTCTC 2164
 DB 1954 TCCAGATGTAAAGAAAGTGAAGAAATCACAATGACATCCCTCATCAACCACTTTGG 1013
 QY 2165 CAGGCCAAGAAAGAGGCGAGCAAGTGAAGAAAGCGCCAGGTGAGAGAGAGATG- 2223
 DB 1014 AAAACATTAAGAAAACTACAAATCAGGTCCTAAATCTTACATGATGATGAGGAAGA 1073
 QY 2224 -----AGGGTCAGAGATCCCGGGAGGCCAGAGCCGAGGGGGGAGCCCGGCAAGAA 2275
 DB 1074 CACACAGCAGAGTACTGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133
 QY 2276 GACCATGAAGCTGTCCGGGCGCTCTCTGACCTGTGTAAGTACCAAGTCCGTGGCCAC 2335
 DB 1134 AACCATGAAGCTGTCCGGGCGCTCTCTGATTTGGTTGGTGTACACAACTCCGTGGCCGC 1193
 QY 2336 CCACGACATAGAGATGAGAGGCGCGCTCCAGCTGAGAGGTGTCTTCCAGAGAGACCA 2395
 DB 1194 TCAGAGCATTTG--TGGATGACGGAACACAGAGAAATGTTATCATTCAGTGAAGCAAG 1250
 QY 2396 GGGCCACAGATTTCTGACAGCAGAGCCGCGCAGTACCTTCAACCAAGCAGACACT 2455
 DB 1251 AGCAGATCAGGTTGTTTCAGCAAAATCAGAGAGTTCATGATTTATCAAAAGCAACT 1310
 QY 2456 CTCCCGCATCTACCCCTCTCTCTACCTGTGATCTCCAGCAACTCAACCCGACGCTT 2515
 DB 1311 CACGAGATTTACCCCTCTCTCTACCGCATGATTCAGTAACTTCAACCCCTCTCCCTCA 1370
 QY 2516 CTGGAACCGCGGCTCCCAATGTGTGCTGATGATACAGAGTCCAGAGGCGGAGTCTGCA 2575
 DB 1371 CTGGAACCGAGGCTCCAGCTGATGAGCACTGAATTTATCAATGAGAGCAAAATGATGCA 1430
 QY 2576 GCTGAACCGAGCAGATTCAGGCGCAGCAGTGTGCTCGGCTACGTAATCAAGCTTGGGTG 2635
 DB 1431 GTTAAACCGAGCAGCAATTCAGGCAATGTGCTATGTGCTCAAAACCCAGCA 1490
 QY 2636 CATGTCAGGCGGCTGTTCAACCCCACTCGAGAGAGACCCCTGCGCGGCGAGCTCAAGAA 2695
 DB 1491 AATGTGCAAGAGTACTTCAACCCCTTCTGTGTGAGACCTCTTCTTCCCAACCCCAAAA 1550
 QY 2696 GCAGCTGTGTCTCCGATCATGATGAGCAGCAGCTTCCCAAGCGCGCAGCTCATGCT 2755
 DB 1551 GCAGCTGTCTGAAAGTTATCAGTGAAGCAACTCCCAAACTCCAGACTCATGTT 1610
 QY 2756 GGGGAGCCGTGGGAGATCATGACCCCTTTGTGAGGTGAGATCAATGGGCTCCCTGT 2815
 DB 1611 TGGAGATCGAGGCGAGATCATGACCCCTTTGTGAGGTGAGATCAATGGATGACAGT 1670
 QY 2816 GGAATGACAGCAGGAGAGACCCCGCTGTGTGAGAGAGAGGAGGAGGAGGAGGAGGAG 2875
 DB 1671 AGATTTGTTAAAGATCAAAACCCGTGTGTGAGATGACAAATGATTTAAACCTGTGTGGA 1730
 QY 2876 GAGAGCCCTGTTTCAATGTGTGACATGCGGAGATCGCGTGTCTCGCTTCTGCTG 2935
 DB 1731 AGAAACCTACATTTTCAATGATGACATGCGGAGAAATAGCTTTGGTTGGTTGCTTGTG 1790
 QY 2936 GAGCAGATCCCATCGGGGGTGTCACTTATTTGCGAGAGACGCTGCTTCCAGACAT 2995
 DB 1791 GGATCAGATCCCATTTGAGAGACTTGTGTGAGCAAAAGAACTGTGACCTTCCAGAGCTT 1850
 QY 2996 GATGCCAGGCTAGACAGACGCTGTACTAGAAAGGAGTGAAGAGGAGGAGGAGGAGGAG 3055
 DB 1851 AGTGCCTGCTACCGGATCTTATTTGGAAGAGCTACAGAAAGCATCATATTTGTACA 1910
 QY 3056 TGTGCTGTAGTGAACCTCAGCGGTAG 3083
 DB 1911 CATTAACCATCAATGAATCTATGAAAG 1938

AC AAH17609;
 XX 26-JUN-2001 (first entry)
 DT Human cDNA sequence SEQ ID NO:17123.
 XX Human, primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 DE Homo sapiens.
 XX EP1074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakematsu A, Nagai K, Otsuki T;
 XX WPI, 2001-318749/34.
 DR
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 PS Claim 8; SEQ ID 17123; 2537bp + CD ROM; English.
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH35893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 1977 BP; 634 A; 429 C; 457 G; 457 T; 0 other;
 Query Match 11.8%; Score 545.2; DB 22; Length 1977;
 Best Local Similarity 61.5%; Pred. No. 1.8e-93;
 Matches 987; Conservative 0; Mismatches 588; Indels 29; Gaps 6;
 QY 1675 CCATGGAAGAAACCACTGACATGATCCAGAGAGAAAGAGGAGGAGGAGGAGGAGGAG 1734
 DB 1 CTATGAGAAATCACTGACATGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 1735 TCTTGGGAGCAAGCTGAGCTGATCATGAGCAGTGAAGATGACCAACACTCCCT 1794
 DB 61 TATTCGAGAGCAAACTGAGACTGCTGATCTGTATATCAGGGGAGTGAAGAGCTTCAA 120

RESULT 7
 AAH17609
 ID AAH17609 standard; cDNA; 1977 BP.

1795 CTCACAGATGCTCAAGGCGAAGATCCTGTAAGGGGAGAGAGCTCCGAGCAATCA 1854
121 GCCCTCAAAAGTTGAAAGGCAAAATCTAGTGAAGGTAAAGAGTTGCTTATCACTTG 180
1855 GCGAGATGCGAGGAGGAGGCGAGGTCTGATGAGGACAGTGTGATGATGAGATG 1914
181 GGGATGATGAGAGGAGGAGGAGTTCCGATGAGGACAGTGCAGATGAAATTTGAAG 240
1915 ACTGCAAGCTC---CTCATGGGATGATCCCAATGAAAGCCTGTAAAGAAACAGT 1971
241 AGTCAAAATTCAGCTTCATTAATATGATGAGGACCACTAGCATGAGTGAATCTTTCA 300
1972 CTAAAGGAGAAATGATATTCCTCATCAAGAGTCAAGATTCGGAAGCTGTGAGACCCCA 2031
301 TAAGGAGAAATCTGAGTACTCTGTTAAAGAAATCTCAATTTGAGATTAAGAAATCT 360
2032 ACAATCTTCTGCTTCACACTGTCCCATCTTGAAAGCTCGAGCGCAAGAGAGGCTG 2091
361 ATAGTTTCAAGTGGGGGACT-----ACTGAGGCGCACGATGAAAGGCTTAAATGCA 413
2092 AAGAGACGTGAGTCTGG--GAGAGATGCCGGGCGAGAGACCAATGAGCGCTGCTC 2150
414 CACCTGAAGAGAGTCAAGTGTAAAGAGAAAGTGAAGAAATCAATGATGATGATCTTC 473
2151 GTGGAGAGCTTCTCCAGGCGCAGAGAAAGGAGGAGGAGCTGAAGAGGCGGCGAGCTG 2210
474 ATGACCACTTTGGAAAAACATAAGAAATCTACAAATCAAGCTTAATCTTAAGTACT 533
2211 GAGAGGAGATGAGGAGTCAAGTCTCCCTC-----GGAGGCGCAAGCGAGGAGG 2261
534 GATGATGAGGAGAACACACAGCAGAGTACTGGCAAGAGGAGTGGCCAGCTGTAACAATG 593
2262 ACCCGGAGAGAGAGACCAATGAGCTGTCCGGGCGCTCTGTAACCTGAGTAACTACCC 2321
594 GGTGCGGAGAGAGAAACATGAGAGCTTGCAGAAATCTCTGATTTGGTGTGTAACA 653
2322 AAGTCCGTGCGCAACCCAGCATAGAGATGAGAGGCGGCTGCAAGCTGCGAGTGTGCTC 2381
654 AACTCGGTGCGCGCTGAGCATTTG---TGTATGACGAAACCAAGAAATGTGTTATCA 710
2382 TTGAGCGAGACCAAGGCGCACAGATTTGAGAGAGAGAGCGGCGAGTACTACCTTC 2441
711 TTGAGTGAACCAAGAGCATCATGAGTGTTCACAGAAATCAAGAGCATTCATGATTTAT 770
2442 AACGAGAGAGAGCTCTCCGATCTACCCCTCCCTACCGTGTGAGTCTACAGCAATCA 2501
771 AATCAAAAGCAATCTCAGAGAGATTTACCCCTGCTTACCGCATTTGATTCAGTAATCT 830
2502 AACCGGAGCGCTTCTTGAAGCGCGGCTGCAATGTTGCCCTGAATCACTACAGTCAAG 2561
831 AACTCTCTCCCTTACTGGAAGGAGGCTGCGAGTATGAGCACTGAATTCATCTGAAG 890
2562 GGGGAGATGCTGCACTGAACCGAGCCAAGTTCAAGCGCAAGTGGCTGCGGTACGTA 2621
891 GAGCAGATGATGAGCTTAACCGAGCCAATTCAGGCAATGCAATTTGCTATGTC 950
2622 CTGAAGCTGGGTGATGATGCGAGGCGGTGTTCAACCCCAATCGAGAGACCCCTGCGCC 2681
951 CTGAAGCCCGAGCAAAATGAGAGTGAAGTACTTTCAACCCCTTCTGTGATGACCTCTTCT 1010
2682 GGGGAGCTCAAGAGAGAGCTGTGCTCCGATCATCATGAGGCGAGCTTCCCAAGCG 2741
1011 GCGCAACCCCAAAAGAGCTATCTGAAAGTTATCATGAGAGCAAGCTCCCAAACT 1070
2742 GCGGATCTCATGCTGGGGAGCGGTGGAGATCATCAACCCCTTGTGTGAGGTGAGATC 2801
1071 CCAAGATCTCATGTTGAGATCGAGGAGATCATTAACCTTTTGTGAAAGTTGAAT 1130
2802 ATTGGGCTCCCTGTGAGCTGAGAGAGGAGAGAGAGCGCGGTGTGAGAGAGAGGCTTC 2861
1131 ATTGGATTTGAGATGATTTGTTGTAAGATTAACCCGCTGTGTGATGATCAATGAGATT 1190
2862 AACCCCACTTGGAGAGAGACCTGTGTTTCAATGTGCAATGCGGAGATGCGCTGCT 2921

1191 AACCTGTGTGGAGAAAGCACTGACATTTACAGTACATGCGCAAAATGACTTGTGTT 1250
2922 GCGTTCCTGCTGTGGAGCAAGATCCCATGGGCTGACTTTCATTTGAGCAGAGAGCTG 2981
1251 GGTTCCTGTGTGAGATCAAGATCCATTTGAGAGAGATTTGTTGAGCAAAAGATCTGT 1310
2982 GCGTTCAGCAGATGATGCGAGCTGACAGACAGTGTACTAGAGGAGATGAGAGAGCC 3041
1311 ACCTTCAGCAGCTTAGTGTGCTGCTACCGGATGTCTATTGGAAGAGCTGACAGAGCA 1370
3042 TCCATCTTGTGCAATGTGCTGTGATGATCAATGAGCGTAAAGTCAAGAGCTTGTGGC 3101
1371 TCCATTTGTGACATTAACCATGAAATTAATGTGAAAGAAACACAACTTCAGAGGT 1430
3102 CTAAAGGCGCTTCTCTCCGAGGCGCAAGCGCGCTGCTGACAGTCAATGCTGTGGG 3161
1431 CTGAAGGAGACTGTTCAATAGAAATCTTAGGACAGTCTTCAAGAAACATTTCCCATAT 1490
3162 GGGCCCCCGGCGCGCTCTGTTAGCCAGGATCTGCGGCGCAGCGCCAGCGCCCG 3221
1491 GTAC-----GGAGCGATTCATTGAGATGAAATTTGCGAGCAGCAGCTAGCGCCCA 1544
3222 ACCAAGAGCCAGAAAGCGGCGCGAGGCTTCCCGAGCTGTG 3265
1545 GCCAAAGGCGAGAGAAAGAGCAAAATGGGCTTCCAAAGAAATGAT 1588

RESULT 8

ABK71572 ID ABK71572 standard; cDNA; 534 BP.

XX AC ABK71572;

XX DT 30-JUN-2002 (first entry)

XX DE Human dithp polynucleotide #38.

KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW skin; testis; thymus.

XX OS Homo sapiens.

XX PN WO20020754-A2.

XX PD 14-MAR-2002.

XX PF 29-AUG-2001; 2001WO-US27127.

XX PR 05-SEP-2000; 2000US-229747P.

XX PR 05-SEP-2000; 2000US-229748P.

XX PR 05-SEP-2000; 2000US-229749P.

XX PR 05-SEP-2000; 2000US-229750P.

XX PR 05-SEP-2000; 2000US-229751P.

XX PR 05-SEP-2000; 2000US-230583P.

XX PR 06-SEP-2000; 2000US-230585P.

XX PR 06-SEP-2000; 2000US-230514P.

XX PR 06-SEP-2000; 2000US-230515P.

XX PR 06-SEP-2000; 2000US-230517P.

XX PR 06-SEP-2000; 2000US-230518P.

XX PR 06-SEP-2000; 2000US-230519P.

XX PR 06-SEP-2000; 2000US-230597P.

XX PR 06-SEP-2000; 2000US-230598P.

XX PR 06-SEP-2000; 2000US-230599P.

XX PR 06-SEP-2000; 2000US-230610P.

XX PR 06-SEP-2000; 2000US-230655P.


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QY 1505 GGTCTGCAAGGCTGGCTGCGCTGGAGGTGACTGCTGGATGGGCGCCGACGGGGA 1564
DB 1010 GGGCCCTGAAGCGGGGGTGGCTGGAGGTGATGATGGGATGAGCTGACGGGGA 1069
QY 1565 GGGCATTTGTGACACAGGTGACACTGCTGACTTCAAGATCTCTTCAAGAACGTCAATGA 1624
DB 1070 ACCGTGCTTTACAGAGGACACACCTGACCTCCGCACTCTCTTCAAGATGCTGGC 1129
QY 1625 AACCATCAACAATATGCTTCTCAAGAAATGATACCAATGATCTGTCCATCGAANA 1684
DB 1130 CACAGTAGACAGATATGCTTCCAGACATGACTACCCAGTATCTTCTCCGAGAC 1189
QY 1685 CCACGTGATGTCATCAGACAGAAATAATGGCCAGTATGACTGACATCTGCGGGA 1744
DB 1190 CCACGTGATGTCAGACAGACAGACATGCGCTCATCTGACTGACATCTGCGGGA 1249
QY 1745 CAGGCTGACCTGTCACTGATGACATGATGACCAACACTCCCTCTCCACAT 1804
DB 1250 GACGCTGTGAGCACCCTTGGATGGGGTGTGCCCATCTGACCTGCTCCGCTGAGGA 1309
QY 1805 GCTCAAGGCGAAGATCTCTGTGAAGGGGAAAGAGCTCCAGCCACATCAGAGAGATC 1864
DB 1310 GCTTCGAGAGAGATCTGTGTGAAGGGGAAAGATTAACATTTGAGGAACCTGGAATA 1369
QY 1865 GGAGGAAGCGAGGTGTCTGATGAGACAGTGTGATGATGATGATGATGATGATGATG 1924
DB 1370 TGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1429
QY 1925 CCTCAATGGGAGATGATCCACCAATGAAAGCGTGAAGAAACATGCTGTAAGAGAAA 1982
DB 1430 TAGAGCTGAGCTGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1489
QY 1983 -----CTGATTCCTCTCAATCAAGAGTGAAG----- 2009
DB 1490 CAAGCCATCTGTGTGCTCAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1549
QY 2010 -----ATTGCGGACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
DB 1550 CCGCAGCTTCAACATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1609
QY 2063 TGGAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2122
DB 1610 AACCAAGGCGAAGCGCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1669
QY 2123 GGCAGCAGACCGCAATGCGCGCTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2182
DB 1670 GGAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1729
QY 2183 C-AGCAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2241
DB 1730 CAAGGTAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1789
QY 2242 GAGGCGCAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2301
DB 1790 GAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1849
QY 2302 CTGACCTG-----TGAAGTACACCAAGTCCGTGAGAGAGAGAGAGAGAGAGAGAG 2351
DB 1850 AGAGAGGACAGATGAATCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1909
QY 2352 GAGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2410
DB 1910 TAGGCGAGGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1969
QY 2411 -----GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466
DB 1970 TATACCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2029
QY 2467 ACCCTCTCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2526
DB 2030 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2089
QY 2527 GCTGCAATATGTTGCTCTGAACTACAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2586

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DB 2090 GCTCCAGATGTGTGCTCATGATATGACAGCTGACAGGCTTGAAGAGACATCTGATG 2149
QY 2587 CCAAGTTACGCGCAACGAGTGTGCTGACAGTACGATCAAGCCGTGGGTGATGTCAGAG 2646
DB 2150 GGCATTTCCGCGAAGATGGGGCTGTGTGTATGTGCTGAGAGAGAGAGAGAGAGAGAG 2209
QY 2647 GCGTGTCAACCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2706
DB 2210 TCCAGAGTTCTTTTCCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2269
QY 2707 TCCGATCATCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2766
DB 2270 TCCAGTGTATGAGGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2325
QY 2767 GGGAGATCATGACCCCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2826
DB 2326 -----ATTGAGATCCACTGTGAAAGTGAAGTCAATCTTTGCGCTTGAAGACAGC 2380
QY 2827 GGGAGCAGACCCGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2886
DB 2381 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2440
QY 2887 TTTTCATGAGCAGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2946
DB 2441 GTTTCGGGCTGTGTGTGCTGAACTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2500
QY 2947 CCA---TCGGGCGTGAATTCATTTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3003
DB 2501 GGAATATCCGAAATGACTTATTTGTCAGTACACCTGCTGCTGAGAGAGAGAGAGAGAG 2560
QY 3004 GCTACAGACAGCTGACCT 3022
DB 2561 GTTACGCGCAGATTCACCT 2579

RESULT 11
AADI7564
ID AADI7564 standard; cDNA; 2289 BP.
AC AADI7564;
DT 10-DEC-2001 (first entry)
XX
DE Novel human phospholipase cDNA #8.
XX
KW Human; novel human protein; NHP; phospholipase protein; phospholipid;
KW phospholipase C delta-4; cell activation; signal transduction; cancer;
KW drug screening; biological disorder; mental disorder; medical disorder;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2289
FT /tag=a
FT /product="Human phospholipase #7"
XX
PN WO200168871-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US07994.
XX
PR 13-MAR-2000; 2000US-0188885.
XX
PR 15-MAR-2000; 2000US-0189693.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B, Donoho G, Hilpun E, Turner CA, Abuin A;
PI Friedrich G, Zambrowicz B, Sands AT;
XX
XX WPI; 2001-582456/65.

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DR P-PSDB: AAE10440.

XX New polynucleotides encoding human phospholipase protein involved in
PT cell activation and signal transduction, useful for drug screening,
PT diagnosis and in gene therapy of biological disorders -

PS Claim 8; Page 40-41; 45pp; English.

XX The present sequence is a cDNA encoding novel human protein (NHP),
CC phospholipase protein. Phospholipases hydrolyse phospholipids and play
CC a key role in the cell activation and signal transduction. NHPs share
CC structural similarity with animal phospholipases, including phospho-
CC lipase C delta-4. NHP oligonucleotides are useful in conjunction with
CC polymerase chain reaction (PCR) to screen libraries, isolate clones,
CC and prepare cloning and sequencing templates, and alternatively as
CC hybridisation probes for screening libraries and assessing gene
CC expression patterns. They are used in the identification, selection
CC and validation of novel molecular targets for drug discovery, where
CC identification and characterisation of human genomic clones is helpful
CC for identifying polymorphisms, determining the genomic structure of a
CC given locus/allele and designing diagnostic tests. The microarray
CC comprising NHP cDNA is useful for screening collections of genetic
CC material from patients having a particular medical condition, which
CC is used to identify mutations associated with a particular disease and
CC also as diagnostic or prognostic assay. NHP nucleotide sequences are
CC useful for drug screening. Nucleotide construct encoding NHP products
CC are used in gene therapy for modulating NHP expression and to produce
CC genetically engineered host cells to express NHP products in vivo. The
CC NHP sequences are useful for generating antibodies, as reagents in
CC diagnostic assays, for identifying other cellular gene products related
CC to NHP and as reagents in assays for screening for compounds that are
CC useful in the treatment of mental, biological or medical disorders and
CC diseases. They can be used to therapeutically augment the efficacy of
CC chemotherapeutic agents used in the treatment of breast or prostate
CC cancer.

CC Sequence 2289 BP; 568 A; 588 C; 623 G; 510 T; 0 other;

CC Query Match 6.7%; Score 308.6; DB 22; Length 2289;

CC Best Local Similarity 54.2%; Pred. No. 7.3e-49; Mismatches 559; Indels 15; Gaps 2;

CC Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

QY 744 TTTCAGGCGTACCTGAGCGGAGCTTTCAGCCCACTGCTGCTTTCAGATTCACACGCG 803
DB 229 TTGCTGCTGAGCTTGGAGAGAGAGCTCCCTGGAGAGGGCTTCAACATGCTTTCAT 288
QY 804 AGCCACCGCGAGTGGCTGAGCTGCTGCTTCACACGAGCGAGTGGCGGACCTGGGCT 863
DB 289 GGCCTGCGCTCCAACTGAGCTGATGGCCAAAGTGTGAGAGGCGCCAGATATGATG 348
QY 864 ACTGGCTGGCTACCTGAGCGGCGGATGAGGAGGAGCGCTGGCTGGCGCGAG 923
DB 349 CGAGGGCTCCAGCTGTTGGTGAATCTTGTACACAGCATGAGCATGAGGCGCT---- 404
QY 924 CGGACGAGGAGCGAGTGGCTGAGAGCAGACCTTTGACGAGGCGCAGCAAGACGGGATGCG 983
DB 405 -----GGACCAATGGCTGAGAGGATGTTTCAACGTGAGCAAAATACTGAGTGGT 456
QY 984 AGCTGAGCATTTGGCCAGTGGCTGAGCTGCTGCAAGCTCAAGTGAACCTGCCCCG 1043
DB 457 AAGATGATTTCCAAAGAGTTCAAGCGGTATTGTCACTAATGATGTGAAATGAGCAAA 516
QY 1044 CAGAGGCTGAAGCATGTTCAAGGAGCGGAGACCGGATGACCAACCAAGGAGCGTGGGT 1103
DB 517 GAAATATGCTTCACTTTTTCAGGAGGAGACAGC---TCCAGTGTGGAACCTTGGA 573
QY 1104 TTTCAGAGTTCCTGCTTCTTACAGATGATGTCACCGCGGAGACTTCACTGCTTC 1163
DB 574 GGAAGAGATTTCTAGAGTCTTATAGGACATTAAGCAATGCTGCTGAGTGACAGAACTG 633
QY 1164 ATGCTGACCTACAGCAACACAGGACCACTGATGCGCGGACCTGACGCGCTTCTG 1223
DB 634 TTTCAGAGTTCCTGCTTCAAGGAGCGGAGCTGCTGCTGGAATTTTGAATTTCTTC 693

QY 1224 CAGGTGAGCAGAGATGAGCGGGTGTGACCTTCGAGAGCTGCCAGACATCATGACAG 1283
DB 694 CAAGAGAGCAGAGAGAGAGAGAGAGCTGACCTTGAAGCTTCTGGAACCTATGACCGC 753
QY 1284 TTTCAGAGTTCCTGCTTCTTACAGATGATGTCACCGCGGAGACTTCACTGCTTC 1343
DB 754 TATGACCTTCAGACAGTGGCAAACTGCGGCAATGCTGTGATGTGATGCTTCTCAGC 813
QY 1344 TACACCGAGAGCCCTGCTGATGATCTTCAACCTTCAGAGACCAACATGTCACAGAC 1403
DB 814 TACCTGCTTCAAGATGAGAGATTTCAACCAACCTGCTTCCCATCTATCAGAT 873
QY 1404 ATGACGAGCGCTGAGACCACTTATCATCACTGCTGCCAACAACCTTCTGTTGGGT 1463
DB 874 ATGACTCAACCCCTGAGAACCACTTATCATGCTTCTTCAACCTTATGATGGG 933
QY 1464 GACCACTCATGCTCCAGATCAAGGCTGAGACATGATGCTTGGTCTGACGCTGCTGC 1523
DB 934 GACCACTTTCGCGCCAGAGCAGCGTGAAGGATATATACGGGCTTGAAGCGGGGTGC 993
QY 1524 GCGTGGCGGAGGAGCTGCTGAGATGGGCGGACGAGGAGCCATTTGTCACATGCG 1583
DB 994 GCGTGGCGGAGGAGATGATGAGATGAGACCTAGCGGAGACCTTCTTACACGGA 1053
QY 1584 TACACTGACCTTCAGAGATCTTTCAGAAACCTCATTTGAAACATCAACAAATATGCC 1643
DB 1054 CACACCCGACCTCCCGCATCTGTTCAAGATGTCGTCGACAGTATGATGCTC 1113
QY 1644 TTTCATCAAGATGATGATCCAGATGATCTGCTCATGCAAAACCTGATGATCATCAG 1703
DB 1114 TTTCAGATCATGATGATCCAGATGATCTTGTCTGAGAGACCACTGACCTGGAGCAG 1173
QY 1704 CAGAGAAATATGAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1763
DB 1174 CAGAGACCATGAGCTCCGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1223
QY 1764 GTGAGCAGTGAAGATGAGCAGACCACTCCCTTCACAGATGCTCAAGGAGATCTTC 1823
DB 1224 TTGATGAGGAGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1293
QY 1824 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1883
DB 1294 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1353
QY 1884 GATGAGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1943
DB 1354 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
QY 1944 ACCAATGCAAGCGTGTGAGAAACATGCTTAAGAGAAATGATTCCTCAT 1996
DB 1414 CAGGAGCAGAACTTCAAGATTAAGGACAAAGAAATCAAGCCATCTT 1466

RESULT 12
AAD23721
ID AAD23721 standard; DNA; 2289 BP.
XX
AC AAD23721;
DT 07-MAR-2002 (first entry)
XX
DE Human phospholipase C delta 5 (PLCD5) DNA #1.
XX
KW Human; phospholipid C delta 5; PLC5 protein; deep vein thrombosis;
KW angina pectoris; percutaneous transluminal coronary angiography; PTCA;
KW thrombo embolic insult; disseminated intravascular coagulation;
KW arteriosclerosis; epilepsy; depression; neurodegenerative disease;
KW stroke; rheumatoid arthritis; immune disorder; chromosome localisation;
KW vaccine; gene therapy; ds.
XX
OS Homo sapiens.

Key Location/Qualifiers
 CDS 1..2289
 FT 12289
 FT /tag= a
 FT /product= "Human PLCD5 protein"
 MO200183771-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 27-APR-2001; 2001MO-EP04784.
 XX
 PR 29-APR-2000; 2000EP-0109318.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Brandt S, Duecker K, Gietz J;
 XX
 DR WPI; 2002-034515/04.
 DR P-PSDB; AAB14268.
 XX
 PT New phospholipase C delta 5 polypeptides, useful for treating deep vein
 PT thrombosis, instable angina pectoris, percutane transluminal coronary
 PT angiography, disseminated intravascular coagulation and epilepsy -
 XX
 PS Claim 4; Page 34-37; 51pp; English.
 XX
 CC The patent discloses phospholipid C delta 5 (PLCD5) proteins and their
 CC corresponding polynucleotides. PLCD5 sequences are useful for treating
 CC deep vein thrombosis, instable angina pectoris, percutane transluminal
 CC coronary angiography (PTCA), thrombo embolic insult, disseminated
 CC intravascular coagulation, arteriosclerosis, epilepsy, depression,
 CC neurodegenerative diseases, stroke, rheumatoid arthritis and immune
 CC disorders. PLCD5 sequences are also useful as vaccines for inducing
 CC immunological response in a mammal. PLCD5 DNAs are also useful for
 CC chromosome localization studies, as valuable tools in tissue expression
 CC studies and in gene therapy. The present sequence is a DNA encoding
 CC human PLCD5 protein.
 XX
 SO Sequence 2289 BP; 568 A; 587 C; 623 G; 511 T; 0 other;

Query Match 6.7%; Score 308.6; DB 24; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 7.3e-49;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

QY 744 TTCCAGCGCTACCGCTGACGCGACGCTTCCAGCCTGCTGCTTCAACCAACGCGC 803
 DB 229 TTCTCTGTAGCTGCTGACGAGGCTCCCTGACGAGGCTTCACTGTCTTCAT 288
 QY 804 AGCCACCGGAGTGTGACCTGTCTCCACGACGAGGTGCGGCACTGGTTC 863
 DB 289 GGGCGCGCTCCAACTGGACCTGATGGCCAACTGTTGAGGAGGCCCAAGATATGATG 348
 QY 864 ACTGGCTGTGCTACCTCATGCGCGCATCAGGACGAGGACAGCTGCTGCGCCAG 923
 DB 349 CGAGGGCTCCAGCTGTGGATCTTGTCAACGATGACATGAGGAGGCGCT--- 404
 QY 924 CGCACCAGGACCGAGTGTGAAAGCAGAGCTTTGACGAGCGGCAAGAAACGGGATGGC 983
 DB 405 -----GACCAATATGGCTGAGCGATTTGTTTCAACGTGAGACAAATAACGATGGT 456
 QY 984 AGCTTGAGCATTTGGAGGTCTGCACTGCTGACAGCTGACAACTCAACCTGACCTGCGG 1043
 DB 457 AAGATGAGTTTCCAAAGATTTAGCGTTATTGCACTATGATGATGAAATGAGCCAA 516
 QY 1044 CAAAGGTGAAGAGATTTTCAGGGAAGGAGACAGGATGACCAACCAAGGACGCTGGGT 1103
 DB 517 GAATATGCTTCACTGCTTTTTCAGGACAGACAG---TCCAGTCTGAAACCTTGGAA 573
 QY 1104 TTGAAGAGTTCTGCTCTTCAAGATGATTTCCACCGCGCGGAGCTTACCTGCTC 1163
 DB 574 GGAAGAGATTTCTAAGTTCTTATGAGCATTTAAACGTGCTGAGGTGAGGAACTG 633
 QY 1164 ATGCTGACCTTACGAAACCAAGACCACTGGATCGCGCAGCTGACGCGCTTCTGT 1223

DB 634 TTGAAAGTTTTCAGCTGATGGGACAAAGGTGACTGTCTGAAATTTTGGATTTCTC 693
 QY 1224 CAGGTGAGCAGAAAGATGCGCGGTGTGACCTCGAGAGCTCCGAGACATCATGAGCAG 1283
 DB 694 CAAGAGAGCAGAAAGAGAGAGACTGCACCTCTGACCTTGTCTGGAACATTTGACCGC 753
 QY 1284 TTTGAGCCATGCCCAAAAACAAGATGAAGGGGCTGTGGGCAATGATGCTTCAACAC 1343
 DB 754 TATGAACCTTCAGACAGTGGCAAACTCGGCGATGTGCTGATGATGATGCTTCTCAGC 813
 QY 1344 TACACAGAGCCCTGCTGGTGAATCTTCAACCTGTAGACCAACATGTGACCCAGGAC 1403
 DB 814 TACCTTCTCTTAAGATGAGACATCTTCAACCCAGCTGCTCCCTCCATCTATCAGGAT 873
 QY 1404 ATGACGACCGCTGAGGCACTTATCATCACTGTGCCAACAACATCACTGTGGGT 1463
 DB 874 ATGACTCAACCCCTGAACCACTTATCTTATGCTCTTCTATTAACATCACTTATGAGGG 933
 QY 1464 GACCACTCATGTCCCACTGACAGGCTGACATGTATGCTTGGTCTTGCAGGCTGCTGC 1523
 DB 934 GACCACTTTGTGGCCAGAGCAGGTGAGGAGATATTAACGGGCTTGAACCGGGGTGC 993
 QY 1524 CGCTGCGTGAAGTGAAGTGTGCTGAGTGGGCGGACGAGGACCATTTGCAACATGCG 1583
 DB 994 CGCTGCGTGAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1053
 QY 1584 TACACTGTGACTTCAAGATCTCTTCAAGAGCTCATTTGAAACATCAACAAATATGCG 1643
 DB 1054 CACACCTGACCTCCGCACTCTCTTCAAGATGTGCTGAGCCACAGTATGATGATGATG 1113
 QY 1644 TTCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1703
 DB 1114 TTCAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1173
 QY 1704 CAGAAAGAAATGAGCCAGTATCTGATGATGATGATGATGATGATGATGATGATGATG 1763
 DB 1174 CAGCAGACCAATGAGCCGCTCATCTGATGATGATGATGATGATGATGATGATGATG 1233
 QY 1764 GTGAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1823
 DB 1234 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1293
 QY 1824 GTGAAGGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1883
 DB 1294 GTGAAGGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1353
 QY 1354 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
 QY 1944 ACCAATGAAAGCTGTGAAGAAACATCTGTAAGAGAACTGATTTCTCTCAT 1996
 DB 1414 CAGAGGAGAACTTCAAGATTAAGAACAAAGAAAGAAATCAAGGCCATCTT 1466

RESULT 13
 ABK10063
 ID ABK10063 standard, cDNA, 2629 BP.
 XX
 AC ABK10063;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DB Human phospholipase C 16816 cDNA.
 XX
 KW Human, phospholipase C; PLC; phospholipase C 16816; brain disorder; gene;
 KW cellular proliferative disorder; differential disorder; prion disease;
 KW glial disorder; cerebrovascular disease; acute meningitis; cirrhosis; ss;
 KW demyelinating disease; degenerative disease; heart disorder; rickets;
 KW ischaemic heart disease; myocardial disease; neoplastic heart disease;
 KW vascular disease; inflammatory disease; bone metabolism disorder;
 KW chronic renal disease; haematopoietic disorder; autoimmune disease;

arthritis; systemic lupus erythematosus; Sjogren's syndrome; psoriasis;
KX Crohn's disease; uveitis; atopic allergy; balloon angioplasty;
KM coronary artery bypass graft surgery.

OS Homo sapiens.

PH Key Location/Qualifiers
FT CDS 257..2545

FT /tag= a
FT /product= "Human phospholipase C 16816"
FT /transl_except= (pos:760..762, aa:Arg)
FT /transl_except= (pos:1981..1983, aa:Gly)
FT /note= "This region is specifically claimed"

XX WO200206302-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US22760.

XX 17-JUL-2000; 2000US-218675P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Meyers R, Rudolph-Owen L, Tsai FY;

XX WPI, 2002-188535/24.

XX P-PSDB; AAU76816.

XX New human phospholipase C protein for diagnosing and treating disorders
PT e.g. Alzheimer's disease, heart failure, cancer, psoriasis, Sjogren's
PT disease, and to identify modulators for therapeutic use

XX Claim 1; Fig 1; 129pp; English.

XX The invention relates to human phospholipase C (PLC) polypeptides 16816
XX and 16839. The polypeptides can be used in the treatment and diagnosis of
XX various disorders including cellular proliferative and/or differentiative
XX disorders (e.g. carcinoma and leukemia), brain disorders including glial
XX disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
XX ischemia and hypertensive encephalopathy), infections (e.g. acute
XX meningitis and prion diseases), demyelinating diseases (e.g. multiple
XX sclerosis), degenerative diseases (e.g. Alzheimer's disease), heart
XX disorders including heart failure, ischaemic heart disease (e.g.
XX myocardial infarction), myocardial disease (e.g. myocarditis), neoplastic
XX heart disease (e.g. angina pectoris), vascular diseases (e.g.
XX atherosclerosis), inflammatory disease (e.g. Kawasaki syndrome), bone
XX metabolism disorders (e.g. osteoporosis), cirrhosis, rickets, chronic
XX renal disease, haematopoietic disorders, autoimmune diseases (e.g.
XX diabetes mellitus), arthritis, systemic lupus erythematosus, Sjogren's
XX syndrome, psoriasis, Crohn's disease, uveitis, atopic allergy, and
XX pathology of therapeutic interventions in vascular disease (e.g. balloon
XX angioplasty and related techniques) and vascular replacement (e.g.
XX coronary artery bypass graft surgery). This sequence represents cDNA
XX encoding the human phospholipase C 16816.

XX Sequence 2629 BP; 648 A; 677 C; 735 G; 569 T; 0 other;

XX Query Match 6.7%; Score 308.6; DB 24; Length 2629;
XX Best Local Similarity 54.2%; Pred. No. 7.5e-49;
XX Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

XX 744 TTCACGCGCTACCTGAGGAGGAGCTTGAGAGCCCAACTGCTTACAGATCTACCGAGC 803
XX 485 TTGCTGCTTACCTGAGGAGGAGCTTCCCTGAGAGGAGGCTTACCATTTGTTTCAT 544
XX 804 AGCCACCGGAGTGGCTGCTGCTTCCACACGACGAGGAGGAGGAGCTTGGCTC 863
XX 545 GGGCGGCTCCACCTGAGCTGATGAGCAACAGTGTGAGAGGAGGAGGAGGAGGATG 604
XX 864 ACTGCGCTGCGTACCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 923
XX 605 CGAGGAGCTTCCAGCTTGTGATCTTGTACCAAGATGAGCAATCAGAGAGGAGGCTT 660

QY 924 CGCACGAGGACGAGTGGCTGGAAGCAGACGTTTGACGAGGCCGACAGAAACGGGATGCG 983
DB 661 -----GGACCAATGGCTGAGGAGTGTGTTTCAACGTGAGACAAATAATCAGATGCT 712
QY 984 AGCCTGAGCATTTGGCGAGGCTGCTGAGCTGCTGACCAAGCTCAACGTGACCTGCCCGG 1043
DB 713 AAGATGAGTTTCCAAAGAAAGTTCAAGCGGTATTGCACTTAATGATGGAATGACCA 772
QY 1044 CAGAGGTTGAAGCATGATGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1103
DB 773 GAATATGCTTTCAGTCTTTTTCAGGACGAGACAGC---TCCAGTGTGGAACCTTGAA 829
QY 1104 TTTGAAGATTCTGCTGCTTCTTCAAGATGATGCAACCCCGGAGGAGCTTCACTGCTC 1163
DB 830 GGAGAGAAATTCGACAGTCTTATTAAGGACATTAAGCTGAGCTGAGCTGACAGAACTG 889
QY 1164 ATGCTGACCTTACAGCAACCAAGGACCACTGATGCTGAGCTGAGGAGGAGGAGGAG 1223
DB 890 TTTGAAGTTTTCAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 949
QY 1224 CAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1283
DB 950 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1009
QY 1284 TTTGAGCCATGCGCAAGAAACAGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1343
DB 1010 TATGAACTTTCAGACAGTGGCAAACTGGCGGATGCTGATGATGAGTGGCTTCCAGC 1069
QY 1344 TACACGAGAGCCCTGCTGCTGAGATCATCTTCAACCTGAGACGACCAATGTCACAGAC 1403
DB 1070 TACCTTCTCTTAAGAGTGAAGAGACATCTTCAACGAGCTGCTTCCATCATACAGAT 1129
QY 1404 ATGACGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1463
DB 1130 ATGATCTCAACCTTGAACCACTTATCTGCTCTTCTTCAACCTTACCTTACCTGAGG 1189
QY 1464 GACGAGCTGATGCTGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1523
DB 1190 GACGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1249
QY 1524 GCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1583
DB 1250 GCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1309
QY 1584 TACACTTGAATCCAGATCTCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1643
DB 1310 CACACCTGATCTCCGAGATCTCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1369
QY 1644 TTTATCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1703
DB 1370 TTTCAAGATCAGACTACCACTGATCTTGTCTGAGAGACCACTGAGAGGAGGAGGAG 1429
QY 1704 CAGAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1763
DB 1430 CAGCAGACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1489
QY 1764 GTGAGCAGTGAAGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1823
DB 1490 TTGAGATGGGAGTGTGCTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1549
QY 1824 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1883
DB 1550 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1609
QY 1884 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1943
DB 1610 CTTGAGTGAAGAGTCAAGATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1669
QY 1944 ACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1996
DB 1670 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1722

QY 1824 GTGAAGGGAGAGAGCTCCACGCAATCAGCGAGATCGGAGAGAGGAGGTCT 1883
DB 1551 GTGAAGGGAGAGAGCTCCACGCAATCAGCGAGATCGGAGAGAGGAGGTCT 1610
QY 1884 GATGAGGAGAGAGCTCCACGCAATCAGCGAGATCGGAGAGAGGAGGTCT 1943
DB 1611 CCGTGAATGGAAGAGTCAATATGCGAGTCCAGCTTTGAGAGCTGAGGCC 1670
QY 1944 ACCAATCGAAGCGTGTAGAAAACACTGCTAAGAGAACTGGATTCCTCAT 1996
DB 1671 CAGAGCAGAACTTCAATTAAGGACAAAGAGAAATCCAGCCCATCTT 1723

RESULT 15
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ID AAD19219 strand: DNA; 1840 BP.
XX AAD19219;
AC AAD19219;
XX 18-DEC-2001 (first entry)
XX Human CG121 (or C592) lipase DNA #1.
DE Human; apolipoprotein; lipase; lipoprotein receptor; ALR; angina;
XX Human; apolipoprotein; lipase; lipoprotein receptor; ALR; angina;
XX Cardiovascular disease; lipid metabolism; myocardial infarction;
XX Cerebral ischaemia; arterial thrombosis; thrombolytic; antilipemic;
XX Coronary artery thrombosis; cerebral artery thrombosis; stroke;
XX Intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
XX Neuroprotectant; cerebroprotective; ds.
OS Homo sapiens.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 140..1840
FT /tag= a
FT /product= "Human CG121 (or C592) lipase protein"
FT /note= "CDS does not include stop codon"
FT /partial
XX MO200179446-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US12529.
XX 14-APR-2000; 2000US-197337P.
XX 20-JUN-2000; 2000US-0598042.
XX 03-AUG-2000; 2000US-0631451.
XX 22-SEP-2000; 2000US-0667298.
XX 17-NOV-2000; 2000US-0714936.
XX (HSE-) HSEQ INC.
XX Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
XX Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
XX Wang D;
XX WPI; 2001-611724/70.
XX P-PSDB; AAE11925.
XX Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
XX receptor polypeptides, useful for preventing diagnosing and treating
XX lipid metabolism disorders, thrombosis and cardiovascular diseases -
XX Claim 1; Page 155-158; 266pp; English.

CC and thrombosis. Antibodies against these proteins are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of these sequences. ALR polypeptides are also
CC useful for identifying agents (agonists and antagonists) that bind to
CC them and cells expressing ALR proteins are useful for identifying a
CC therapeutic agent for use in treatment of a pathology related to
CC aberrant expression or physiological interactions of this polypeptide.
CC Vectors comprising these DNA and protein sequences are also useful for
CC producing ALR proteins. The nucleic acids and polypeptides of the
CC invention are also useful for the treatment of occlusive cardiovascular
CC diseases, myocardial infarction, cerebral ischaemia, angina, arterial
CC thrombosis, coronary artery thrombosis and cerebral artery thrombosis
CC or intracardiac thrombosis and stroke. The nucleic acids of the invention
CC are used in gene therapy. The present sequence is human CG121 (or C592)
CC lipase DNA.
XX
SQ Sequence 1840 BP; 455 A; 483 C; 508 G; 394 T; 0 other;

Query Match 6.6%; Score 307; DB 22; Length 1840;
Best Local Similarity 54.1%; Pred. No. 1.4e-48;
Matches 678; Conservative 0; Mismatches 560; Indels 15; Gaps 2;

QY 744 TTCAGGCTTACCTGACGAGCTTGCACCCCACTGCTTACACATCTACACGCG 803
DB 368 TTGCTGCTTACCTGACGAGAGAGCTTCCCTGAGGAGGCTTACATTTCTCAT 427
QY 804 AGCAGCGCGAGTGGCTGAGACTGCTTCCACAGCAGGAGTGGCGGCTGAGTGC 863
DB 428 GGGCGCGCTTCACTGAGCTGATGAGCTTCAAGAGTGTGAGAGGCGGAGATGATG 487
QY 864 ACTGCGCTGCTTCTATGAGCGGCGATCAGCAGAGAGAGAGCTGCTGCGCGCAG 923
DB 488 CGAGGCGCTCAGCTGTTGAGATCTTGTCAACAGATGACATCAGAGCGCT---- 543
QY 924 CGCAGCAGAGCGAGTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
DB 544 -----GAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
QY 984 AGCTGAGCATTTGCGAGAGTCTGCTGAGCTGCTGAGAGAGAGAGAGAGAGAGAG 1043
DB 596 AAGATGAGTTTCCAGAGAGTTCAGCGGTTATGCACTTAATGATGAGAGAGAGAG 655
QY 1044 CAGAGGAGAGAGAGAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
DB 656 GAATATGCTTCACTTCTTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
QY 1104 TTTGAGAGTCTGCTGCTTTCAGAGATGATTCACCGCGGAGAGAGAGAGAGAG 1163
DB 713 GGAGAGAGATTCGATCAGTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
QY 1164 ATGCTGAGCTTACAG 1223
DB 773 TTTGAGAGTTTTCAG 832
QY 1224 CAGGTGAG 1283
DB 833 CAG 892
QY 1284 TTTGAG 1343
DB 893 TATGAG 952
QY 1344 TACAGCAG 1403
DB 953 TACCTTCTTCAAGAT 1012
QY 1404 ATGAGCAG 1463
DB 1013 ATGACTCAACCCCTGAG 1072
QY 1464 GACGAGCTTATGCTTCAAG 1523
DB 1073 GACGAGCTTATGCTTCAAG 1132

QY 1524 CGCTGGGTGAGGTGAGCTGCTGGGATGGGGCCGAGGGGAGCCCATGTGACCATGSC 1583
Db 1133 CGCTGGGTGAGGTGAGTGTGATGGATGGACTAGCGGGAACTGTGTTTACACGSA 1192
QY 1584 TACACTGTGACTTCCAGATCTCTTCAAGAGCGTCATTGAAACCATCAACAATATGCC 1643
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QY 1644 TTGATCAAGATATGATACCATGATCTGTCCATGAAAAACCATGCAGTGTCATCCAG 1703
Db 1253 TTCAGACATCAGACTACCCAGTCATCTGTCTCCGTGAGAGCCCATGCACTGGGAGCAG 1312
QY 1704 CAGAGAAAATGGCCAGTATCTGACTGACATCTTGGGGACAAGCTGGACCTGTATCA 1763
Db 1313 CAGCAGACATGGCTCCCTCTCTGACTGAGATCTGGGGAGCAGCTTGTGAGCACCAACC 1372
QY 1764 GTGAGCAGTGAAGATGCAACCACTCCCTCTTCAAGATGCTCAAGGGCAAGATCTTC 1823
Db 1373 TTGGATGGGGTGTGCTGCTCAGCTGCTGCTGAGAGCTTGGAGAAAGATCTTG 1432
QY 1824 GTGAAGGGGAAGAAGCTCCAGCCAAATAGAGAGATGCGAGAGGAGCGAGTGTCT 1883
Db 1433 GTGAAGGGGAAGAAGTTAACAATTGAGAGACCTGAAATATGAGAGAGAGGAGCAGAA 1492
QY 1884 GATGAGACAGTGTGATGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCC 1943
Db 1493 CTTGATTTGAGAGATCAGATTTGGCGCTGAGATCCAGTTTGAAGCTGAGCTGAGCCC 1552
QY 1944 ACCAATCGAAAAGGTGTAGAAAACTGTGTAAGAGGAAAAGTGTCTCAT 1996
Db 1553 CAGGAGCAGAACTTCAGATTAAGACAAAAAGAGAAAATCCAAAGCCCATCTT 1605

Search completed: March 28, 2003, 16:33:51
Job time : 1148 secs

Query No.	Score	Match	Length	DB	ID	Description
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2	610.4	13.2	930	14	B0960462	B0960462 AGENCOUR
3	588.8	12.7	759	12	BG472146	BG472146 602513865
4	580.8	12.5	1016	12	BG334784	BG334784 602457129
5	570.4	12.3	663	12	BG619793	BG619793 602781835
6	550	11.9	561	10	BE255177	BE255177 60111571

FEATURES	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
LOCUS	BO946757				
DEFINITION	BO946757				889 bp
ACCESSION	AGNCOURT_8924326				NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466785
VERSION	BO946757				5', mRNA sequence.
KEYWORDS	BO946757.1				GI:22362235
SOURCE	EST.				house mouse.
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 889)				
	NIH-MGC http://mgc.nci.nih.gov/ .				
	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs-remail.nih.gov				
	Tissue Acquisition: The Cepko Laboratory				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LINTL at:				
	http://image.llnl.gov				
	plate: L1AM1391 row: k column: 10				
	High quality sequence stop: 676.				
	Location/Qualifiers				
	1. 889				

QY 2380 CCTTCAGCAGACCAAGCCCAACCAAGTTCTGACGAGAAAGCCGGCCAGTACTACGCT 2439
 DB 345 CTTTCAGTGAACCAAGGCCCATCATGATCTGACGAGAAAGCCCACTAGTACTGCT 404
 QY 2440 TCAACGACGACGCTTCCCGCATCTACCCCTCTCTTACCGTGTGACCTCCAGCACT 2499
 DB 405 TCAACGACGACGCTTCCCGCATATATACCCCTCTCTTACCGTGTGACCTCCAGCACT 464
 QY 2500 ACAACCCGACGCTTGTGAAAGCCGCTGCCAAATGTTGCCCTGAACTACAGTACAG 2559
 DB 465 ACAATCCAAACCTTTGTGAAGGCTGTGTCAGATGATGTTGCCCTGAACTACAGTACAG 524
 QY 2560 AGGGGCGGATGCTGACGCTGAACCGACCAAGTTCAAGGCGCAACGATGCTGCGCTACG 2619
 DB 525 AGGGGCGGATGCTGACGCTGAACCGACCAAGTTCAAGGCGCAACGATGCTGCGCTACG 584
 QY 2620 TACTCAAGCTGGTGTATGTCCAGGGGCTGTTCAACCCCACTCGAGAGAACCCCTGCG 2679
 DB 585 TGCTCAAAACCCAGTGTATGTCCAGGGGCTGTTCAACCCCACTCGAGAGAACCCCTGCG 644
 QY 2680 CCGGCGGACTCAAGACGAGCTGGTGTCTCCGGAATCATGAGGCGACAGCTTCCCAAGC 2739
 DB 645 CCGGCGGACTCAAGACGAGCTGGTGTCTCCGGAATCATGAGGCGACAGCTTCCCAAGC 704
 QY 2740 CGCGGACTCCATGCTGCGGGGACCGTGGGAGATCATGACCCCTTTGTGAGGTGAGA 2799
 DB 705 CAGCGGACTCGGTGCTGCGGGGACCGTGGGAGATCATGACCCCTTTGTGAGGTGAGA 764
 QY 2800 TCATT-GGGCTCCCTGTGAGTGTGACGAGGAGGAGACCCGCTGTGTGACGACAAAGGG 2858
 DB 765 TCATTGGGGGCTCCCGGTGACTGACGAGGAGGAGACCCGAGTGTGAGGAGCAAGAGGG 824
 QY 2859 --TTCAACCCCACTGGAGGAGGAGACCCGCTGTTT 2890
 DB 825 ATTCAACCCCACTGGAGGAGGAGCACTGTTGT 858

RESULT 3
 LOCUS BG472146 759 bp mRNA linear EST 21-MAR-2001
 DEFINITION 602513869P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645721 5',
 mRNA sequence.
 ACCESSION BG472146
 VERSION BG472146.1 GI:13404520
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 759)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM1419 row: 1 column: 18
 High quality sequence stop: 683.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:4645721"
 /clone_id="NIH_MGC_16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally

BASE COUNT 148 a 248 c 256 g 107 t
 ORIGIN
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Query Match 12.7%; Score 588.8; DB 12; Length 759;
 Best Local Similarity 99.7%; Pred. No. 5.4e-106;
 Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2795 GGAGATCATTGGGCTTCCTGTGAGTGTGACGAGGAGGAGACCCGCTGTGTGACGACAA 2854
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 QY 2855 CCGGTTCAACCCCACTGGGAGGAGACCCCTGTTTCAATGAGCAATGCGGAGATGCG 2914
 DB 62 CCGGTTCAACCCCACTGGGAGGAGACCCCTGTTTCAATGAGCAATGCGGAGATGCG 121
 QY 2915 GCTGTGCGCTTCTCTGTCTGTGAGCAACGATCCATCGGGGCTGATCATTTGGCCAGAG 2974
 DB 122 GCTGTGCGCTTCTCTGTCTGTGAGCAACGATCCATCGGGGCTGATCATTTGGCCAGAG 181
 QY 2975 GACGCTGGCTTTCAGCAGATGATGCAAGGCTTACAGACGTTTACTTAAAGGATGGA 3034
 DB 182 GACGCTGGCTTTCAGCAGATGATGCAAGGCTTACAGACGTTTACTTAAAGGATGGA 241
 QY 3035 AAGAGCTTCATCTTCTGTCATGTCGTCATGTCATGTCATGTCATGTCATGTCATGTC 3094
 DB 242 AAGAGCTTCATCTTCTGTCATGTCGTCATGTCATGTCATGTCATGTCATGTCATGTC 301
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 DB 302 TCTGGGCTTAAAGGCTTCTCTGTCATGTCGTCATGTCATGTCATGTCATGTCATGTC 361
 QY 3155 TGTGGGCGGCGCCCGGCGCCGCTTCTGTTAGCCAGGATCTTGTGCGGCGGCGGCGG 3214
 DB 362 TGTGGGCGGCGCCCGGCGCCGCTTCTGTTAGCCAGGATCTTGTGCGGCGGCGGCGG 421
 QY 3215 CGGCCCGACCAAGAGCCGAGACCGGGCGGCGGAGGCTTCCGAGCTGTGCTGGGTAC 3274
 DB 422 CGGCCCGACCAAGAGCCGAGACCGGGCGGCGGAGGCTTCCGAGCTGTGCTGGGTAC 481
 QY 3275 ACAGGACACAGGCTCCAAAGGAGGTGAGCAGACGATGTGCTCCCGGAGCCGAGCTTC 3334
 DB 482 ACAGGACACAGGCTCCAAAGGAGGTGAGCAGACGATGTGCTCCCGGAGCCGAGCTTC 541
 QY 3335 TCCGGAAGCCCGACGAGGAGGCGGCGGCGGAGGCTTCCGAGCTGTGCTGGGTAC 3386
 DB 542 TCCGGAAGCCCGACGAGGAGGCGGCGGCGGAGGCTTCCGAGCTGTGCTGGGTAC 593

RESULT 4
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 DEFINITION 602457129P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579663 5',
 mRNA sequence.
 ACCESSION BG394794
 VERSION BG394794.1 GI:13288242
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1016)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM1297 row: 1 column: 08
 High quality sequence stop: 599.

FEATURES

Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_1ib="NIH MGC 16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 324 a 302 c 247 g 143 t

ORIGIN

Query Match 12.5%; Score 580.8; DB 12; Length 1016;
 Best Local Similarity 99.3%; Pred. No. 2.2e-104;
 Matches 604; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

FEATURES

source

1..663
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="IMAGS:493248"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 133 a 199 c 212 g 119 t

ORIGIN

Query Match 12.3%; Score 570.4; DB 12; Length 663;
 Best Local Similarity 96.5%; Pred. No. 2.2e-102;
 Matches 637; Conservative 0; Mismatches 16; Indels 7; Gaps 5;

QY 1280 GCAGTTTGAGCCATGCCCCAGAAAAAGATAGAGGGGCTGTGGGCGATTGATGGCTTCAC 1339
 DB 2 GCAGTTAGAGCCATGCCCCAGAAAAAGATAGAGGGGCTGTGGGCGATTGATGGCTTCAC 61
 QY 1340 CAACCTACACAGAGAGCCCTGTGTGTGATCTTCAACCTCTGAGACACCACTATGTGACCA 1399
 DB 62 CAACCTACACAGAGAGCCCTGTGTGTGATCTTCAACCTCTGAGACACCACTATGTGACCA 121
 QY 1400 GGCATGACGACGACGCGCTGAGCCACTACTACTCATCCTGCTCCCAACAGCACTGCTGT 1459
 DB 122 GGCATGACGACGACGCGCTGAGCCACTACTACTCATCCTGCTCCCAACAGCACTGCTGT 181
 QY 1460 GGGTGAACGAGCTCATGTCCAGTCAAGGGTGAACATGTATGCTTGGGCTCTCAGGCTGG 1519
 DB 182 GGGTGAACGAGCTCATGTCCAGTCAAGGGTGAACATGTATGCTTGGGCTCTCAGGCTGG 241
 QY 1520 CTGGCCCTCCGTGAGAGTGAAGTGTGGGATGGGCGGAGCCGATTTGTGACCA 1579
 DB 242 CTGGCCCTCCGTGAGAGTGAAGTGTGGGATGGGCGGAGCCGATTTGTGACCA 301
 QY 1580 TGGCTACCTGATCTTCAAGATCTCTTCAAGAGCTCATTTGAAACCATCAACAATA 1639
 DB 302 TGGCTACCTGATCTTCAAGATCTCTTCAAGAGCTCATTTGAAACCATCAACAATA 361
 QY 1640 TGGCTTCACTGAAGATGAGTACCAGTGTCTGTTCATGAAAAACACTGAGTGTCAAT 1699
 DB 362 TGGCTTCACTGAAGATGAGTACCAGTGTCTGTTCATGAAAAACACTGAGTGTCAAT 421
 QY 1700 CCAGAGAGAGAAATGGCCCAAGATCTGATGATCTCTTGGGAGCAAGTGAAGTCTGTC 1759
 DB 422 CCAGAGAGAGAAATGGCCCAAGATCTGATGATCTCTTGGGAGCAAGTGAAGTCTGTC 481
 QY 1760 ATCAGTGAAGAGATGAGTGCACACACTCCCTCTCCAGAGATGCTCAAGGCAAGAT 1819
 DB 482 ATCAGTGAAGAGATGAGTGCACACACTCCCTCTCCAGAGATGCTCAAGGCAAGAT 541
 QY 1820 CCTGTGAAGAGAGAGCTCCAGCC-AACATCAGCAGAGATGCGAGG-AAAGCGAG 1877
 DB 542 CCTGTGAAGAGAGAGAGCTCCAGCCAAACATCAGCAGAGATGCGAGGAAAGCGAG 601
 QY 1878 GTGTCTGA 1885
 DB 602 GTGTCTGA 609

RESULT 5
 LOCUS 663 bp mRNA linear EST 22-MAY-2001
 DEFINITION 602781835F1 NCI CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4932488
 5', mRNA sequence.

ACCESSION BG819793
 VERSION BG819793.1 GI:14167380
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 663)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM10858 row: f column: 09
 High quality sequence stop: 649.

QY 2523 GCCGGCTGCCAAATGGTTGCTGAACTACAGTCAAGAGGGGGGATGTGCGACCTGAAAC 2582
 DB 4 GCCGGCTGCCAAATGGTTGCTGAACTACAGTCAAGAGGGGGGATGTGCGACCTGAAAC 63
 QY 2583 CGAGCCAAAGTTCA-GCGCCAAAGGCTGCGGCTCAAGTCAAGCCCTGGGTGATGTG 2641
 DB 64 CGAGCCAAAGTTCAAGGCGCCAAAGGCTGCGGCTCAAGTCAAGCCCTGGGTGATGTG 123
 QY 2642 CCAGGGGCTGTTCAACCCCACTCGAGAGACCCCTGCGGCGGCACTCAAGAGAGAGCT 2701
 DB 124 CCAGGGGCTGTTCAACCCCACTCGAGAGACCCCTGCGGCGGCACTCAAGAGAGAGCT 183
 QY 2702 GGTGCTCCGATCATGATGAGGCGAGCA-GCTTCCAAAGCGCGGCACTCATGCTGGGG 2760
 DB 184 GGTGCTCCGATCATGATGAGGCGAGCACTGCTTCCAAAGCGCGGCACTCATGCTGGGG 243
 QY 2761 ACCGTGGAGATCATGACCCCTTTGTGAGGTGAGATCATTTGGGCTCCCTGTGACT 2820
 DB 244 ACCGTGGAGATCATGACCCCTTTGTGAGGTGAGATCATTTGGGCTCCCTGTGACT 303
 QY 2821 GCAGCAGGAGCAGACCCCGGTGTGAGAGCAGCAAGGGTTCAACCCCACTGGAGAGAA 2880
 DB 304 GCAGCAGGAGCAGACCCCGGTGTGAGAGCAGCAAGGGTTCAACCCCACTGGAGAGAA 363

QY	2881	CCGGTTTTCATGGTGTGACATGCCGAGAGATCGCGCTGTCGCGTTCTCTGCTTGGAGCC	2940
Db	364	CCCTGGTTTTTCATGGTGTGACATGCCGAGATCGCGCTGTCGCGTTCTCTGCTTGGAGCC	423
QY	2941	ACGATCCCATCGGGCGGTGACTTCATTTGGCCAGAGAGCGCTGAGCTTTTGACAGCATGATGC	3000
Db	424	ACGATCCCATCGGGCGGTGACTTCATTTGGCCAGAGAGCGCTGAGCTTTTGACAGCATGATGC	483
QY	3001	CAGGTACAGACAGCTGTAACCTAGAAAGGAGTGAAGAGCGCTCCATCTTTCGTGCA-TGTG	3059
Db	484	CAGGTACAGACAGCTGTAACCTAGAAAGGAGTGAAGAGCGCTCCATCTTTCGTGCACTGTG	543
QY	3060	GCTGTCACTGTACA--TCAGCGGTAAGGTCAAGCAGGCTCTGTGGCCTTAAGAGGCTCTTTC	3117
Db	544	GCTGTCACTGTACAATCAACGAGTAGTCTCAAGCAAGGCTCTGTGGCCTTAAGAGGCTCTTTC	603
QY	3118	TCCGAGGCCCAAAGGCC--GGTGCCTGGACAGTATGTTGTGGCGAGCCCGCGGCCG	3175
Db	604	TCCGAGGCACCAAGGCCAGGCTCGCATGTGACAGTATGTTGTGGCGAGCCCGGACCG	663

RESULT 6	BE255177	561 bp	mRNA	linear	EST_13-JUL-2000
LOCUS	60111517171	NIH_MGC_16	Homo sapiens	CDNA clone IMAGE:3356063 5',	
DEFINITION	mRNA sequence.				
ACCESSION	BE255177				
VERSION	BE255177.1	GI:9125614			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 561)	NIH-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-r@mail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Ling Hong/Rubin Laboratory			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov			
	Plate: L10CM161 row: b column: 06			
	High quality sequence stop: 559.			

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FEATURES
source
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3356069"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pOTB1; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGACG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT
101 a 185 c 191 g 84 t
ORIGIN

```

OY	2874	GAGAGACCCTCGTTTTCATGCTGACATGCGGAGATCGGGCTGATCGGCTCTCGTC	2933
Db	60	GAGGAGACCCCTGGTTTTCATGCTGACATGCGGAGATCGGGCTGATCGGCTCTCGTC	119
OY	2934	TGGGACCAACGATATCCATCGGGGCTGACTTCAATTGGCCAGAGAGCGTGGCTTCAGCAGC	2993
Db	120	TGGGACCAACGATATCCATCGGGGCTGACTTCAATTGGCCAGAGAGCGTGGCTTCAGCAGC	179
OY	2994	ATGATGCCAGGCTACAGACACGTGTACTTAAAGGATGAGAAAGGCTCCATCTTCTGTG	3053
Db	180	ATGATGCCAGGCTACAGACACGTGTACTTAAAGGATGAGAAAGGCTCCATCTTCTGTG	239
OY	3054	CATGTGCTGTCTAGTGAATCAGCGGTAAAGTCAAGCAGGCTCTGGGGCTTAAAGGCTC	3113
Db	240	CATGTGCTGTCTAGTGAATCAGCGGTAAAGTCAAGCAGGCTCTGGGGCTTAAAGGCTC	299
OY	3114	TTTCCTCCAGAGGCCAAAGCCCGGCTCGCTGAGCAGTCAATGCTGCTGGGCGGCCCCGGCC	3173
Db	300	TTTCCTCCAGAGGCCAAAGCCCGGCTCGCTGAGCAGTCAATGCTGCTGGGCGGCCCCGGCC	359
OY	3174	CGGCTCTCCGTTAGCCAGCGGATCTCTGGCGGCAAGCGCAGCGCCCCGACCAAGAGCCAG	3233
Db	360	CGGCTCTCCGTTAGCCAGCGGATCTCTGGCGGCAAGCGCAGCGCCCCGACCAAGAGCCAG	419
OY	3234	AAGCCGGGCGCCAGGAGGCTCTCCGGAGCTGTCTTGGGTACAGGGACACAGGCTTCCAG	3293
Db	420	AAGCCGGGCGCCAGGAGGCTCTCCGGAGCTGTCTTGGGTACACAGGGACACAGGCTTCCAG	479
OY	3294	GGGGTGGCAGAGATGTGTGCCCCCGGGCGCCGGACCTGTCTCGGAAAGCCCAATCCGAG	3353
Db	480	GGGGTGGCAGAGATGTGTGCCCCCGGGCGCCGGACCTGTCTCGGAAAGCCCAATCCGAG	539
OY	3354	GAGGGGCGCCGAGCGGCGAGCC	3375
Db	540	GAGGGGCGCCGAGCGGCGAGCC	561

RESULT 7
 BE255354
 LOCUS
 DEFINITION
 BE255354 801 bp mRNA linear EST 13-JUL-2000
 60111536991 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:3355889 5',
 mRNA sequence.
 BE255354
 BE255354.1 GI:9125792
 EST.
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 801)
 NIH-MGC http://mgc.nci.nih.gov/.
 Unpublished (1998)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L16C160 row: j column: 18
 High quality sequence stop: 576.
 Location/Qualifiers
 1
 801

cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 153 a 251 c 239 g 89 t 1 others

Query Match 10.0%; Score 465; DB 14; Length 733;
Best Local Similarity 78.9%; Pired. No. 1.5e-81;
Matches 381; Conservative 0; Mismatches 146; Indels 9; Gaps 2;

3116 CCTCCGAGGAGCCAAAGCCCGCTCGCTGACAGTCACTGCTGGGCGGCGCCGCGCG 3175
1 CTTCCGAGGAGCAGCAGCAGGCTCGCTGACAGTCACTGCTGGGCGGCGCCGCGCG 60
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61 GCGCTCTGTTAGCCAGGAGTCTCTGGGCGGCGCAGCCAGGCGCGCGAGGAGGAGG 120
3236 GCGGCGCGGAGGAGGAGTCTCTGGGAGTCTCTGGGAGCAGGAGCAGGAGGAGG 3295
121 GCGGAGTCTGAGGAGGAGTCTCTGGGAGTCTCTGGGAGCAGGAGCAGGAGGAGG 180
3296 GGTGGAGCAGCAGTGTGTGTCGCGCGCGCGCGCGAGCTCTCTCGGAGAGCCGCGAG 3355
181 GCGAGCTGATGAGTGTGTCGCGCGCGCGCGCGAGCTCTCTGAGAGGCGCGCTCA 240
3356 GGGGCGCGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 3409
241 GAGGTGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 300
3410 GAGGCGCTGTGTCGAGTGTGTCGCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 3469
301 GAGGCGCTGTGTCGAGTGTGTCGCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 360
3470 GCGCAGTGTGTCGAGTGTGTCGCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 3529
361 GCGCAGTGTGTCGAGTGTGTCGCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 420
3530 GAGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 3589
421 AAGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 480
3590 GCGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 3649
481 GAGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 540
3650 GAGGAGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 3709
541 AAGGAGGAGGAGGAGGAGGAGGAGTGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGG 597
3710 GCGGCTCATGCTCTCTGAGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 3769
598 GCGGCTCATGCTCTCTGAGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 657
3770 GCGGCTCATGCTCTCTGAGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 3829
658 GCGGCTCATGCTCTCTGAGTGTGTCGCGCGCGCGCGAGCTCTCTGAGAGGAGG 717
3830 GTTGTGCTCAAGAGCTG 3845
718 GTTGTGCTCAAGAGCTG 733

RESULT 11
BB430723 696 bp mRNA linear EST 31-AUG-2001
LOCUS BB430723 RIKEN full-length enriched, adult male hippocampus Mus
DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS COMMENT

musculus cDNA clone C630034J05 3', mRNA sequence.
BB430723
BB430723.2 GI:15412030
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
'Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyu, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Osaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jul 18, 2000 this sequence version replaced gi:9270450.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y., and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Funct. Genomics 2, pre. 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Location/Qualifiers
1..696
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630034J05"
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/sex="male"
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/dev_stage="adult"
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/note="Site 1: Xhol; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in

FEATURES Source

RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCCTGAGATTAATTAATTCCTTCCCTCCCTCCCT 3']"

BASE COUNT 184 a 175 c 202 g 134 t 1 others

Query Match 10.0%; Score 462; DB 10; Length 696;
Best Local Similarity 83.7%; Pred. No. 5.7e-81;
Matches 555; Conservative 0; Mismatches 86; Indels 22; Gaps 2;

QY 1530 GTGAGCTGAGCTCTGGAGTGGGCGGAGAGCCATTTGTGACCATGCTCACT 1589
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QY 1590 CTGACTTCCAAAGTCTCTTCAAGAGTCAATTAACCAATATGCTTCACT 1649
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DB 154 AAGATAGTACCAAGTCTCTTCAAGAGTCAATTAACCAATATGCTTCACT 213
QY 1710 AAAATGGCCCAAGTCTCTTCAAGAGTCAATTAACCAATATGCTTCACT 1769
DB 214 AAGATGGCCCAAGTCTCTTCAAGAGTCAATTAACCAATATGCTTCACT 273
QY 1770 AGTGAATAGTACCAAGTCTCTTCAAGAGTCAATTAACCAATATGCTTCACT 1829
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QY 1830 GCGAAGAGTCTCCAGCCCAATCAGGAGAGTCCGAGAGAGGAGTGTCTGATGAG 1889
DB 334 GCGAAGAGTCTCCAGCCCAATCAGGAGAGTCCGAGAGAGGAGTGTCTGATGAG 393
QY 1890 GACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1949
DB 394 GACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 453
QY 1950 CGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
DB 454 CGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 513
QY 2010 ATTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2069
DB 514 ATTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 573
QY 2070 CTGCGAGCA-----AGAGCAAGGCTGAAGAGAGTGTGATGATGATGAT 2108
DB 574 CTGCGAGCA-----AGAGCAAGGCTGAAGAGAGTGTGATGATGATGATGAT 633
QY 2109 GGGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2168
DB 634 GGGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
QY 2169 GGC 2171
DB 694 GGC 696

RESULT 12
LOCUS BG299246 711 bp mRNA linear EST 21-FEB-2001
DEFINITION 603395735P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4507377 5',
ACCESSION BG299246
VERSION BG299246.1 GI:13064707
KEYWORDS EST.

SOURCE
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL NIH-MGC
COMMENT NIH-MGC
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10384 row: e column: 10
High quality sequence start: 4
High quality sequence stop: 660.
Location/Qualifiers

FEATURES
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."

BASE COUNT 179 a 204 c 211 g 116 t 1 others

Query Match 9.8%; Score 456.4; DB 12; Length 711;
Best Local Similarity 84.5%; Pred. No. 7.3e-80;
Matches 595; Conservative 0; Mismatches 101; Indels 8; Gaps 7;

QY 2168 GCGAAG 2227
DB 12 GCGAAG 71
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QY 2288 GTCCGGGGCCCTCTGACCTGTGAGTGAAGTACCAAGTCCGAGGCGCACCAGATGAG 2347
DB 132 GTCCGGGGCCCTCTGACCTGTGAGTGAAGTACCAAGTCCGAGGCGCACCAGATGAG 191
QY 2348 GATGAGAGGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2407
DB 192 GATGAGAGGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 251
QY 2408 TCTGAG 2467
DB 252 CTTGAG 311
QY 2468 CCGCTCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2527
DB 312 CCGCTCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 370
QY 2528 CTGCAAAATGTTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2587
DB 371 TTGCAAGATGTTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 428
QY 2588 CAAATTGAGGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2647
DB 429 CAAATTGAGGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 488
QY 2648 CTTGTTCAACCCCAACTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2707

	TITLE	JOURNAL	COMMENT
Dp	489	IGHCTTCAACCCCAACTCGAGGATGCCCTTG-CGGGSCAGCTCAAGAAGAGCTGGCCCT	547
Oy	2708	CCGATCATCATTAGTGGCCAGAGAGCTTTCCCAAGCCGCAGATTCATGTGGGGAGCCTGG	2767
Dp	548	GAGATCATCATGAAGGCGCAGAGCTGCCAAG-CAAAGGATCTCGTCTGGGCACACCTGG	606
Oy	2768	GGAGATCATCAGACCCTTTGTGAGGTGGAGATCATTTGGGCT--CCCTGTGACTGG--AG	2824
Dp	607	GGAGATCATCAGAACATTAAGTGGAGGTGGAGATCATTTGGGCTCCCCCGTAGCTGCCAG	666
Oy	2825	CAGGAGCACAGACCCCGGTGTGGACGACAAGGGTTCAACCCA	2868
Dp	667	AACGAAGCAGACCCGAGTGTGTGACGACTCAAGAAATTAACCA	710
RESULT 13			
LOCUS	BB624082	667 bp mRNA linear EST 26-OCT-2001	
DEFINITION	BB624082 RIKEN full-length enriched, adult male eyeball Mus musculus clone 7530433C13 5', mRNA sequence.		
ACCESSION	BB624082		
VERSION	BB624082.1 GI:16462692		
KEYWORDS	EST		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 667)		
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakita,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki.Y.		
	RIKEN Mouse BSTs (Arakawa,T., et al. 2001)		
	Unpublished (2001)		
	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gscl.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayasaka,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wegl,K., Fujiwara,S., Inoue,K., Togawa,Y., Ikawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Komno,H., Fukuishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-285 (2001) Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamana,K., Itzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,U., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers		

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	/strain="C57BL/6Jr"	
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	/clone_1ib="RIKEN full-length enriched, adult male eyeball"	
	/sex="male"	
	/tissue_type="eyeball"	
	/dev_stage="adult"	
	/lab_host="DH10B"	
	/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAAGATCCACAGAGCTCTTTTGTTCCTTTTTCVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCTCGAATTAAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PhC I. Cloning script, 5' end: SalI; 3' end: BamHI"	
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ORIGIN		
Query Match	9.7%; Score 451.8; DB 10; Length 667;	
Best Local Similarity	88.7%; Pred. No. 5.8e-79;	
Matches 489; Conservative	0; Mismatches 62; Indels 0; Gaps 0;	
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OY	666 CCTTACGCCAAGAACAGAGAAGGCCAAGTCTTCATTCGATTCATCCAGAGAGTGATGAG	725
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OY	846 GTGGGCGGCACTGTGGTTCATCTGGCGCTGCGCTCACTCATGTGGCGGCACTACGACGAGAC	905
Db	417 GAGGACGCTACTCTGGTGTACAACGCGCTTCGCTCACTCATGTGGCGGCACTACGAGTAGAAG	476
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OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 200000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	176.4	3.8	3870	1	US-08-138-133-1 Sequence 1, Appl1
3	176.4	3.8	3893	1	US-08-138-641-3 Sequence 3, Appl1
4	176.4	3.8	3893	1	US-08-138-133-3 Sequence 3, Appl1
5	77.2	1.7	13953	4	US-09-738-884-3 Sequence 3, Appl1
6	55.9	1.3	7218	1	US-08-232-463-14 Sequence 14, Appl1
7	51.6	1.1	1288	1	US-08-440-856A-9 Sequence 9, Appl1
8	49.8	1.1	1926	4	US-09-249-585A-4 Sequence 4, Appl1
9	49.8	1.1	1931	2	US-09-130-114-2 Sequence 2, Appl1
10	49.4	1.1	3624	1	US-07-951-715A-6 Sequence 6, Appl1
11	49.4	1.1	3624	2	US-08-459-448A-6 Sequence 6, Appl1
12	49.4	1.1	3624	3	US-08-459-595A-6 Sequence 6, Appl1
13	49.4	1.1	3624	3	US-08-459-504B-6 Sequence 6, Appl1
14	49.4	1.1	3624	3	US-08-459-444-6 Sequence 6, Appl1
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16	49.4	1.1	3624	4	US-09-547-422-6 Sequence 6, Appl1
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18	48.2	1.0	1652	4	US-09-220-528-68 Sequence 68, Appl1
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ALIGNMENTS

RESULT 1
US-08-138-641-1
; Sequence 1, Application US/08138641
; Patent No. 5474921
; GENERAL INFORMATION:
; APPLICANT: Koblan, Kenneth S.
; APPLICANT: Pompliano, David L.
; TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
; TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Muchard
; STREET: P.O. Box 2000, 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,641
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muchard, David A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18937
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4720
; TELEFAX: (908) 594-3903
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3870 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-138-641-1

Query Match 3.8%; Score 176.4; DB 1; Length 3870;
Best Local Similarity 62.7%; Pred. No. 1.7e-27;
Matches 292; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1403 CATGACGAGCGCGGAGGCACTACTTCACTACCTGTCGCCACACACTGCTGCTGAGG 1462
DB 963 CATGACACACCCACGCTCTCATTTGATCTCTTCTCGCATATATGCTATCTGACTG 1022

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RESULT 2

US-08-138-133-1
 ; Sequence 1, Application US/08138133

; GENERAL INFORMATION:
 ; APPLICANT: GIBBS, JACKSON B.
 ; APPLICANT: KOBLAN, KENNETH S.
 ; APPLICANT: MACLEOD, ANGUS M.
 ; APPLICANT: MERCHANT, KEVIN J.
 ; TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
 ; TITLE OF INVENTION: PHOSPHOLIPASE C
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID A. MUTHARD
 ; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: U.S.A.
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/138,133
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MUTHARD, DAVID A.
 ; REGISTRATION NUMBER: 35,297
 ; REFERENCE/DOCKET NUMBER: 18938
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-3903
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3870 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-138-133-1

Query Match 3.8%; Score 176.4; DB 1; Length 3870;
 Best Local Similarity 62.7%; Pred. No. 1.7e-27;
 Matches 292; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1403 CATGACGAGCGCGTGAAGCCATCTTCTATCTACCTGCTCCCAACAACTTACCTGCGGG 1462
 DB 963 CATGAACACCCATCTCTCTATCTATGATCTCTCTCTGATTAATGATATCTGATCTG 1022
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 QY 1763 AGTAGAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1822
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 DB 1380 GATTAGCATGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1425

RESULT 3

US-08-138-641-3
 ; Sequence 3, Application US/08138641

; GENERAL INFORMATION:
 ; APPLICANT: Koblman, Kenneth S.
 ; APPLICANT: Pompliano, David L.
 ; TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
 ; TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Muthard
 ; STREET: P.O. Box 2000, 126 E. Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/138,641
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Muthard, David A.
 ; REGISTRATION NUMBER: 35,297
 ; REFERENCE/DOCKET NUMBER: 18937
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-3903
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3893 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-138-641-3

Query Match 3.8%; Score 176.4; DB 1; Length 3893;
Best Local Similarity 62.7%; Pred. No. 1.7e-27;
Matches 292; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1403 CATGACGACGACGCTGAGCCAGTACTTCACTACCTGCTCCCAAAACCACTACCTGCTGGG 1462
DB 963 CATGAACAACCCACTGCTCTACTATGATCTCTCTCCGCAATAATACGATATGACTG 1022
QY 1463 TGACACGCTCATCTCCAGTCAAGGCTGACATGTAATGCTTGGGCTCTGACGCTGCTG 1522
DB 1023 GGAACAGTTCTCCAGAGATCTCTCCGAAAGCTTACGCTGCTGCTGAGGATGGGCTG 1082
QY 1523 CCGCTGCTGAGGTGATCTGCTGGATGGGCCGACGGGAGCCCATTTGCAACATGG 1582
DB 1083 TCGCTGATGATGATGAGTCTGCTGGATGGGCCAGATGGGATCCAGTCAATTACCATGG 1142
QY 1583 CTACACTCTGATCTCCAGATCTCTCTTCAAAAGATCTATTGAAACCATCAAAATATGC 1642
DB 1143 GCACACCTTCACCAACAAATTAATGTTCTGAGATGCTGACACACATCAAGAGACAGC 1202
QY 1643 CTTCATCAAGATGATGATCCAGTATCTGCTCATGCAAAACCACTGACATGCTATCCA 1702
DB 1203 GTTCGATGCTCAGAGATCTCTGCTCATCTCTGCTCATGAGGACATGACGATTTGCCA 1262
QY 1703 GCAGAGAAAATGAGCCAGTATCTGATCTGATCTGCTGGGAGCAAGCTGATCTATC 1762
DB 1263 GCAGAGAAACATGGCCAGACATTCAGAGAGTGTGCTGACACAGCTCTCCACCAAGCC 1322
QY 1763 AGTGAAGATGAGATGATCCACACATCTCCCTCTCCACAGATCTCAAGGCAAGATCT 1822
DB 1323 CGTGAACATTTGCGCTG---ATGGGCTCCCTTCTCCCAACCACTCAAGAGAAATCT 1379
QY 1823 CGTGAAGGAGAGAGTCTCCAGCCATCATCAGAGAGATGGGAG 1868
DB 1380 GATTAAACATTAAGAGCTGCTGAGGAGCTGCTATGAGAGGCTG 1425

RESULT 4
US-08-138-133-3

Sequence 3, Application US/08138133
Patent No. 5519163
GENERAL INFORMATION:
APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MERCHANT, KEVIN J.
TITLE OF INVENTION: INHIBITORS OF PHOSPHODIESTERASE C
TITLE OF INVENTION: PHOSPHODIESTERASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DAVID A. MUTHARD
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MUTHARD, DAVID A.

REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3893 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-138-133-3

Query Match 3.8%; Score 176.4; DB 1; Length 3893;
Best Local Similarity 62.7%; Pred. No. 1.7e-27;
Matches 292; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1403 CATGACGACGACGCTGAGCCAGTACTTCACTACCTGCTCCCAAAACCACTACCTGCTGGG 1462
DB 963 CATGAACAACCCACTGCTCTACTATGATCTCTCTCCGCAATAATACGATATGACTG 1022
QY 1463 TGACACGCTCATCTCCAGTCAAGGCTGACATGTAATGCTTGGGCTCTGACGCTGCTG 1522
DB 1023 GGAACAGTTCTCCAGAGATCTCTCCGAAAGCTTACGCTGCTGCTGAGGATGGGCTG 1082
QY 1523 CCGCTGCTGAGGTGATCTGCTGGATGGGCCGACGGGAGCCCATTTGCAACATGG 1582
DB 1083 TCGCTGATGATGATGAGTCTGCTGGATGGGCCAGATGGGATCCAGTCAATTACCATGG 1142
QY 1583 CTACACTCTGATCTCCAGATCTCTCTTCAAAAGATCTATTGAAACCATCAAAATATGC 1642
DB 1143 GCACACCTTCACCAACAAATTAATGTTCTGAGATGCTGACACACATCAAGAGACAGC 1202
QY 1643 CTTCATCAAGATGATGATCCAGTATCTGCTCATGCAAAACCACTGACATGCTATCCA 1702
DB 1203 GTTCGATGCTCAGAGATCTCTGCTCATCTCTGCTCATGAGGACATGACGATTTGCCA 1262
QY 1703 GCAGAGAAAATGAGCCAGTATCTGATCTGATCTGCTGGGAGCAAGCTGATCTATC 1762
DB 1263 GCAGAGAAACATGGCCAGACATTCAGAGAGTGTGCTGACACAGCTCTCCACCAAGCC 1322
QY 1763 AGTGAAGATGAGATGATCCACACATCTCCCTCTCCACAGATCTCAAGGCAAGATCT 1822
DB 1323 CGTGAACATTTGCGCTG---ATGGGCTCCCTTCTCCCAACCACTCAAGAGAAATCT 1379
QY 1823 CGTGAAGGAGAGAGTCTCCAGCCATCATCAGAGAGATGGGAG 1868
DB 1380 GATTAAACATTAAGAGCTGCTGAGGAGCTGCTATGAGAGGCTG 1425

RESULT 5

US-09-738-884-3

Sequence 3, Application US/09738884
Patent No. 6391606
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00849
CURRENT APPLICATION NUMBER: US/09/738, 884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 13953
TYPE: DNA
ORGANISM: Human
US-09-738-884-3

Query Match 1.7%; Score 77.2; DB 4; Length 13953;
Best Local Similarity 74.6%; Pred. No. 6.6e-07;

[illegible][illegible]

QY 740 GGTCTTCCAGCGCTTACCTGAGCGAGCTTGCACCCCACTGCTTGCAGATCTACCA 799
 Db 712 CGCTTACACCGCTTCCAGAGCAGCCATCGTGGGCTTCCAGAAATCGCCCTCGAGCT 771
 QY 800 CGGACAGCAGCGGAGTCCGTGAGCTTGTCTTCCACAGAGCGAGTGGCGGCACTG 859
 Db 772 SSGCGSAGCGGRTCCGRTCTCACTGCTCTTCCCTTCCGCTGCGCAGCSCATGCT 831
 QY 860 GGTCTACTGCTGCTGCTTACTTCACTGCGGATCAGAGAGAGAGAGCTTGGCTGCGG 919
 Db 832 CATCAACGCTGCGCGAGGCGGCGACCAACGACGCGCGAGCGAGAGAGAGAGAGAG 891
 QY 920 CCAAGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 979
 Db 892 CMTGCACTGAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
 QY 980 TGGCAGCTTGGAGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1029
 Db 952 CAGGGGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1001

RESULT 8

US-09-249-585A-4/c
 ; Sequence 4, Application US/09249585A
 ; Patent No. 6417002
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotlick, Robert
 ; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
 ; FILE REFERENCE: 0867/0D905
 ; CURRENT APPLICATION NUMBER: US/09/249,585A
 ; CURRENT FILING DATE: 1999-02-11
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1926
 ; TYPE: DNA
 ; ORGANISM: Epstein Barr Virus
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(1926)
 ; OTHER INFORMATION: template strand of EBNA-1 DNA
 US-09-249-585A-4

Query Match 1.1%; Score 49.8; DB 4; Length 1926;

Best Local Similarity 44.9%; Pred. No. 0.18; Mismatches 232; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

QY 1856 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1915
 Db 740 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 681
 QY 1916 CTGCAAGCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1975
 Db 680 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
 QY 1976 GAGGAACTGATTCCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2035
 Db 620 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 561
 QY 2036 CTTCTCCGCTTCCACACTGTCCTCCATCTGAAAGCTCGAAGCGCAAGAGCAAGGCTGAGA 2095
 Db 560 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 501
 QY 2096 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2155
 Db 500 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 441
 QY 2156 AAGCTTCTCCAGGCGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2215
 Db 440 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 381
 QY 2216 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2275

Db 380 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 321
 QY 2276 G 2276
 Db 320 G 320

RESULT 9

US-09-130-114-2/c
 ; Sequence 2, Application US/09130114
 ; Patent No. 5976807
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotlick, Robert A.
 ; APPLICANT: Damaj, Bassam B.
 ; APPLICANT: Robbins, Alan K.
 ; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
 ; FILE REFERENCE: 0867/1D903US1
 ; CURRENT APPLICATION NUMBER: US/09/130,114
 ; CURRENT FILING DATE: 1998-08-06
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PasteSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: EBNA
 US-09-130-114-2

Query Match 1.1%; Score 49.8; DB 2; Length 1931;

Best Local Similarity 44.9%; Pred. No. 0.18; Mismatches 232; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

QY 1856 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1915
 Db 740 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 681
 QY 1916 CTGCAAGCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1975
 Db 680 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
 QY 1976 GAGGAACTGATTCCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2035
 Db 620 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 561
 QY 2036 CTTCTCCGCTTCCACACTGTCCTCCATCTGAAAGCTCGAAGCGCAAGAGCAAGGCTGAGA 2095
 Db 560 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 501
 QY 2096 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2155
 Db 500 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 441
 QY 2156 AAGCTTCTCCAGGCGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2215
 Db 440 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 381
 QY 2216 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2275
 Db 380 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 321
 QY 2276 G 2276
 Db 320 G 320

RESULT 10

US-07-951-715A-6
 ; Sequence 6, Application US/07951715A
 ; Patent No. 5625136
 ; GENERAL INFORMATION:
 ; APPLICANT: Kozziel, Michael G.
 ; APPLICANT: Desai, Nalini M.

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621 /product= "Full-length, maize"
OTHER INFORMATION: optimized cry1B
OTHER INFORMATION: /note= "Disclosed in Figure 6."
US-08-459-448A-6

Query Match 1.1%; Score 49.4; DB 2; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

Qy 743 CTTCCAGGCGTACCTGAGCGGAGCTTGAACCCCACTGCTGCTTCACTTCAACGCG 802
Db 2487 CTTGAGTGAACCCGACCTGAGCTGAGCTGCGGAGCGGAGGAGGCGCCACCA 2546
Qy 803 CAGCCACCGGAGTGGTGAACCTGCTCCACGAGCGAGGTGGCGGACCTGGGT 862
Db 2547 CAGCCACCTTCACTGAGCATGCACTGGGCTGACGACCTGCAAGAACTGGG 2606
Qy 863 CACTGGCTGGCTAAGCTGAGCGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGG 922
Db 2607 CGTGTGGGTGTGTTCAAGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2666
Qy 923 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 979
Db 2667 GTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2726
Qy 980 TGGGAGCTGAGCAATGGCGAGGCTGCGAGCTGCTGCAAACTGAACTGGC 1039
Db 2727 GAGTGGGCGGAGCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2786
Qy 1040 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1099
Db 2787 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2846
Qy 1100 GGGTTTGAAGGTTCTGCTCTTCAAGATGATGCAACCGCGGAGGAGGAGG 1159
Db 2847 CAACATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2906
Qy 1160 GCTCATGCTGAGCTTCAAGCAACCAAGAGGAGGAGGAGGAGGAGGAGGAG 1219
Db 2907 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2966
Qy 1220 CTT 1222
Db 2967 CAT 2969

RESULT 12
US-08-459-595A-6
Sequence 6, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.

APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John U.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutcliffe, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621 /product= "Full-length, maize"
OTHER INFORMATION: optimized cry1B
OTHER INFORMATION: /note= "Disclosed in Figure 6."
US-08-459-595A-6

Query Match 1.1%; Score 49.4; DB 3; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

Qy 743 CTTCCAGGCGTACCTGAGCGGAGCTTGAACCCCACTGCTGCTTCACTTCAACGCG 802
Db 2487 CTTGAGTGAACCCGACCTGAGCTGAGCTGCGGAGCGGAGGAGGAGGAGGAGGAGG 2546

QY 803 CAGCACCAGGAGTGGCTGAGACCTGATCTCCACAGACGAGTGGCCGACCTGGGT 862
 DB 2547 CAGCCACCACTTACAGCTTGAACATGACGTGGCTGACCGACCTCAACAGAACTTGGG 2606
 QY 863 CACTGGCTGCGCTACCTCAATGACCGGCATCAGCAGAGAGAGAGCTGCTGCGCCCA 922
 DB 2607 CATTGGGTGTGTTCATTAAGATCAAGACCCAGAGAGGGGCAAGCCGCTGGGCACTTGA 2666
 QY 923 GCGCACCAGGAGCAG---TGCTGAAAGCAGAGCTTTACAGAGCGGCAAGAGCGGGGA 979
 DB 2667 GTTCATTCAGAGAAAGCCCTGCTGGAGGCGCTGAGCGCGCTGAAGCGCGCCAGAA 2726
 QY 980 TGGCAGCTGAGCATTGGCGAGGTCTGACGTGCTGACCAAGCTCAAGTGAACCTGTC 1039
 DB 2727 GAAGTGGCGGAGCAAGCGGAGAGAGCTGACGTGAGAGACCAAGCGCTGTACACGAGGC 2786
 QY 1040 CCGGCAAGAGGTGAGCAAGATGTTCAAGGGAAGCGGACAGATGACCAAGAGAGCGCT 1099
 DB 2787 CAGGAGGCGCTGAGACCCCTGTTCTGGGACAGCCAGTACAGACCGCTGACAGCGGAC 2846
 QY 1100 GGGTTTGAAGATTCTGTCCTTCTTCAAGATGATGTCACCCCGCGGACCTTACTT 1159
 DB 2847 CAACATCGCATGATCCAGCGCCGCAAGAGCTGTGACCGCATCCGAGAGCGCTTACTT 2906
 QY 1160 GCTCATGCTGACCTTACAGCAACCAAGACCAAGCACTGATGCGCGCAGCTGAGGCTT 1219
 DB 2907 GAGCGAGCTGCCGTGATCCCGGCTGAAACCGCCAGATCTTGAAGAGCTGAGAGGCCA 2966
 QY 1220 CCT 1222
 DB 2967 CAT 2969

RESULT 13
 US-08-459-504B-6
 ; Sequence 6, Application US/08459504B
 ; Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Lannis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6075185artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,504B
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/459,595
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 TELEPHONE/DOCKET INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3624 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Synthetic DNA"
 HYPOTHEICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3621
 OTHER INFORMATION: /product= "Full-length, maize
 OTHER INFORMATION: optimized cry1B"
 OTHER INFORMATION: /note= "Disclosed in Figure 6."
 US-08-459-504B-6

Query Match 1.1%; Score 49.4; DB 3; Length 3624;
 Best Local Similarity 45.3%; Pred. No. 0.25;
 Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

QY 743 CTTCAGACGCTACCTCGAGGAGGAGCTTCCAGCCCACTGCTTACAGATCTTACACGG 802
 DB 2487 CTTCAGATGAGAACCCGACCTGAGCTGACGTGCGCGAGGAGAGAGTGGCTACCA 2546
 QY 803 CAGCACCAGGAGTGGCTGAGACCTGCTTCACAGCAGGAGTGGCGCACCTGGGT 862
 DB 2547 CAGCCACCACTTACAGCTGAGCATGACGTGGGCTGACCGACCTGAGAGACCTGGG 2606
 QY 863 CACTGGCTGCGCTACCTATGAGCGCGCATCAGCAGAGAGAGAGCTTGGCTGCCCA 922
 DB 2607 CATTGGGTGTGTTCATTAAGATCAAGACCCAGAGAGGGCCAGCCGCTGGGCACTTGA 2666
 QY 923 GCGCACCAGGAGCAG---TGCTGAAAGCAGAGCTTGAAGGCGGCAAGAGCGGGGA 979
 DB 2667 GTTCATTCAGAGAAAGCCCTGCTGGAGGCGCTGAGAGCAAGCCGCTGACAGGCG 2726
 QY 980 TGGCAGCTGAGCATTGGCGAGGTCTGAGCTGCTGACCAAGCTCAAGTGAACCTGTC 1039
 DB 2727 GAAGTGGCGGAGCAAGCGGAGAGAGCTGAGAGCAAGCCGCTGACAGGCG 2786
 QY 1040 CCGGCAAGAGGTGAGCAAGATGTTCAAGGGAAGCGGACAGATGACCAAGAGAGCGT 1099
 DB 2787 CAGGAGGCGCTGAGACCCCTGTTCTGGGACAGCGAGTACGAGCGCTGACAGCGGAC 2846
 QY 1100 GGGTTTGAAGATTCTGTCCTTCTTCAAGATGATGTCACCCCGCGGACCTTACTT 1159
 DB 2847 CAACATCGCATGATCCAGCGCCGCAAGAGCTGTGACCGCATCCGAGAGCTTACTT 2906
 QY 1160 GCTCATGCTGACCTTACAGCAACCAAGACCAAGCACTGATGCGCGCAGCTTGGAGCTT 1219
 DB 2907 GAGCGAGCTGCCGTGATCCCGGCTGAAACCGCCAGATCTTGAAGAGCTGAGAGGCCA 2966
 QY 1220 CCT 1222
 DB 2967 CAT 2969

RESULT 14
US-08-459-444-6
; Sequence 6, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Kozie, Michael G.
; Desai, Nalin M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CCCL577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cry1B"
; /note= "disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-459-444-6
Query Match 11%; Score 49.4; DB 3; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;
QY 743 CTTCCAGCCTTACCTGAGCGAGCTTGCACCCCACTGCTTACGATCTACACGG 802
DB 2487 CTTCCAGTGAAGCCGACCTGAGCTGACGCTGCCGACGCGAGAACTGCGCCACCA 2546
QY 803 CAGCCACCGGAGTGGCTGACCTGCTTCCACGACGAGCGAGTGGCGCGACCTGGGT 862

DB 2547 CAGCCACCACTTTCAGCCTTGACATGACGAGGCTTGACCGACCTTGACGAGAACTGGG 2606
QY 863 CACTGCGCTGCGCTACCTCAATGCGCGGATCAGGACGAGAGACAGCTGAGCTGCCGCA 922
DB 2607 CGTGGGTGTGTTCATCAAGATCAAGACCCAGAGAGGCGCACCGCCGCTGGGCAACTGGA 2666
QY 923 GCGCACCAAGGAGCCAG--TGCTGAAGACAGACGTTTGAAGAGCGGACAGAAACGGGGA 979
DB 2667 GTTCATGAGAGAAAGCCCTGCTGGCGAGGCGCCCTGAGCGGTGAAGGCGCGGAGAA 2726
QY 980 TGGCAGCTGAGCAATTTGGCCAGGCTCTGAGCTGCTCAAGCTCAAGCTGAACCTGCC 1039
DB 2727 GAAATGGGCGCAGCAAGCGCAGAGAGCTGAGACCAAGGCGCTGTACACCGAGGC 2786
QY 1040 CCGGACAGGGTGAAGACAGATGTTTCAAGGAAGCGGACACGATGACCAACCAAGGAGCT 1099
DB 2787 CAAGAGGCGCTGAGACGCGCTTTCGTGAGACGACGATGACGCGCTTGAGGCGGACAC 2846
QY 1100 GGGTTTGAAGATTTGTGTGCTTTCACAGATGATGTCACCGCGGACCTTACTT 1159
DB 2847 CAACATCGGATGATTCACGCGCGGACCAAGCTGTGACCGATCGGAGGCTTACTT 2906
QY 1160 GCTATGCTGACCTTACGCAACCAAGACACACCTGATGCCGCGGACCTGACGCTT 1219
DB 2907 GAGGAGCTGCCGTGATCCCGGCTGAACGCGGAGATCTTGAGAGCTGAGAGGCGCA 2966
QY 1220 CCT 1222
DB 2967 CAT 2969
RESULT 15
US-09-053-549-7
; Sequence 7, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalin
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121521artis Corporation
; STREET: 3054 Cornwallis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:

NAME/KEY: CDS
LOCATION: 1..3621
OTHER INFORMATION: /product= "Full-length, maize
OTHER INFORMATION: optimized cry1B"
OTHER INFORMATION: /note= "disclosed in Figure 6."
US-09-053-549-7

Query Match 1.1%; Score 49.4; DB 3; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

QY 743 CTTCCAGCGCTACCTGAGCGGACCTTGACCCCACTGCTGCTTCAAGCATCTACCAAG 802
DB 2487 CTTGAGTGGAGACCCGACCTGAGCTGAGCTGCGGACGAGAAAGTCCGCCACCA 2546
QY 803 CAGCCACCGGAGTCCGTGAGCCTGCTCCACAGCAGAGGTGGCGGCACTGGGT 862
DB 2547 CAGCCACCACTTCAAGCTGACATGACGTGGGCTGCACTGCAAGAACTTGG 2606
QY 863 CACTGCGCTGCGTACTCAATGCGCGCATCAGCAGAGACAGCTTGCTCGCGCCA 922
DB 2607 CAGTGGGTGTGTGTCAGATCAAGACCAAGAGGCAAGCCGCTGGGCAACTGGA 2666
QY 923 GCGCACCAGGAGCAG--TGGCTGAAGCAGACCTTTGACGAGCGCAAGAAAGGGA 979
DB 2667 GTTCATGAGAGAGAGCCCTGCTGGCGAGGCCCTGAGCGCTGAAGCGCGCGAGAA 2726
QY 980 TGGCAGCTGAGCATTTGGCAGGCTCTGCAAGCTGCTCAAGCTCAACGTGAACCTGCC 1039
DB 2727 GAAGTGGCGGACAGCGGCAAGAGCTGCAAGCTGGAACCAAGCGCTGTACACCGAGGC 2786
QY 1040 CCGGACAGAGGAGTGAAGCAGATGTTCAAGGGAAGCGGACAGATGACCAAGGAGAGCT 1099
DB 2787 CAGGAGGCGCGTGAAGCGCCCTGTTCGTGACAGCAGATGAGACCGCTGCAAGCGCAC 2846
QY 1100 GGGTTTGAAGAGTTCTGTGCTTTTCAAGATGATGTCAACCCCGGAGCTTCTACT 1159
DB 2847 CAACATGCGCATGATCCACGCGCGCAAGCTGTGACCGCATCCGCGAGGCTTACT 2906
QY 1160 GCTCATGCTGACCTTACGCAACCAAGAGCAACCTGATGCGGCAAGCTGCAAGCGCTT 1219
DB 2907 GAGCGAGCTGCGGTGATCCCGGCGTGAACGCCGAGATCTTGAAGAGCTGAGAGGCCA 2966
QY 1220 CCT 1222
DB 2967 CAT 2969

Search completed: March 28, 2003, 21:31:55
Job time : 395 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 16:34:17 ; Search time 399 Seconds
(without alignments)
9885.362 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
Sequence: 1 tgcgactctagactagctg.....ggtacaggggccaccgccccg 4635

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	3624	78.2	3624	10	US-09-927-112-3
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4	308.6	6.7	2289	10	US-09-908-664-3
5	308.6	6.7	2629	10	US-09-908-664-1
6	308.6	6.7	2709	10	US-09-804-969-20
7	307	6.6	1840	10	US-09-835-996A-7
8	301.8	6.5	2211	10	US-09-800-971-3
9	301.8	6.5	3425	10	US-09-800-971-1
10	289.8	6.3	2627	10	US-09-880-107-3293
11	276.8	6.0	3068	10	US-09-728-952-35
12	276.8	6.0	3068	10	US-09-728-952-64
13	195.4	4.2	567	9	US-09-764-868-24
14	195.4	4.2	567	9	US-09-955-999-31
15	146	3.1	1490	10	US-09-728-952A-18
16	144.2	3.1	5273	10	US-09-728-952-78
17	144.2	3.1	5430	10	US-09-822-635-3
18	144.2	3.1	10172	10	US-09-822-635-1
19	143.6	3.1	1827	10	US-09-908-664-6

20	143.6	3.1	2171	10	US-09-908-664-4	Sequence 4, Appli
21	106.4	2.3	981	10	US-09-867-550-1333	Sequence 1333, Ap
22	106.4	2.3	1505	10	US-09-728-952-59	Sequence 59, Appl
23	105.8	2.3	2547	10	US-09-765-298A-9	Sequence 9, Appli
24	100	2.2	278	9	US-09-796-692-3034	Sequence 3034, Ap
25	100	2.2	279	9	US-09-796-692-8940	Sequence 8940, Ap
26	91	2.0	2139	10	US-09-828-447-7	Sequence 7, Appli
27	77.2	1.7	13953	9	US-10-096-961-3	Sequence 3, Appli
28	76	1.6	760	10	US-09-828-447-1	Sequence 1, Appli
29	76	1.6	2276	10	US-09-828-447-6	Sequence 6, Appli
30	73.6	1.6	285	10	US-09-764-870-1561	Sequence 5561, Ap
31	71.6	1.5	582	10	US-09-764-870-112	Sequence 112, Appl
32	71.6	1.5	582	10	US-09-764-860-50	Sequence 50, Appli
33	68.8	1.5	503	10	US-09-764-870-92	Sequence 92, Appli
34	68.4	1.5	2517	10	US-09-476-242-16	Sequence 16, Appli
35	68.4	1.5	2517	10	US-09-476-242-17	Sequence 17, Appli
36	68.4	1.5	2523	10	US-09-476-242-15	Sequence 15, Appli
37	68.4	1.5	2529	10	US-09-476-242-14	Sequence 14, Appli
38	68.4	1.5	2535	10	US-09-476-242-13	Sequence 13, Appli
39	68.4	1.5	2541	10	US-09-476-242-9	Sequence 9, Appli
40	68.4	1.5	2541	10	US-09-476-242-10	Sequence 10, Appli
41	68.4	1.5	2541	10	US-09-476-242-11	Sequence 11, Appli
42	68.4	1.5	2541	10	US-09-476-242-12	Sequence 12, Appli
43	64.8	1.4	819	10	US-09-804-969-18	Sequence 18, Appli
44	57.2	1.2	1680	9	US-09-938-842A-787	Sequence 787, App
45	56.4	1.2	773	10	US-09-910-943-594	Sequence 594, App

ALIGNMENTS

RESULT 1
US-09-927-112-1
Sequence 1, Application US/09927112
Patient No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32544, a novel human phospholipase C and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 38155-20048.00
CURRENT APPLICATION NUMBER: US/09/927,112
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/246,808
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4635
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (435) ... (4058)
US-09-927-112-1

Query Match 100.0%; Score 4635; DB 10; Length 4635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	TGCGATCTAGAACTAGTGGCAAGCGCTCTGCACTCCCACTCCGAGAACTGCTCAGG	60
QY	61	AACCTGCGGCTCTCCGCTGGGACGCTGCTGATCAAGTCAAGCTCCAGGCGCTTAA	120
DB	61	AACCTGCGGCTCTCCGCTGGGACGCTGCTGATCAAGTCAAGCTCCAGGCGCTTAA	120
QY	121	GCTGAGGGCTGAGTCTTATTCACAGCCCTCGGGGAAACCGGGCTGGAGACCCCATG	180
DB	121	GCTGAGGGCTGAGTCTTATTCACAGCCCTCGGGGAAACCGGGCTGGAGACCCCATG	180

[illegible]

Db	1261	GGTGCAGAGACATCATCAGAGATTGTAGCGCATGCCAGAAAAAACAAGACTAAGGGGCTTGC	13220
Qy	1321	TGGGACATGATATGGCTTCAACAACTACAACGAGAGGCCCTGTGGTGTGACATCTTCAACCCCTG	13800
Db	1321	TGGGACATGATATGGCTTCAACCAACTACAACGAGAGGCCCTGTGGTGTGACATCTTCAACCCCTG	13800
Qy	1381	AGCACCCACATGTGACCCAGGACATGACGAGCCGCTGAGGCCATCTACTTCATCACCCTCGT	14400
Db	1381	AGCACCCACATGTGACCCAGGACATGACGAGCCGCTGAGGCCATCTACTTCATCACCCTCGT	14400
Qy	1441	CCCAACAACCCATCCCTGTGGGTGTACCAAGCTCATGTGTCCAGTCAAGGGGTGACATGTTATG	15000
Db	1441	CCCAACAACCCATCCCTGTGGGTGTACCAAGCTCATGTGTCCAGTCAAGGGGTGACATGTTATG	15000
Qy	1501	CTTGGGATCTGACAGGCTTGGCTGCGCTGCGCTGGAGGTGACATGCTGGGATGGGACCCGAG	15600
Db	1501	CTTGGGATCTGACAGGCTTGGCTGCGCTGCGCTGGAGGTGACATGCTGGGATGGGACCCGAG	15600
Qy	1561	GGGAGCCCATTTGTGCACCATGATGTCACTCTGACTTCCAAAGTCCCTCTTCAAAAGCTCA	16200
Db	1561	GGGAGCCCATTTGTGCACCATGATGTCACTCTGACTTCCAAAGTCCCTCTTCAAAAGCTCA	16200
Qy	1621	TTGAAACCATCAAAATATGCTTCATCAAGAATAGTACCAGATCTCTGCTCATCG	16800
Db	1621	TTGAAACCATCAAAATATGCTTCATCAAGAATAGTACCAGATCTCTGCTCATCG	16800
Qy	1681	AAAACCACTGCAGTGTCAATCAGACAGAGAAAATGGCCAGATCTGACTGACATCTTGG	17400
Db	1681	AAAACCACTGCAGTGTCAATCAGACAGAGAAAATGGCCAGATCTGACTGACATCTTGG	17400
Qy	1741	GGGACAACTGTGACCTGTGCATCAGTGGACGTGAATGCACACACATCCCTCTCCAC	18000
Db	1741	GGGACAACTGTGACCTGTGCATCAGTGGACGTGAATGCACACACATCCCTCTCCAC	18000
Qy	1801	AGATCTCAAGGGGCAAGATCTCTGTGAGGGGAGAAAGCTCCAGCCAAATCAGCGAGG	18600
Db	1801	AGATCTCAAGGGGCAAGATCTCTGTGAGGGGAGAAAGCTCCAGCCAAATCAGCGAGG	18600
Qy	1861	ATGCGAGAGAAAGGAGAGTGTCTGATGAGAGACGAGTGTATGAGATTGACATGACTGCA	19200
Db	1861	ATGCGAGAGAAAGGAGAGTGTCTGATGAGAGACGAGTGTATGAGATTGACATGACTGCA	19200
Qy	1921	AGCTCTCAATGGGGATGCATCCACCAATCGAAGCGGTAAAAAACTGTGAAGAGA	19800
Db	1921	AGCTCTCAATGGGGATGCATCCACCAATCGAAGCGGTAAAAAACTGTGTGAAGAGA	19800
Qy	1981	AACCTGATTCCTCTCATGAAGAATGCCAATTCGGGACTGTGAGGACCCCAACAATCTTCT	20400
Db	1981	AACCTGATTCCTCTCATGAAGAATGCCAATTCGGGACTGTGAGGACCCCAACAATCTTCT	20400
Qy	2041	CCGTCTCCACACTGTCCCAATCTGGAAGCTGCGAGCGCAAGAGCAAGGCTGAAGAGACG	21000
Db	2041	CCGTCTCCACACTGTCCCAATCTGGAAGCTGCGAGCGCAAGAGCGAAGGCTGAAGAGACG	21000
Qy	2101	TGGAATCTGGGAGAGATGCGGGGCCAGACGACATGTGCGCCTCGTCTGGGAACT	21600
Db	2101	TGGAATCTGGGAGAGATGCGGGGCCAGACGACATGTGCGCCTCGTCTGGGAACT	21600
Qy	2161	TCTCCAGGCGCAAAAGAGGAGGACGAGGTGAAGAAAGGCGGCGCGTGAAGAGGAG	22200
Db	2161	TCTCCAGGCGCAAAAGAGGAGGACGAGGTGAAGAAAGGCGGCGCGTGAAGAGGAG	22200
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Db	2221	ATGAGGCTCAGAGACTCCCGGGAGGCCAAGCGCGAAGGGCGACCCGGAGAAAGACCA	22800
Qy	2281	TGAAGCTGTCCCGGGCCCTCTTGAAGTGTGAAGTACCAAGTCCGTGGCCACCAAG	23400
Db	2281	TGAAGCTGTCCCGGGCCCTCTTGAAGTGTGAAGTACCAAGTCCGTGGCCACCAAG	23400
Qy	2341	ACATAGATGAGAGCGGCGCTCAGCTGGCAGGTGTCTTCAAGCAGACCAAGGCC	24000

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Q	y	2401	ACCAGATTTCTGCACGACGAAAGCCGGCCGCACTACCTTACGCTTCAACCAAGACAGCTCTTCC	2460
D	b	2401	ACCGAGATTTCTGCACGACGAAAGCCGGCCGCACTACCTTACGCTTCAACCAAGACAGCTCTTCC	2460
Q	y	2461	GCATCTACCCCTCTCTCTTACCGTGTGGACTCCAGAACCTAACCCCGAGCCCTTCTGGA	2520
D	b	2461	GCATCTACCCCTCTCTCTTACCGTGTGGACTCCAGAACCTAACCCCGAGCCCTTCTGGA	2520
Q	y	2521	ACGCGGCTCCCAATAGTTGCTGCTTGAACCTACAGTCAGAGGGGGGATGTCTGACGTGA	2580
D	b	2521	ACGCGGCTCCCAATAGTTGCTGCTTGAACCTACAGTCAGAGGGGGGATGTCTGACGTGA	2580
Q	y	2581	ACCGAGCCAAAGTTTCAGGCGCAACGCTGGCTGGCTGACTCAAGCTTGGGTGATGT	2640
D	b	2581	ACCGAGCCAAAGTTTCAGGCGCAACGCTGGCTGGCTGACTCAAGCTTGGGTGATGT	2640
Q	y	2641	GCACGGGGGGTTCACACCCCACTGGAGAGACCCCTGGCCGGGAGGCTCAAGAAAGACG	2700
D	b	2641	GCACGGGGGGTTCACACCCCACTGGAGAGACCCCTGGCCGGGAGGCTCAAGAAAGACG	2700
Q	y	2701	TGGTGCTCCGGAATCATCAGTGGCGACAGCTTCCCAAGCCGGCGCACTCAATGCTGGGGG	2760
D	b	2701	TGGTGCTCCGGAATCATCAGTGGCGACAGCTTCCCAAGCCGGCGCACTCAATGCTGGGGG	2760
Q	y	2761	ACCGTGGGGAGATCATGACCCCTTGTGTGAGGTGAGATCATTTGGCTCTCTGTGACT	2820
D	b	2761	ACCGTGGGGAGATCATGACCCCTTGTGTGAGGTGAGATCATTTGGCTCTCTGTGACT	2820
Q	y	2821	GCACGACGAGACAGACCCCGGTGTGTGAGACAGACGGGTTCACCCCACTGGGAGAGAG	2880
D	b	2821	GCACGACGAGACAGACCCCGGTGTGTGAGACAGACGGGTTCACCCCACTGGGAGAGAG	2880
Q	y	2881	CCCTGTGTTTTCATGATGTACATGCTCCGAGATCGCGCTGGTCCGCTCTCTGCTGGAC	2940
D	b	2881	CCCTGTGTTTTCATGATGTACATGCTCCGAGATCGCGCTGGTCCGCTCTCTGCTGGAC	2940
Q	y	2941	ACGATCCCATCGGGCTGACTTCAATTGAGCCAGAGACGCTGGCTTCAAGCAGCATGATG	3000
D	b	2941	ACGATCCCATCGGGCTGACTTCAATTGAGCCAGAGACGCTGGCTTCAAGCAGCATGATG	3000
Q	y	3001	CAGGCTACAGACACGTGTACTTGTGAAGGATGGAAGAGGCTTCCATCTTGTGATGTGG	3060
D	b	3001	CAGGCTACAGACACGTGTACTTGTGAAGGATGGAAGAGGCTTCCATCTTGTGATGTGG	3060
Q	y	3061	CTGTGAGTACATCAGGAGGTAAAGTCAAGAGGCTCTGGGCTTAAAGAGGCTCTTCTCC	3120
D	b	3061	CTGTGAGTACATCAGGAGGTAAAGTCAAGAGGCTCTGGGCTTAAAGAGGCTCTTCTCC	3120
Q	y	3121	GAGGCCCCAAAGCCCCGGCTGTGCTGGAACGTATGCTGTGGGCGGCCCCCGGCCCGGCCCT	3180
D	b	3121	GAGGCCCCAAAGCCCCGGCTGTGCTGGAACGTATGCTGTGGGCGGCCCCCGGCCCGGCCCT	3180
Q	y	3181	CCGTTTACGACGAGGATCTCTGGGGCGCACGAGCCGCCCAACAGACAGAAAGCCGG	3240
D	b	3181	CCGTTTACGACGAGGATCTCTGGGGCGCACGAGCCGCCCAACAGAGCCAGAAAGCCGG	3240
Q	y	3241	GCCCGAGGGGCTTCCGGGAGCTGTCTCTGGGTCAAGGAGACAGGCTCAAGGGGGTGG	3300
D	b	3241	GCCCGAGGGGCTTCCGGGAGCTGTCTCTGGGTCAAGGAGACAGGCTCAAGGGGGTGG	3300
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D	b	3301	CAGACGATGTGTGCCCCCGCGGCGCGGACCTTGTCCGGAAGCCCGAGCCAGAGAGGGG	3360
Q	y	3361	CCGGACGCGGACGCCCCCGAGGTAAAGCGCCAGACTCGGTGCGAGAGAAAGACCTTGTGC	3420
D	b	3361	CCGGACGCGGACGCCCCCGAGGTAAAGCGCCAGACTCGGTGCGAGAGAAAGACCTTGTGC	3420
Q	y	3421	GAGTGGGGGCCCCCGGTGTCTGTGAAGGGCCCGGGGCTGTGTGGATGTGCGCGCATATCA	3480
D	b	3421	GAGTGGGGGCCCCCGGTGTCTGTGAAGGGCCCGGGGCTGTGTGGATGTGCGCGCATATCA	3480

Qy	3481	TGAGGTGTGTGGAGATCTCTGGCCGCGCTGTAA	CACCGGGGGGCTGTGACAGGGAGCGGC	3540
Db	3481	TGAAGTGTGTGGATCTCTGGCCGCGGTAA	CACGGGGGCTGTGACAGGAGCGGC	3540
Qy	3541	CACCGACCCGGGGGCTGTGACAGGACAGGACCATTC	TGGCAGAGCCCGGGCCCGG	3600
Db	3541	CACCGACCCGGGGGCTGTGACAGGACAGGACCATTC	TGGCAGAGCCCGGGCCCGG	3600
Qy	3601	CTGACTGTGGGGGGCCCCCTGTGTGGCTTGAACCTTC	ACGCTATCCCGGGAGAAACA	3660
Db	3601	CTGACTGTGGGGGGCCCCCTGTGTGGCTTGAACCTTC	ACGCTATCCCGGGAGAAACA	3660
Qy	3661	GAGAGGCCCCCAAGGCTCTGTGGGGCTTGAAGGACAGGGTTC	AGCGGCTACAGT	3720
Db	3661	GAGAGGCCCCCAAGGCTCTGTGGGGCTTGAAGGACAGGGTTC	AGCGGCTACAGT	3720
Qy	3721	CCTCGACTCCAGACAGCCAGACGCCGGGACATCCCGAAAGGCTCCCGCTGGAGCTG	3780	
Db	3721	CCTCGACTCCAGACAGCCAGACGCCGGGACATCCCGAAAGGCTCCCGCTGGAGCTG	3780	
Qy	3781	AGGGTGCCTTCAGGCAACCGGGGGCCCTTCAGGAGAGATGATGCTTGTGTTTCTCAA	3840	
Db	3781	AGGGTGCCTTCAGGCAACCGGGGGCCCTTCAGGAGAGATGATGCTTGTGTTTCTCAA	3840	
Qy	3841	AGCTGAGAGATCAGAGATTAATCCCCCATGTCTTCGCGCGGTATGAGCCCTCTTGGCCT	3900	
Db	3841	AGCTGAGAGATCAGAGATTAATCCCCCATGTCTTCGCGCGGTATGAGCCCTCTTGGCCT	3900	
Qy	3901	GGGTGTCTCCCGACGCCCTGTGGATGGCTGGGGCTGTGGGTACATGCTGTGCTTCTG	3960	
Db	3901	GGGTGTCTCCCGACGCCCTGTGGATGGCTGGGGCTGTGGGTACATGCTGTGCTTCTG	3960	
Qy	3961	CGTGAAGGTGTGGCTCGCTGTGTGCTGTGCTGTGTGCTGTATCCGTGACATGTCTCC	4020	
Db	3961	CGTGAAGGTGTGGCTCGCTGTGTGCTGTGCTGTGTGCTGTATCCGTGACATGTCTCC	4020	
Qy	4021	GTGGACACTGTCTTCCTTGGCTTGTGTGGCCCATAGCCCAAGCCCTCTGTCTGAGCT	4080	
Db	4021	GTGGACACTGTCTTCCTTGGCTTGTGTGGCCCATAGCCCAAGCCCTCTGTCTGAGCT	4080	
Qy	4081	TGAAGCCCTGTGGACTTGGGTGTGGGTGTGTATAGGCGGACAGGCTGGGAAAGAACAGCT	4140	
Db	4081	TGAAGCCCTGTGGACTTGGGTGTGGGTGTGTATAGGCGGACAGGCTGGGAAAGAACAGCT	4140	
Qy	4141	GCTCTGTGTGAGGCTCTGGGGCCGGGACTGTGGCTGTGACATCTGTGGGCCCTCCGGCTGG	4200	
Db	4141	GCTCTGTGTGAGGCTCTGGGGCCGGGACTGTGGCTGTGACATCTGTGGGCCCTCCGGCTGG	4200	
Qy	4201	GGCGTTCCTCCCAACTCACTCTCTGGGGCTGGCGACTGTGACCTGTGATGCTTTC	4260	
Db	4201	GGCGTTCCTCCCAACTCACTCTCTGGGGCTGGCGACTGTGACCTGTGATGCTTTC	4260	
Qy	4261	CTGGGACTGGGGGCTCATGTACCATTCCTTCCACTCTCCCTCTAAGGGCAGGCTCCAGGGG	4320	
Db	4261	CTGGGACTGGGGGCTCATGTACCATTCCTTCCACTCTCCCTCTAAGGGCAGGCTCCAGGGG	4320	
Qy	4321	TCCCTACTGGGAAGTGTGATGTGGGACAGGTGAGCACTGTGGGCGTCTCTGGGCCCC	4380	
Db	4321	TCCCTACTGGGAAGTGTGATGTGGGACAGGTGAGCACTGTGGGCGTCTCTGGGCCCC	4380	
Qy	4381	TGGGACGCTGTGAAGCTGTGAGTGTGCTGTGGAGTGAATTCCTGTGGGCCCGAGGGCTTC	4440	
Db	4381	TGGGACGCTGTGAAGCTGTGAGTGTGCTGTGGAGTGAATTCCTGTGGGCCCGAGGGCTTC	4440	
Qy	4441	GCTGCTTGGGCTGTAGCACTCCCATTAAGAAAGGTGTCTCTTAAGCTGTGAGGAGGAGCA	4500	
Db	4441	GCTGCTTGGGCTGTAGCACTCCCATTAAGAAAGGTGTCTCTTAAGCTGTGAGGAGGAGCA	4500	
Qy	4501	TACACGAGGCCCCCGCACACACCCGTGCCCTCCAGACCCCCCTGTACCAAGCTTTCCT	4560	
Db	4501	TACACGAGGCCCCCGCACACACCCGTGCCCTCCAGACCCCCCTGTACCAAGCTTTCCT	4560	

Qy 4561 TCTGCCCCCAACCCAGCTGCTCCGTAAGTAACTAGAGCGGCGAGTACAGATA 4620
Db 4561 TCTGCCCCCAACCCAGCTGCTCCGTAAGTAACTAGAGCGGCGAGTACAGATA 4620
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Db 4621 CGGGGCCCGAGCCCG 4635

RESULT 2

US-09-927-112-3
; Sequence 3, Application US/09927112
; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Siles-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-927-112-3

Query Match 78.2%; Score 3624; DB 10; Length 3624;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 435 ATGGCTCCCGCAAGCCGCGCCCTTCTGCGCCAGCTTCTCCGCTGAGAGCCAGAG 494
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Qy 495 CCGGATCCCGAGAGAGAGGCTTTTCTTGAAGCCCAATTTGCGCGTGTGAGAGCG 554
Db 61 CCGGATCCCGAGAGAGAGGCTTTTCTTGAAGCCCAATTTGCGCGTGTGAGAGCG 120
Qy 555 TGCATGGGTGCACTGCAAGAGGAGATGAGATGTAAGTGTGAGGAGCTTCAAGAG 614
Db 121 TGCATGGGTGCACTGCAAGAGGAGATGAGATGTAAGTGTGAGGAGCTTCAAGAG 180
Qy 615 CTGCTCCGCTTCTACTACTGAGAGACCGCTCTGCAATCCGCTGAGAGCCCTTCA 674
Db 181 CTGCTCCGCTTCTACTACTGAGAGACCGCTCTGCAATCCGCTGAGAGCCCTTCA 240
Qy 675 AAGAAAGAGAGGCGCAAGATCTCATTGACCTCATCAGAGAGTGAAGAGGCGAG 734
Db 241 AAGAAAGAGAGGCGCAAGATCTCATTGACCTCATCAGAGAGTGAAGAGGCGAG 300
Qy 735 TCGAGAGTCTTCAGAGGCTACCTGACGAGAGCTTGAACCCCACTGCTTCAAGCAT 794
Db 301 TCGAGAGTCTTCAGAGGCTACCTGACGAGAGCTTGAACCCCACTGCTTCAAGCAT 360
Qy 795 TACCAAGAGAGCCAGAGAGTGTGAGACTGTGTCTCAACAGAGAGAGTGTGAG 854
Db 361 TACCAAGAGAGCCAGAGAGTGTGAGACTGTGTCTCAACAGAGAGAGTGTGAG 420
Qy 855 ACCTGGGTGCTGAGAGCTGAGTACCTGAGTGTGAGAGAGAGAGAGAGAGAGAG 914
Db 421 ACCTGGGTGCTGAGAGCTGAGTACCTGAGTGTGAGAGAGAGAGAGAGAGAGAG 480
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Db 541 GGGGATGAG 600
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Db 601 CTGCCCGGAG 660
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Db 661 ACGCTGGGTGTTTGAAGAGTGTGAGCTTCTCAAGATGATGATGATGATGATGATG 720
Qy 1155 TACCTGCTCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1214
Db 721 TACCTGCTCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 1215 CGCTTCTGAG 1274
Db 781 CGCTTCTGAG 840
Qy 1275 ATCAGAGAGTGTGAG 1334
Db 841 ATCAGAGAGTGTGAG 900
Qy 1335 TTCAACCACTACACAG 1394
Db 901 TTCAACCACTACACAG 960
Qy 1395 CACCAAG 1454
Db 961 CACCAAG 1020
Qy 1455 CTGCTGGGTGAG 1514
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Qy 1515 GCTGCTGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1574
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Qy 1635 AATATGCTTCTCATCAAGATGAGTACCAAGATGATGATGATGATGATGATGATG 1694
Db 1201 AATATGCTTCTCATCAAGATGAGTACCAAGATGATGATGATGATGATGATGATG 1260
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Qy 1755 CTGCTATCAG 1814
Db 1321 CTGCTATCAG 1380
Qy 1815 AAGATCTCTGTAAG 1874
Db 1381 AAGATCTCTGTAAG 1440
Qy 1875 GAGGTGTCTGATGAG 1934
Db 1441 GAGGTGTCTGATGAG 1500
Qy 1935 GATGATCCAG 1994
Db 1501 GATGATCCAG 1560
Qy 1995 ATCAAG 2054
Db 1561 ATCAAG 1620
Qy 2055 TCCCATCTGAG 2114

Db 1621 TCCCATCTTGAAGAGCTCGAGCGCAAGAGCAAGGCTGAAGAGGACGTGAGTCTGAGGAG 1680
Qy 2115 GATGCGGGGGCCGAGAGCCCAATGCGCGCTGTGTGAGGAACTTCCAGGCGCAAG 2174
Db 1681 GATGCGGGGGCCGAGAGCCCAATGCGCGCTGTGTGAGGAACTTCCAGGCGCAAG 1740
Qy 2175 AAGAGGGGCGAGAGCTGAAGAGCGCGCAGCGTGAAGAGGAGATGAGGATGAGAGC 2234
Db 1741 AAGAGGGGCGAGAGCTGAAGAGCGCGCAGCGTGAAGAGGAGATGAGGATGAGAGC 1800
Qy 2235 TCCCGGGAGGCGAGAGCCGAGGGGCGACCCGCGAGAGAGCACTGAAGCTGTCTCCG 2294
Db 1801 TCCCGGGAGGCGAGAGCCGAGGGGCGACCCGCGAGAGAGCACTGAAGCTGTCTCCG 1860
Qy 2295 GCGCTCTCTGAAGCTGAGAGTCAACCAAGTCCGTGGGCCCAACAGCACTAGAGATGAG 2354
Db 1861 GCGCTCTCTGAAGCTGAGAGTCAACCAAGTCCGTGGGCCCAACAGCACTAGAGATGAG 1920
Qy 2355 GCGGCGTCAAGTGGAGAGTGTGTCTTTCAGCGAGAGCAAGGCGCGACAGATTTGAG 2414
Db 1921 GCGGCGTCAAGTGGAGAGTGTGTCTTTCAGCGAGAGCAAGGCGCGACAGATTTGAG 1980
Qy 2415 CAGAGAGCGGCGAGTCACTACCTGTTCAACAGAGAGCTTCTCCGCACTTACCTCC 2474
Db 1981 CAGAGAGCGGCGAGTCACTACCTGTTCAACAGAGAGCTTCTCCGCACTTACCTCC 2040
Qy 2475 TCTTACCGTGTGAGTCTCAAGCACTACACCGAGCGCTTGTGAAGCGCGGCTGCA 2534
Db 2041 TCTTACCGTGTGAGTCTCAAGCACTACACCGAGCGCTTGTGAAGCGCGGCTGCA 2100
Qy 2535 ATGGTTCCTCTGAAGTCACTACAGTCAAGAGGGGCGAGTGTGAGCTGAACCGAGCAAGTTC 2594
Db 2101 ATGGTTCCTCTGAAGTCACTACAGTCAAGAGGGGCGAGTGTGAGCTGAACCGAGCAAGTTC 2160
Qy 2595 AGCGCCAAAGTGTGTGTGCGGCTGCTACTCAAGCTGTGTGTGTGTGTGTGTGTGTGT 2654
Db 2161 AGCGCCAAAGTGTGTGTGCGGCTGCTACTCAAGCTGTGTGTGTGTGTGTGTGTGTGT 2220
Qy 2655 AACCCGAACTCGAGAGAGCGCGCTGCGGGGAGCTCAAGAGAGAGCTGTGTGTGTGTGTGT 2714
Db 2221 AACCCGAACTCGAGAGAGCGCGCTGCGGGGAGCTCAAGAGAGAGCTGTGTGTGTGTGTGT 2280
Qy 2715 ATCAGTGGCGAGAGCTTCCCAAGCGCGAGCTCACTGTGTGTGTGTGTGTGTGTGTGT 2774
Db 2281 ATCAGTGGCGAGAGCTTCCCAAGCGCGAGCTCACTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Qy 2775 ATGCAAGCTTGT 2834
Db 2341 ATGCAAGCTTGT 2400
Qy 2835 ACCGCGGT 2894
Db 2401 ACCGCGGT 2460
Qy 2895 GTGCAAGT 2954
Db 2461 GTGCAAGT 2520
Qy 2955 CGTGAAGT 3014
Db 2521 CGTGAAGT 2580
Qy 3015 GTGTAAGT 3074
Db 2581 GTGTAAGT 2640
Qy 3075 AGCGGTAAAGTCAAGAGAGCTTGTGGGCTTAAAGAGCTTCTTCCAGAGCTCAAGAGCT 3134
Db 2641 AGCGGTAAAGTCAAGAGAGCTTGTGGGCTTAAAGAGCTTCTTCCAGAGCTCAAGAGCT 2700
Qy 3135 GCGT 3194
Db 2701 GCGT 2760

Qy 3195 ATCTGTGCGGCGCAGAGCTTC 3254
Db 2761 ATCTGTGCGGCGCAGAGCTTC 2820
Qy 3255 CCGAGAGCTGT 3314
Db 2821 CCGAGAGCTGT 2880
Qy 3315 CCGCGAGGTTAAAGCGCGCAGCTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3374
Db 2881 CCGCGAGGTTAAAGCGCGCAGCTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940
Qy 3435 CCGT 3494
Db 3001 CCGT 3060
Qy 3495 GATCTGT 3554
Db 3061 GATCTGT 3120
Qy 3555 CCGTGAAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 3614
Db 3121 CCGTGAAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 3180
Qy 3615 GCGCGCTGT 3674
Db 3181 GCGCGCTGT 3240
Qy 3675 GGTCTGT 3734
Db 3241 GGTCTGT 3300
Qy 3735 AGCCGAGAGCGCGCGCGAGTCCCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3794
Db 3301 AGCCGAGAGCGCGCGCGAGTCCCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3360
Qy 3795 CAAGCGGGGGCGCGCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3854
Db 3361 CAAGCGGGGGCGCGCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
Qy 3855 AGAGTAAATCCCATGT 3914
Db 3421 AGAGTAAATCCCATGT 3480
Qy 3915 CAGCGCGCGCGAGT 3974
Db 3481 CAGCGCGCGCGAGT 3540
Qy 3975 CCGT 4034
Db 3541 CCGT 3600
Qy 4035 CCGT 4058
Db 3601 CCGT 3624

RESULT 3

US-09-969-14
; Sequence 14, Application US/09804969
; Patent No. US20020081595A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Donoho, Gregory
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abulin, Alejandro

APPLICANT: Friedrich, Glenn
 APPLICANT: Zambrowicz, Brian
 APPLICANT: Sands, Arthur T.
 TITLE OF INVENTION: No. US20020081595A1el Human Phospholipases and Polynucleotides En
 FILE REFERENCE: LEX-0148-USA
 CURRENT APPLICATION NUMBER: US/09/804,969
 PRIOR FILING DATE: 2001-03-13
 PRIOR APPLICATION NUMBER: US 60/188,885
 PRIOR FILING DATE: 2000-03-13
 PRIOR APPLICATION NUMBER: US 60/189,693
 PRIOR FILING DATE: 2000-03-15
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 2289
 TYPE: DNA
 ORGANISM: homo sapiens
 US-09-804-969-14

Query Match 6.7%; Score 308.6; DB 10; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 2.2e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

744 TTCCAGGCGTACCTGACGCGACGCTTCGACCCCACTGCTGCTTCGACATCTACCGCGC 803
 229 TTGCTGTGATGCTTGGAGAGAGCTCCCTCGAGCAGGCGCTTCACCATGTCTTTCAT 288
 804 AGCCACCGCGAGTGTGCTGACCTGTCTCCACGACGAGGATGAGCGGCACTGGGTC 863
 289 GCGCGCGCTCCCACTGACCTGATGGCCCAAGATGTTGAGAGGCGCCAGATATGAGATG 348
 864 ACTGCGCTGCGTCACTCATGCGCGCATGACGACGAGACAGCTGTGCGCGCCAG 923
 349 CGAGGCGCTCAGCTGTGGTGTGATCTTGTCCACGACATGACCATCAGAGGCGCT --- 404
 924 CGACACGAGGACGAGTGTGCTGAAGCAGACGTTTGAAGAGCGGACGAGAGACGGAGTGC 983
 405 -----GACCAATAGCTGAGACGATGGTTTCAACGTGAGACAAATACAGATGTGT 456
 984 AGCCTTGAAGTGGAGGCTGCTGACGCTGACGCTGACCAAGCTCAACGTGACCTGCGCGG 1043
 457 AAGATAGATTTCCAGAAAGTTACGGGTTATTTGACCTATGATGTGAAATGAGACCA 516
 1044 CAGAGGCTGAAGCAGATGTTTCAGGAGGCGGACACGAGATGACCAACGAGGACGCTGGT 1103
 517 GAATATGCTTCAAGTCTTTTTCAGGACGACACG---TCCAGTCTGGAACCTCTGGA 573
 1104 TTGAAGAGTCTGTGCTCTTCTACAGATGATGTCCACCGCGGAGCTCTTACCTGCTC 1163
 574 GAGAGAGATTTGTACAGTCTTATTAAGGCAATTGACTAAACGTGCTGAGGAGGAACTG 633
 1164 ATGCTGACCTTAAGCAACCAAGACCACTGATGCGGACGCGGACGCTGACGCTTCTG 1223
 634 TTTGAAAGTTTTCAGCTGATGGGAGAGGCTGACTGCTGGAATTTTGGATTTCCCT 693
 1224 CAGGTGACCAAGATGCGCGGCTGTGACCTTCGAGAGCTGCCAGACATCTACGACGAG 1283
 694 CAGAGAGACCAAGAGAGAGACGACCTGACCTTGTGCTGGAACCTCAATTCACCGC 753
 1284 TTTGAGCCATGCGCCAGAAACAAAGATTAAGGGGCTGCGGAGATTGATGGCTTCCCAAC 1343
 754 TATGAACCTTTCAGACAGTGGCAAACTGCGGCACTGTGCTGATGATGATGGCTTCTCAGC 813
 814 TACCTGTGCTTAAGATGAGACATCTTCAACCCAGCTGCTGCCATCTATAGAGAT 873
 1404 ATGAGCGACCGCTGAGCAGCTATCTTCACTACCTGCTCCCAACAACCTACTGCTGGGT 1463
 874 ATGATCTCAACCCCTGAAACCACTTCACTCTCTTCTCATACCACTACTACTAGTGGGG 933
 1464 GACCAAGCTATGCTCCAGTCAAGGAGGAGCATGTATGCTGTGGGTCTTGAAGGCTGGCTGC 1523

Db 934 GACCACTTTGGCGGACAGACAGGCTGAGGATATATACGGGCTTGAACGCGGGTGC 993
 1524 CGCTGCTGAGAGTGAAGTGTGAGATGGGCGGACGAGGAGCCATTGTGCCAATGAGC 1583
 Db 994 CGCTGCTGAGAGTGAAGTGTGAGATGGGCGGACGAGGAGCCATTGTGTTCACGGA 1053
 1584 TACACTGACTTCCAGAGTCTTTCAGAAAGCTCATTTGAACCATCAACATATATGCC 1643
 Db 1054 CACACCTGACCTCCCGATCTCTTTCAGAAAGTGTGCGCCACAGATGACAGATATGCC 1113
 1644 TTTCAAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1703
 Db 1114 TTTCAAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1173
 1704 CAGAAAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1763
 Db 1174 CAGAGACCATGAGCGCGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1233
 1764 GTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1823
 Db 1234 TTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1293
 1824 GTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1883
 Db 1294 GTGAAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1353
 1884 GATGAGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1943
 Db 1354 CTTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1413
 1944 ACCAATGAAAGCTGTGAAGAAACCTGTAAGAGAAACTGTGATTCCTCAT 1996
 Db 1414 CAGAGAGCAACCTTCAAGATTAAGACAAAGAAATCCAAAGCCCATCTT 1466

RESULT 4
 US-09-908-664-3
 Sequence 3, Application US/09908664
 Patent No. US20020115178A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Meyers, Rachel
 APPLICANT: Rudolph-Owen, Laura
 APPLICANT: Tsai, Fong Yin
 TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
 FILE REFERENCE: 38155-20022.00
 CURRENT APPLICATION NUMBER: US/09/908,664
 CURRENT FILING DATE: 2001-07-17
 PRIOR APPLICATION NUMBER: US 60/218,675
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 2289
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-908-664-3

Query Match 6.7%; Score 308.6; DB 10; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 2.2e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

744 TTCCAGGCGTACCTGACGCGACGCTTCGACCCCACTGCTGCTTCGACATCTACCGCGC 803
 229 TTGCTGTGATGCTTGGAGAGAGCTCCCTCGAGCAGGCGCTTCACCATGTCTTTCAT 288
 804 AGCCACCGCGAGTGTGCTGACCTGTCTCCACGACGAGGATGAGCGGCACTGGGTC 863
 289 GCGCGCGCTCCCACTGACCTGATGGCCCAAGATGTTGAGAGGCGCCAGATATGAGATG 348
 864 ACTGCGCTGCGTCACTCATGCGCGCATGACGACGAGACAGAGCTGTGCGCGCCAG 923

Db 349 CGAGGCTCCAGCTGTTGGATCTTTGACACGATGAGACCATGAGGCGCT---- 404
 Qy 924 CGCACCAGGACCAAGTGGCTGAACAGACCTTTGACAGAGCCGACAAAGCGGATGCG 983
 Db 405 -----GGACCAATGGCTGAGCGATGGTTTCAAGTGAGAACAAATCAGATGCT 456
 Qy 984 AGCTGAGCATTTGGCCAGGCTCTGAGCTGCTGACAGCTCAACGTGAACCTGCCCGG 1043
 Db 457 AAGATGATTTCCAAAGATTCAGCGGTATTTACCTTAATGATGGAAATGACCAA 516
 Qy 1044 CAGAGGTGAAGCAGATGTTTCAAGGAAACGAGATGACCAAGGACGCTGGGT 1103
 Db 517 GAATATGCTTCACTGCTTTTTCAGGACGAGACAG---TCCAGTCTGGAACCTTGAA 573
 Qy 1104 TTTGAAGATTTCTGTGCTTTTCAAGATATGTCACCTCCGCGGACCTTACCTGCTC 1163
 Db 574 GGAGAAATTCGATCAGTTCTATTAAGGCATTTGAACGTCTGAGGAGGAGAACTG 633
 Qy 1164 ATGTGACCTTACGACCAACCAAGGACCACTGGATGCGGCGACGCTGACGCTCTG 1223
 Db 634 TTTGAAAGTTTTCAGCTGATGGGACAGAGCTGACTGCTGGAATTTTGGATTTCTC 693
 Qy 1224 CAGGTGAGCAGAAAGATGCGGGGTGAGACCTCGAGAGCTGCGAGACATCATGAGCAG 1283
 Db 694 CAGAGGAGCAGAAAGAGAGAGACTGCACTCTGAGCTTCTCTGGAACCTCATTTGACCGC 753
 Qy 1284 TTTGAGCCATGCCAGAAAACAGATTAAGGGGTGCTGGGACATTTGATGCTTACCAAC 1343
 Db 754 TATGAACTTTCAGACAGTGTGCAAACTGGCATGTGCTGATGATGATGCTTCTCAGC 813
 Qy 1344 TACACCGAGAGCCCTGCTGGTGAATCATCTTCAACCTGAGACCAACATGTCACAGAC 1403
 Db 814 TACTTCTGCTTAAGATGAGAGACATTTCAACCACTGCTGCTCCCACTTATCAGGAT 873
 Qy 1404 ATGACGAGCCGCTGAGGACCTACTTATCACTGTGCTCAACCAACTTACTGTGGGT 1463
 Db 874 ATGATCAACCCCTGAAACACTTACTTCTGCTCTTCTATTAACACTTACTGTGGGT 933
 Qy 1464 GACCACTCATGTCCCACTGACAGGCTGAGCATGTATGCTTGGGTCTGAGGCTGCTG 1523
 Db 934 GACCACTTTCGCGGACAGAGAGGCTGAGGATTAATACGGGCTCTGAAAGGGGGGTGC 993
 Qy 1524 CGCTGCTGAGGAGTGAATGCTGAGGATGGGCGGAGCGGACCTATTTGACATGCG 1583
 Db 994 CGCTGCTGAGGAGTGAATGATGAGATGAGACTTACGGGGAACCTGTCTTACACGGA 1053
 Qy 1584 TACACTCTGACTTCCAAAGATCTCTTCAAGAGCTCATTTGAACCTTACCAAAATATGCC 1643
 Db 1054 CACACCTGACCTCCCGCATCTGTTCAAAGATGCTGTCGACAGATGACACATATGCC 1113
 Qy 1644 TTTCACTGAATGAGTACCCAGTATCTGTTCATCGAAAACATGAGTGCATCCAG 1703
 Db 1114 TTTCCAGATCAGACTACCCAGTCACTTGTCTGAGAGCCACTGAGCTGGAGAG 1173
 Qy 1704 CAGAAAGAAATGGCCCACTATCTGACATCTTGGGGAACAAGTGAACCTTATCA 1763
 Db 1174 CAGCAGACCAATGGCCCTGATCTGATGATCTGAGGAGAGAGCTGCTAGACACACC 1233
 Qy 1764 GTGACAGTGAAGATGACCACTCTCTCTTCCAGATGCTCAAGGGCAAGATCTCTC 1823
 Db 1234 TTTGATGGGGTCTCCCACTCACTGCTGCTGAGAGCTTCCGAGAGAAAGTCTCTG 1293
 Qy 1824 GTTGAAGGGAAGAACTCCCGCAACATCAGCGAGAGTGGGAGAGAGGAGAGTGTCT 1883
 Db 1294 GTTGAAGGGAAGAACTTCACTTGAAGAGACCTGGAATATGAGAAAGAGAGAGAGAA 1353
 Qy 1884 GATGAGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
 Db 1354 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
 Qy 1944 ACCAATGAAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1996
 Db 1414 CAGGAGCAGAACTTCAAGATTAAGACAAAGAAAGAAATCCAACTCATTT 1466

RESULT 5
 US-09-908-664-1
 ; Sequence 1, Application US/0908664
 ; Patent No. US20020115178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura
 ; APPLICANT: Tsai, Fong Yin
 ; TITLE OF INVENTION: 16818 AND 16839, NOVEL HUMAN
 ; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 38155-20022.00
 ; CURRENT FILING DATE: US/09/908,664
 ; PRIOR APPLICATION NUMBER: US 60/218,675
 ; PRIOR FILING DATE: 2001-07-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2629
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (257)...(2545)
 US-09-908-664-1
 Query Match 6.7%; Score 308.6; DB 10; Length 2629;
 Best Local Similarity 54.2%; Pred. No. 2.3e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;
 Qy 744 TTCACGCTTACCTTGAAGGAGGAGCTTTCACACCCCACTGCTGCTGAGCATTCACAGCGC 803
 Db 485 TTGCTGCTGAGCTTGGCAGAGAGAGCTCCCTCGAGAGAGGCTTACCATTTGCTTCAT 544
 Qy 804 AGCACCAGGAGTGGCTGAGAGCTGCTTTCACACAGAGAGAGTGGCGGACCTGGGT 863
 Db 545 GGGCGCGCTCCAACTGAGACCTGATGAGCAACAGTGTGAGAGAGGCGCCAGTATGATG 604
 Qy 864 ACTGCGCTGCTTACTTATGCGCGGACATCAGCAGAGAGAGAGAGCTGCGTGGCGCAG 923
 Db 605 CGAGGCTCCAGCTGTGTGATCTTGTACACAGATGAGACATCAGAGGCTCT---- 660
 Qy 924 CGACACAGGACCAAGTGGCTGAGAGAGCTTTCAGAGGCTGACAGCTCAAGTGAACCTGCCG 983
 Db 661 -----GGACCAATGGCTGAGAGAGCTTGTTCACAGCTGAGAGACAAATATGAGATGCT 712
 Qy 984 AGCTGAGCATTTGGCCAGGCTCTGAGCTGCTGACAGAGCTCAAGTGAACCTGCCG 1043
 Db 713 AAGATGATTTCCAAAGATTCAGCGGTATTTGACCTTAATGATGAGAAATGAGACCAA 772
 Qy 1044 CAGAGGTGAAGCAGATTTTCAGAGAGAGGAGACAGAGATGACCAACAGAGAGGCTGGGT 1103
 Db 773 GAATATGCTTCAAGTCTTTTTCAGGAGAGAGAG---TCCAGTCTGAAACCTTGA 829
 Qy 1104 TTTGAAGATTTCTGTGCTTTCACAGATGATGCTCAGCCGCGGACCTTACCTGCTC 1163
 Db 830 GGAGAAATTCGATCAGATTTTAAGGATGATGATGATGATGATGATGATGATGATGATG 889
 Qy 1164 ATGTGACTTACAGCAACCAAGAGCACTGAGATGCCGACAGCTGAGAGGCTTCTG 1223
 Db 890 TTTGAAAGTTTTCAGCTGATGAGGAGAGAGCTGACTCTGGAATTTTGGATTTCTC 949
 Qy 1224 CAGGTGAGCAGAAAGATGCGGGGTGAGACCTCGAGAGCTGCGAGACATTCAGAGAG 1283
 Db 950 CAGAGGAGCAGAAAG 1009
 Qy 1284 TTTGAGCCATGCCAGAAAACAGATTAAGGGGTGCTGGGACATTTGATGCTTACCAAC 1343
 Db 1010 TATGAACTTTCAGACAGTGTGCAAACTGGCGCATGTGCTGATGATGATGATGATGATG 1069

1344 TACACGAGAGCCCTGCTGATCATCTTCAACCTGAGACCAACATGTCACAGAC 1403
1070 TACCTGCTCTAAGATGAGATCTTCAACCTGAGCTCTCCCATCTATCGAGAT 1129
1404 ATGACGAGCCGCTGAGCCATCTATCTATCCTGCTCCCAACAACCTATCTGAGT 1463
1130 ATGACTCAACCCCTGAAACCACTACTTCTCTTCTCAATACCTATCTATGAGG 1189
1464 GACCACTCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1523
1190 GACCACTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1249
1524 CGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583
1250 CGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1309
1584 TACACTCTGATCTTCAAGATCTCTTCAAGATCTCTTCAAGATCTCTTCAAGAT 1643
1310 CACACCTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1369
1644 TACATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1703
1370 TTTCAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1429
1704 CAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1763
1430 CAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1489
1764 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1823
1490 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1549
1824 GTGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1883
1550 GTGAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1609
1884 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
1610 CCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1669
1944 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1996
1670 CAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1722

RESULT 6
US-09-804-969-20
Sequence 20, Application US/09804969
Patent No. US20020081595A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomichy, Boris
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuin, Alejandro
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides En
FILE REFERENCE: LEX-0148-USA
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/188,885
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 60/189,693
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 2709
TYPE: DNA
ORGANISM: homo sapiens

US-09-804-969-20
Query Match 6.7%; Score 308.6; DB 10; Length 2709;
Best Local Similarity 54.2%; Pred. No. 2,3e-65;
Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;
744 TTCCAGGCTTACCTGAGCGGAGGATGATGATGATGATGATGATGATGATGATG 803
486 TTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 545
804 AGCCAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
546 GGGCGGCTTCAACCTGAGCTGATGATGATGATGATGATGATGATGATGATGATG 605
864 ACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 923
606 CAGAGGCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 661
924 CGCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 983
662 -----GACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 713
984 AGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1043
714 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 773
1044 CAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1103
774 GAATATCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 830
1104 TTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1163
831 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 890
1164 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1223
891 TTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 950
1224 CAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1283
951 CAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1010
1284 TTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1343
1011 TATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1070
1344 TACACGAGAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1403
1071 TACCTGCTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1130
1404 ATGAGCAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1463
1131 ATGACTCAACCCCTGAAACCACTACTTCTCTTCTCAATACCTATCTATGAGG 1190
1464 GACCACTCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1523
1191 GACCACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1250
1524 CGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583
1251 CGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1310
1584 TACACTGATCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1643
1311 CACACCTTACCTCCGATCTCTTCAAGATGATGATGATGATGATGATGATGATGATG 1370
1644 TTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1703
1371 TTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1430
1704 CAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1763
1431 CAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1490

QY 1764 GTGAGCAGTGAAGATGCAACCACTCCCTCTCCACAGATGCTCAAGGGCAAGATCTTC 1823
DB 1491 TTGATAGGGGTGCTGCTCCACTCAGTCCCTCCCTGAGAGCTTTGAGAGAGATCTTC 1550
QY 1824 GTGAGGGGGAAGAGCTCCAGCCCAATGACGAGATGCGAGAGAGAGAGAGTGTCT 1883
DB 1551 GTGAGGGGGAAGAGTAACTTGAACCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1610
QY 1884 GATGAGCAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
DB 1611 CTGAGTGTGAAGAGTCAATTTGCGCTGAGTCCAGTGTGAGCTGAGCTGAGCC 1670
QY 1944 ACCAATGGAAGCTGTGAAGAACCTGCTAAGAGAGAGAGAGAGAGAGAGAGAG 1996
DB 1671 CAGAGCAGAACCTTCAGATTAAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAG 1723

RESULT 7

US-09-835-996A-7
Sequence 7, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyen
APPLICANT: Qian, Xiaohong
APPLICANT: Mang, Duntui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835, 996A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714, 936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667, 298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631, 451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598, 042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 1840
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (140)..(1840)
US-09-835-996A-7

Query Match 6.6%; Score 307; DB 10; Length 1840;
Best Local Similarity 54.1%; Pred. No. 5.2e-65;
Matches 678; Conservative 0; Mismatches 560; Indels 15; Gaps 2;
QY 744 TTCAGCGCTACCTGAGCGAGCTTGCAGCCCACTGCTTCAAGCATATACAGCGC 803
DB 368 TTGCTGCGTGAAGCTGAGAGAGAGCTCCCTGAGAGAGAGAGAGAGAGAGAGAGAG 427
QY 804 AGCCAGCGGAGTCCGTGAGCTGTCTTCACAGAGAGAGAGAGAGAGAGAGAGAGAG 863
DB 428 GGCCGCGCTCCAGCTGAGCTGATGAGCAAGGTGTTGAGAGAGAGAGAGAGAGAGAG 487

QY 864 ACTGCTCCGCTTACCTTATGCGCGGATCAGCGAGAGAGAGAGAGAGAGAGAGAGAG 923
DB 488 CGAGGCGCTCCAGCTGTGTGTGATCTTGTGACCCAGATGAGCATCAGAGAGCGCT---- 543
QY 924 CGCACAGAGAGACAGTGTCTTAAGACAGAGCTTTTACAGAGCGCCGCAAGAGAGAGAG 983
DB 544 -----GGACCAATGAGCTGAGAGATTTGTTTCAAGTGAAGCAAAATCAGAGATGT 595
QY 984 AGCCGAGCATTTGGGAGAGGTCTGAGCTGCGCAAGAGCTCAAGTGAAGCTTCCCGG 1043
DB 596 AAGATGAGTTTCAAGAGAGTTCAGAGGTTTATTTGACCTTAATGATGGAATGAGACCA 655
QY 1044 CAGAGGTGAAGCAGATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
DB 656 GAATATGCTTCAAGCTTTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
QY 1104 TTTGAGAGTGTGTGCTTTTCAAGAGATGATGTCACCCGCGGAGAGCTTACCTGCTC 1163
DB 713 GAGAGAGAGATTCGATCAGATTTATTAAGAGATTTGAAGAGTGTGAGTCAAGAGAG 772
QY 1164 ATGCTGACCTACAGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
DB 773 TTTGAAAGTTTTCAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
QY 1224 CAGGTGAGCAG 1283
DB 833 CAAAG 892
QY 1284 TTTGAG 1343
DB 893 TATGAAGCTTCAG 952
QY 1344 TACACAG 1403
DB 953 TACCTGTGCTTAAG 1012
QY 1404 ATGAGCAG 1463
DB 1013 ATGACTCAACCCCTGAAACCACTTCACTGCTCTTCTTCAACCACTTCACTTGTGGG 1072
QY 1464 GACAGCTATGCTCCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
DB 1073 GACAGCTTGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1132
QY 1524 CGTGTGAG 1583
DB 1133 CGTGTGAG 1192
QY 1584 TACACTCTGACTTCAAGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
DB 1193 CACACCTGACCTCCGCACTCTGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1252
QY 1644 TTTATCAAGATGAGTACCAAGTATCTGTCATGCAAGAGAGAGAGAGAGAGAGAG 1703
DB 1253 TTTCAAGATCAGACTTCAAGTATCTGTCATGTCATGCAAGAGAGAGAGAGAGAG 1312
QY 1704 CAG 1763
DB 1313 CAG 1372
QY 1764 GTGAG 1823
DB 1373 TTGATAGGGGTGCTGCTCCACTCAGTCCCTGCGCTGAGAGAGAGAGAGAGAGAG 1432
QY 1824 GTGAG 1883
DB 1433 GTGAG 1492
QY 1884 GATGAGCAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
DB 1493 CTGAGTGTGAAGAGTCAAGATTTGGCGCTGAGAGTCCAGTTTGAAGAGAGAGAGAG 1552

FEATURE:
; NAME/KEY: CDS
; LOCATION: (153) ... (2360)
US-09-800-971-1

Query Match 5.5%; Score 301.8; DB 10; Length 3425;
Best Local Similarity 54.0%; Pred. No. 1.1e-63;
Matches 743; Conservative 0; Mismatches 607; Indels 27; Gaps 5;

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QY 545 GGTGAGCGGTGATGGTCCATGCAAGAGGAGATGCAAGTGTAAAGTCTGTCGCG 604
DB 164 GAGAGAGAGAGAGTGTGGCCATGCTGGGGCTCCGGCTCCGCAAGATCCGCTCGCG 223
QY 605 CTCCAGAGGCTGTGCTGCTTTACTTACTTGAACGAGAC-----CGCTCCGCAATCCG 658
DB 224 CAGGTGCAACAAGAGCGGCTGTACCGGCTGCAAGAGAGAGCGCTGAGCTGTGTTCGA 283
QY 659 CTGAGGCGCTTCAACGAGAAACGAGAGGCAAGATCTTCATGCACTCCAGAGAGGT 718
DB 284 GCGGCGCATCCGCTGCGGCGCATGCGACATCTTCTGTGCAAGACATCGAGGGGT 343
QY 719 GAGTGAAGGCGGCGAGTCGAGAGTCTTTCAGCGCTACCTGACGCGACTTTCAGCCCAA 778
DB 344 CCGGAGAGGCGCACAGTCCAGAGGCGCTGCGGCGCTTC---GGGGGTGCTTTCGCGCAGC 400
QY 779 CTGCTGCTTACGATCTTACCAACGCGACCCAGAGTCCGTGAGCTTCCACAG 838
DB 401 GCGCTGCTTCAACCTTCCTTCAAGGCGCGCGCAAGAACTTGAACTTGGGCGGCCAC 460
QY 839 CAGGAGGTGCGCGCACCTGAGTCACTGCGCTGCTACCTCATGCGCGCATCAGCGA 898
DB 461 GCGTGAAGAGCGACGCGCTGGGCTGCGCGCTTCAACAGTCCGCGCGCGCTGAGCGC 520
QY 899 CGAGAGCAGCCTGCTGCGCGCGCACGCGCACAGGAGACCAAGTGTGAAGCAGCTTGA 958
DB 521 CATGAGCGAGGCGGCGGCT-----AGACCACTGAGATTCACCTCTATCTGCA 568
QY 959 CGAGGCGCAACAAGCGGGGATGCGAGCTTGGAGATTTGGAGGCTTCGAGCTGCTGCA 1018
DB 569 CCGGCTTACTTCAACGAGACAGAGATGAGCTTCAAGAGATCAAGAGCTGCTGAG 628
QY 1019 CAAGCTCAACGTGAACCTGCGCGGCAAGAGGAGTGAAGCAGATGTTTCAGAGGAGCGGAC 1078
DB 629 AATGATCAACGTGAGATGAAGAGATGATAGGCTTCTCTTCAAGAGAGTGTGAC-- 686
QY 1079 GGATGACCAACAAGAGCGCTGGGTTTGAAGATTTGTGCTTCTTCAAGATGATGTC 1138
DB 687 -CACTCCAACAACGACCGTCTAGAGGGGCTGAGATCGAGAGTTCGCGCGGCTGCT 745
QY 1139 CACCGCGCGGAGCTTCACTGCTCATGCTGACCTACAGCAACCAAGACCACTGGA 1198
DB 746 GAAAGCGCGGAGCTGAGAGAGATTTTCATATGATCTCGGCGAGAGACCGCTGTAG 805
QY 1199 TCCCGCCAGCTGCAAGCGCTTCTCAGGTGAGCAAGATGCGGGGTGTGACCTTGA 1258
DB 806 TCCCTTGAAGCTGTGAGATTCCT---GGAGGACCAAGGCGGAGGCGGCACTGCGC 862
QY 1259 GAGCTGCCAGGACATATGAGACAGTTTGAAGCATGCCCCAAGAAAACAAGATGAAGGGCT 1318
DB 863 CCGCGCGCGAGGCTCATTCAGACCTATGAGCTCAACGAGACGCAAGACAGACATGAGGT 922
QY 1319 GCGTGGCATTTGATGGCTTACCAACATACCAAGAGCGCTGCTGTGACATTTCAACC 1378
DB 923 GATGACACTGATGCTTATGATGATGATCTGTGTGCGCGAGGGGGGCTGCTTGAACA 982
QY 1379 TGAGCAACAACATGTGACACAGACATGACGAGCGCGCTGAGGCACTACTTATCACTC 1438
DB 983 CACCAACAGGTGTGTCTCAGAGACATGAACGAGCGCTTGGCCACTACTTCTTCTTC 1042
QY 1439 GTCCCAACAACCTACTCTGTGTGTGACAGGCTCATGTCCAGTCAACGGGTGAACATGA 1498
DB 1043 CTCACAACAACCTATCTGATGATCTCCAGATGCGGGGGCGGACAGACGAGGCGCTA 1102

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QY 1499 TGCTTGGTCTTCGAGAGGCTGCGCTGCGTGTGAGGTGACTGTCTGGATGGGCCGA 1558
DB 1103 TGTTAGGGCTTTTGCCAGGAGATCCGCTGTGTGAGTGTGATGCTGGAGGGGCGAGG 1162
QY 1559 CCGGAGGCCCATTTGTGACCATTTGCTACACTTGAACCTTCAAGATCTCTTCAAGAGCT 1618
DB 1163 AGGGAGGCCCTGTATCTATGATGAGCCATACCTTCAAGATTTCTTTCGGGAGCT 1222
QY 1619 CATTGAACCATCAACAATATGCTTTCATCAAGATGATGATGATGATGATGATGATGAT 1678
DB 1223 GGTCCAGGCTGCGGCGGACCATGCTTTCAGCTGTCCCTTACCTGTATCTATCCCT 1282
QY 1679 CGAAAAACATGCTGCTGATCTGATCAGAGAGAAATATGCTTCAAGTGTGATGATCT 1738
DB 1283 GGAAGAACCATGCTGCGGCTGAGACAGGCTGCGCATGCGCCGCGCATCTTGCACATCT 1342
QY 1739 TGGGACAAAGCTGACCTGTATCATGAGAGAGTGAAGATGCAACACATCCCTCTCC 1798
DB 1343 GGGGACATGCTGTGTGACACAGGCGCTGACCTCCCAATTCGAGAGCTGCTATCC 1402
QY 1799 ACAGATGCTCAAGGCGCAAGATCTCTGTGAAGGGAGAAAGCTCCCAACATCAGCGA 1858
DB 1403 AAGACAGCTGAAGGCGCGGCTCTGTGAGAGGAAAGAGCTGCGCGCTGCTGAGCGA 1462
QY 1859 GGAATGCGAGAGAGGCGAGGTGTCTGATGAGAGACGTCTGATGATGATGATGATGA 1915
DB 1463 GGATGGCGCGGCTCTGTGTGATGAGAGAGAGAGAGAGATGACGAGAGAGAGA 1519

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RESULT 10

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US-09-880-107-3293
; Sequence 3293, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3293
; LENGTH: 2627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U09117
US-09-880-107-3293

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Query Match 6.3%; Score 289.8; DB 10; Length 2627;
Best Local Similarity 54.2%; Pred. No. 8.2e-61;
Matches 744; Conservative 0; Mismatches 587; Indels 42; Gaps 6;

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QY 564 GCCATGCAAGAGGAGATGAGATGAGAGCTGTCGCGCTCCAAAGGCGCTGTCCGC 623
DB 155 GCGCTGTGAAGGACACCGAGCTCTGAAGGTGAAGTCCAGCTCATGAGAGAGAGCGG 214
QY 624 TTCTACTACTGACGAGACCGCTCTGATCCG-----CTGAGGCGCTTACGCG 674
DB 215 TTCTACAAAGTTGACGAGAGGACTGCAAGACCATGCGAGAGAGTCCGCAAGATCAGCGG 274
QY 675 AAGAACGAAAGGCAAGATTCATGATGATCTCATTCAGAGAGTGTGAGGGGCGGAG 724
DB 275 ACCCGAGGTCCCAAGCTGTCTTCATGAGAGCATTTAGAGAGGTGCAATGGGGCACCG 334
QY 735 TCGAGGCTTTCAGCGCTACCTGACGAGAGCTTCAGACCCAACTGCTTCAAGATC 794

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QY 1019 CAAGCTCAAGTGAACCTGCCCCGAGAGAGGTGAAGACAGATGTTCAAGGAAACGAGAC 1078
 Db 763 AATGCTCAAGTGAACCTGCCCCGAGAGAGGTGAAGACAGATGTTCAAGGAAACGAGAC 820
 QY 1079 GATGACCAACCAAGGAGACGCTGGGTTTGAAGATTCTGTGCTTCTTCAAGATGATGTC 1138
 Db 821 -CACTCCAAACCAAGGAGACGCTGGGTTTGAAGATTCTGTGCTTCTTCAAGATGATGTC 879
 QY 1139 CACCCGCGGGAGCTTACTGCTGCTGACCTTACAGAACCAAGACCAAGACCACTGGA 1198
 Db 880 GAAGCGGCGGAGCTGAGAGGATCTTCAATCAGTACTCGGGGAGAGCCGCTGTGAG 939
 QY 1199 TGCCGCGAGCTGCTGAGGCTTCTGAGGTGAGAGAAAGATGGCGGTGTGACCTTCGA 1258
 Db 940 TGCCGCGAGCTGCTGAGGCTTCTGAGGTGAGAGAAAGATGGCGGTGTGACCTTCGA 996
 QY 1259 GAGCTGCGAGGACATCATCAGAGAGTTTGAAGCCATGCCCCAAGAAACAGATGAGGCT 1318
 Db 997 CCGGGCCAGACGCTCATTCAGACCTTATGAGCTCAACAGACAGCCAGACGATGAGCT 1056
 QY 1319 GCTGGGATGATGAGCTTCAACCACTTACACAGAGAGCCCTGCTGTGACATCTTCAACC 1378
 Db 1057 GATGACCACTGATGAGCTTCAATGATGATCTGTTGTGCGCGAGAGGAGCTGCTTGAACA 1116
 QY 1379 TGAGCACCAACATGTCAGACAGGACATGACGAGCCGCTGAGCCACTTCACTTCACTTC 1438
 Db 1117 CACCCACACGCTGTGTCTTCAAGAGACAGAACGAGCCCTTGTCCCACTTCACTTCACTTC 1176
 QY 1439 GTCCCAACACCTTACTCTGTGTGTCACAGCTCATGTCCCACTGACGAGGTGACATGTA 1498
 Db 1177 CTCCCAACACCTTACTCTGTGTGTCACAGCTCATGTCCCACTGAGGAGCCAGACGACCA 1236
 QY 1499 TGCT-----TGGGTCTGAGAGGCTGTGCGGCTGTGAGGAGGAGCTG 1543
 Db 1237 TGTTAGTACTGTAAGAGGAGGAGGCTTGTGCGGAGAGGAGGAGGAGGAGGAGGAGGAG 1296
 QY 1544 CTGGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1603
 Db 1297 CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1356
 QY 1604 CCTTTCAAGAGCTCATTTGAACCATCAACAAATATGCTTCTCATCAAGATGATGATGCC 1663
 Db 1357 TCTTTCCGGAGCTGTGTCAGAGCCGTGCGGAGCATGCTTCAAGCTGTCTTCCCTTATCC 1416
 QY 1664 AGTATCTCTGCTCATGAAAACCATGCACTGAGTGTATCCAGAGAGAAATGAGCCAGTA 1723
 Db 1417 TGTATCTCTTCTCTGAGAACCACTGCGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAG 1476
 QY 1724 TCTGACGACATCTTGGGAGCAAGCTGACCTGTCTATCAGTGAAGTGAAGTGCAC 1783
 Db 1477 CCTGTCACATCTTGGGAGCAAGCTGACCTGTGTGTACACAGGCGGTGAGCTCCCAATTC 1536
 QY 1784 CACACTCCCTCTCTCAAGATGCTCAAGGAGAGATCTCTGTGAAGGAGAGAGTCTCC 1843
 Db 1537 GAGGCTGCTATCCCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1596
 QY 1844 AGCCAACTCAAGAGAGTGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1903
 Db 1597 CGCTGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1656
 QY 1904 GATTGACGATGA 1915
 Db 1657 CGAGAGAGAGAG 1668

RESULT 12
 US-09-728-952-64
 ; Sequence 64, Application US/09728952
 ; Patent No. US20020111302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Y. Tom
 ; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Kyle
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yamazaki, Yuki
 ; APPLICANT: Ujwal, Manusha U.
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. US20020111302A1 Nucleic Acids and
 ; FILE REFERENCE: 799
 ; CURRENT APPLICATION NUMBER: US/09/728,952
 ; CURRENT FILING DATE: 2000-11-30
 ; NUMBER OF SEQ ID NOS: 101
 ; SOFTWARE: pc_Fl_genes Version 2.0
 ; SEQ ID NO 64
 ; LENGTH: 3068
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (128)..(2512)
 US-09-728-952-64

Query Match 6.0%; Score 276.8; DB 10; Length 3068;

Best Local Similarity 53.4%; Pred. No. 1.2e-57; Mismatches 607; Indels 42; Gaps 6;

QY 545 GGTGAGGCGGTGCATGAGTGCATGCAAGAGGAGATGAGATGAGTGAAGTGTGAGCGG 604
 Db 298 GAGAGACAGAGACGATGCGGCGCATGCTGCGGCGCTCCGCGTCCGCAAGATCCGCTGCG 357
 QY 605 CTCAAGGCGCTGTGCTCGCTTCTACTACTGAGAGAGC-----CGCTCTGATCCG 658
 Db 358 CAGTGGACAGAGAGCGGCTGTACCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 QY 659 CTGAGAGCCCTTACCCAG 718
 Db 418 GCGGCGCATCCGCGTGGCGCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
 QY 719 GAGTGAAGGAGGAG 778
 Db 478 CCGAGAGGAG 534
 QY 779 CTGCTGCTTCAAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 838
 Db 535 GCGCTGCTTCAAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594
 QY 839 CAGCAGAGTGGGCGGAG 898
 Db 595 GCGTGAAG 654
 QY 899 CGAG 958
 Db 655 CATGAG 702
 QY 959 CGAGGCGGAG 1018
 Db 703 CCGGCTGACTCCAAACAG 762
 QY 1019 CAAGCTCAACGTGAACTTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078
 Db 763 AATGCTCAACGTGAGATGAACGATGATGATGATGATGATGATGATGATGATGATGATG 820
 QY 1079 GATGACCAACCAAGGAGACGCTGGGTTTGAAGATTCTGTGCTTCTTCAAGATGATGTC 1138
 Db 821 -CACTCCAAACCAAGGAGACGCTGGGTTTGAAGATTCTGTGCTTCTTCAAGATGATGTC 879
 QY 1139 CACCCGCGGGAGCTTACTGCTGCTGACCTTACAGAACCAAGACCAAGACCACTGGA 1198
 Db 880 GAAGCGGCGGAGCTGAGAGAGATCTTCCATCAGTACTCGGCGAGAGAGAGAGAGAGAG 939
 QY 1199 TGCCGCGAGCTGACAGCGCTTCTGAGGTGAGAGAGAGATGAGGAGGAGTGTGATCGA 1258

Db	940	TCGCCCTGAGCTGCTGAGATTCTCT---GGAAGA-CGAGGGGAGAGAGGGGCCCAACTGGCC	996
Qy	1259	GAGCTGCGCAGAGACATCATCGACAGCTTTGAGCCATGCCAGAAAACAAGATGAGGGGCT	1316
Db	997	CGGCCCCCAGCAGCTCATTTCAAGCCCTTAGAGCTTACGAGACAGCAAGAGCATGAGCT	1056
Qy	1319	GCTGGGCACTGATGAGCTCTTCAACCAACTACACGAGAGGCCCTGAGTGACATCTTCAACC	1376
Db	1057	GATGACACTGAGATGGCTCTCATGATGATCTTGTGTCCGCCGAGAGGGGCTGCTTTGACAA	1116
Qy	1379	TCAGCAACCAATGTGACACGAGACATGACGACCCGCTGAGCACTTACCTTCACTTC	1433
Db	1117	CACCCACAGTGTGTGTTCCAGAGACATGAAACAGGCCCTTGCCCACTACCTTATCTCTTC	1176
Qy	1439	GTCCCAACAACCTACCTCGTGGGTGACCAAGCTCATGTCTCCATCTACGGGTGACATGTA	1499
Db	1177	CTCCCAACAACCTATCTGACTGACTCCCAAGATCGGGGGGCCAGAGACGAGAGCCTTA	1236
Qy	1499	TGCT-----TGGGTCTGACAGGCTGCGCTGCGCTGAGTGAAGTGAAC	1543
Db	1237	TGTTAGTACTGTAGCAGAGGGGGGCTTTGGCCAGAGGATGCCGCTGCTGAGACTGACTG	1296
Qy	1544	CTGGGATGGGCCCGACGGGGAGCCCATATTGTGACCAATGAGCTACCTTCAAGAT	1603
Db	1297	CTGGGAGGGGGCAGAGAGGGGGCCCGCTCATCTTATGAGCCATACTCTCACTCCAGAT	1356
Qy	1604	CCTCTTCAAAAGCGCATGTGAAACCATCAACAAATATGCTTCATCAAGATGACTACC	1666
Db	1357	TCTCTTCCGGGACGTGGTTCAGGCCGTGCGGACCATGCTTACCGCTTCTCCCTTACC	1416
Qy	1654	AGTGATCTGTGCATTCGAAAACCACTGCAGTGTCACTCAGCAGAAAGAAATGGCCAGTA	1723
Db	1417	TGTCACTCTTATCCCTGGAGAACCACTGCGGGCTGGAGACAGCAGCGTCATGGCCCGCA	1476
Qy	1724	TCTGACTGACATCTCTGGGGACAAGCTGGAACCTGTCTATCAATGATGAGCATGAAAGTCCAC	1783
Db	1477	CCTTCGACACATCTCTGGGGACAAGCTGATGACACAGCGCTGGAATCTCCCAATTCGGA	1536
Qy	1784	CACACTCCCTCTCCACAGATGTCCAGAGGCAAGATCTCTGGAAGGGGAAAGACTCC	1843
Db	1537	GGAAGTGCATCTCCCAAGACAGCTGAAAGGGCCGGGTCTCTGTGAAAGGAAGAACTCC	1586
Qy	1844	AGCCAACTACGCGAGGATGCGGAGGAAGGCGAGGTGTCTATGAGACAGTGTCTGATGA	1903
Db	1597	CGCTGCTCGAGCGAGGATGGCGGGCTCTGTGGAATCGGAGAGGAGAGAGAGATGA	1656
Qy	1904	GATTGACGATGA 1915	
Db	1657	CGAGAGGAGAA 1668	

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RESULT 13
US-09-764-868-24
; Sequence 24, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c

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; NAME/KEY: SITE
; LOCATION: (1238)
; OTHER INFORMATION: n equals a,t,g, or c
;
; NAME/KEY: SITE
; LOCATION: (542)
; OTHER INFORMATION: n equals a,t,g, or c
;
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
;
US-09-764-868-24

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Query Match	4.28;	Score 195.4;	DB 9;	Length 567;
Best Local Similarity	70.98;	Pred No 4	70-38;	

Matches 270; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

Qy	699	ATGACATCCATCCAGAGAGTGTAGAGAGGCGGAGTCGAGGCTTCCA -GGCTACCC	75
Db	187	ATTGATTTCCATTTTCAAAGATGACTGAGGGCCGGAGCTTGAAATATTTCCNCTTACAAGC	246
Qy	758	TGACGGACGTTTCGACCCCACTGCTGCTTCAGCATCTACACGCGAGCCACCGGAGTC	817
Db	247	TGAGGGGAACTTCGACCCGAGCTGTGTTCCATCTACATGGAACCATGAGATC	306
Qy	818	GCTGGAACCTTGCTTCACACGAGAGCGAGTGGGCGCACCTGGGTCACTGGCTGCGCTA	877
Db	307	CTGGAACCTTCATCACCTTCCAACCCCGAGGAGGCCGACCTGGATTCACAGGCTCTAAGTA	366
Qy	878	CTCATAGGCGGGCATTCACGCGACGAGGACACACCTGGCTCGCCCGCCAGCGACCCAGGAGACA	937
Db	367	CTTGATGGCTGGCACTACGTGATGAAAGCTCCCTTGGCCAAAAGCGAGAGGCCCATGACCA	426
Qy	938	GTGCTGTAAGCAGACGTTTGAACGAGCGCCCAACAAGACGGGGATGGCAGCTGAGCATTTGG	997
Db	427	ATGGGTGAAGAGAGACCTTTGAGAGAGCTGATTAAGATGGTGAACGGCTTGCTGAAATATTTGA	486
Qy	998	CGAGGTCCTGCGACGCTGCTGCAACAAGCTCAACGTGAACCTTGCCCGGCGAGAGGGTGAAGCA	1051
Db	487	AGGATACATCTGCGATGAGCACTAACTGAATGTATCTGCCCCGAGAAAAGTCGACCA	546
Qy	1058	GATGTTCCAGGAGCGGACAC	1078
Db	547	AATGTTTCANAGAGCCGACAC	567

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RESULT 14
US-09-955--999-31
; Sequence 31, Application US/099555999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptides
; TITLE OF INVENTION: Antibodies, and Methods Based Thereon
; FILE REFERENCE: PT086P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (238)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (542)
; OTHER INFORMATION: n equals a,t,g, or c

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NAME/KEY: SITE
LOCATION: (556)
OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-31

Query Match 4.2%; Score 195.4; DB 9; Length 567;
Best Local Similarity 70.9%; Pred. No. 4.7e-38;
Matches 270; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

QY 699 ATGACCTCCATCCAGAGTGAAGAGGAGCGAGCTCGAGGTCTTCCA-GCGTACCC 757
DB 187 ATTGATTCCTTTACAAAGTGAAGAGGCGCGAGCTTAAATATTCNCNTTACAGC 246
QY 758 TGACGAGCTTGACCCCACTGCTTTCAGCATTCACAGGACCGACCGAGTC 817
DB 247 TGAGGGAGCTTGACCCCACTGCTTTCAGCATTCACAGGACCGACCGAGTC 306
QY 818 GCTGACCTGTCTCCACAGCAGCGAGGCGGCGGCTGCTGCTGCTGCTGCTGCT 877
DB 307 CTGAGCTTCATCACTCCAAAGGAGGAGGCGGCGGCTGCTGCTGCTGCTGCTGCT 366
QY 878 CCGATGAGCGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 937
DB 367 CCGATGAGCGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426
QY 938 GTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 997
DB 427 ATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486
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RESULT 15

US-09-835-996A-18

Sequence 18, Application US/09835996A

Patent No. US20020142953A1

GENERAL INFORMATION:

APPLICANT: Ballinger, Dennis

APPLICANT: Loeb, Debra

APPLICANT: Montgomery, Julie

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Aundt, Vinod

APPLICANT: Zhao, Qing

APPLICANT: Wehrman, Tom

APPLICANT: Drmanac, Radoje

APPLICANT: Ren, Feiyang

APPLICANT: Qian, Xiaohong

APPLICANT: Wang, Dunru

TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM

FILE REFERENCE: 28110/35915A

CURRENT APPLICATION NUMBER: US/09/835, 996A

CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: US 60/197,137

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: US 09/714,936

PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: US 09/667,298

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US 09/631,451

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 09/598,042

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 45

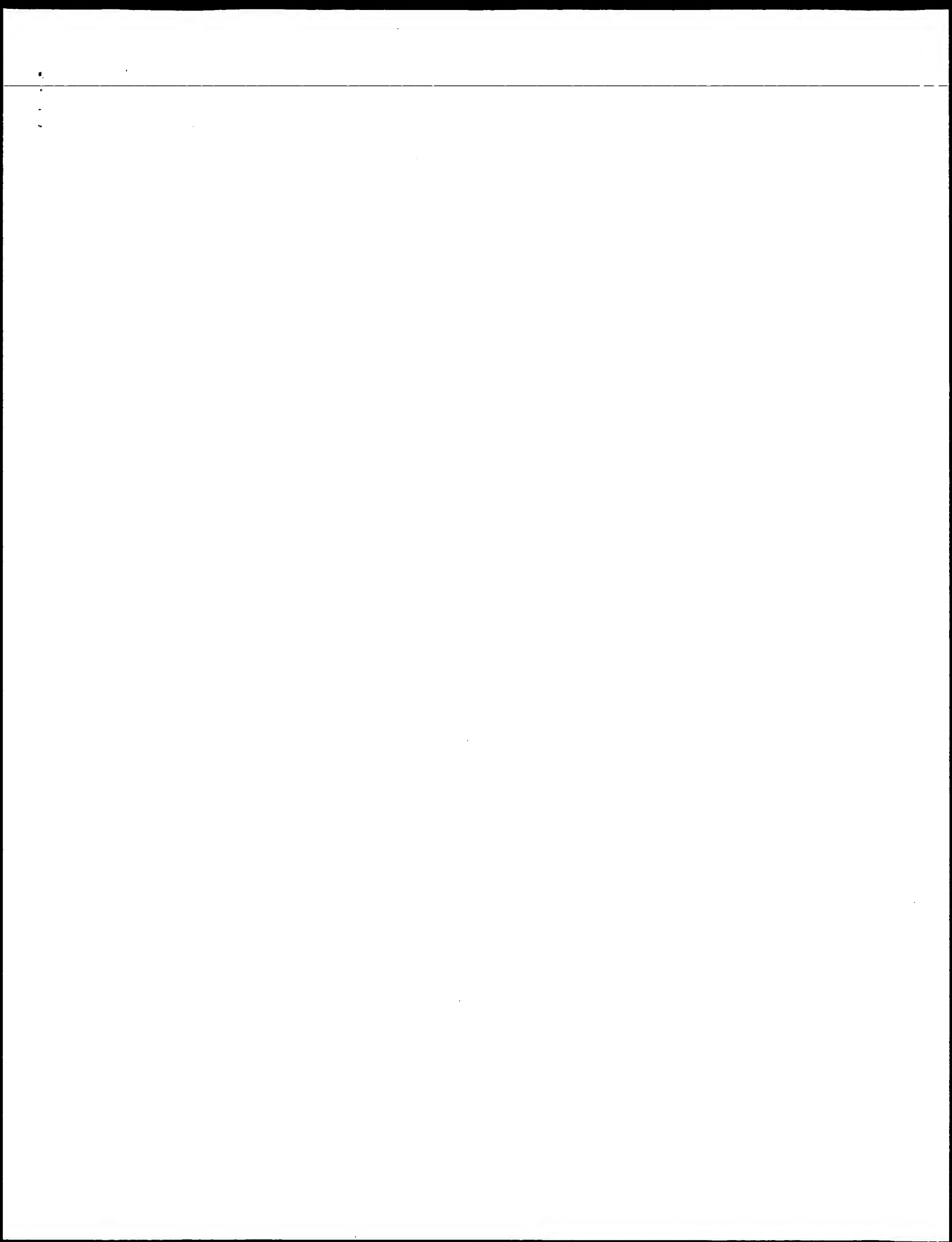
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LOCATION: (151)..(1170)
US-09-835-996A-18

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Job time : 449 secs



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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

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41: em_hgt_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2274	49.1	4411	6 AK074149	AK074149 Homo sapi
3	2112	45.6	2243	6 AX402958	AX402958 Sequence
4	1579	34.1	6551	6 AX392825	AX392825 Sequence
5	1446	31.2	6946	6 AB007919	AB007919 Homo sapi
6	1446	31.2	154736	9 AL139246	AL139246 Human DNA
7	861	18.6	2480	9 BC019679	BC019679 Homo sapi
8	242	5.2	106323	9 AL513477	AL513477 Human DNA
9	97	2.1	245	11 HS776M4T	HS776M4T Mus muscu
10	62	1.3	976	10 MM0296951	MM0296951 Mus muscu
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13	28	0.6	621	9 HSA338904	HSA338904 Homo sapi
14	24	0.5	176291	2 AC023583	AC023583 Homo sapi
15	23	0.5	17863	2 AC121463	AC121463 Rattus no
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17	22	0.5	1525	9 AF110821	AF110821 Homo sapi
18	18	0.5	2419	9 HSM800908	HSM800908 Homo sapi
19	22	0.5	2512	4 OCPLCMR	OCPLCMR Homo sapi
20	22	0.5	2614	17 AF111852	AF111852 Homo sapi
21	22	0.5	3111	9 HSG6PT2	HSG6PT2 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 10 from Patent WO0185956.
ACCESSION AX304472
VERSION AX304472.1 GI:17383843
KEYWORDS
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ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE
1 Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Tribouley, C.M.,
Yue, H., Khan, F.A., Gandhi, A.R., Au-Young, J., Lai, P., Kearney, L.,
Elliot, V.S., Ding, L. and Thornton, M.

TITLE Lipid metabolism enzymes
JOURNAL Patent: WO 0185956-A 10.15-NOV-2001;
Incyte Genomics, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db xref="taxon:9606"
/note="Incyte ID No: 7472768CB1"
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1127 CAAGATGATGTCACCCGCGGGACCTTACCTGCTCATGCTGACGCTTACAGCAACCA 1186
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AUTHORS	Tang, Y.T., Azimzai, Y., Das, D., Thornton, M., Lu, D.A., Tribouniey, C.M., Yue, H., Gandhi, A.R., Walia, N.K., Khan, F.A., Lu, Y., Yao, M.G., Hatalib, A.J., Elliott, V.S., Patterson, C., Lal, P., Ramkumar, J., Nguyen, D.B. and Baugh, M.R.					
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 REFERENCE
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 Griffith, J.A., Patterson, C., Gandhi, A.R., Lu, Y., Yao, M.G.,
 Baughn, M.R., Walla, N.K., Hatfield, A.J., Ding, L., Tribouley, C.M.,
 Das, D., Thornton, M., and Lal, P.
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 JOURNAL Lipid metabolism enzymes
 Patent: WO 0216597-A 12-28-FEB-2002;
 Incyte Genomics, Inc. (US)
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VERSION	AL139246.20	GI:16973797			
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SOURCE	human.				

REFERENCE 1 (bases 1 to 154736)
AUTHORS Moore, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,

COMMENT On Nov 17, 2001 this sequence version replaced gi:15912352.

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPep; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Ch1>

RP3-395M20 is from the library RPCT-3 constructed by the group of Plier de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-395M20. The true left end of clone RP4-755G5 is at 90075 in this sequence. The true right end of clone RP4-755G5 is at 90078 in this sequence. The true right end of clone RP11-361M21 is at 135438 in this sequence.

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source

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QY 3502 GCGCGCGCGTGAACACCGGGGCTTGCAGAGGAGCGGCCACCCGCGCGGCGCTTGC 3561
DB 55720 GCGCGCGCGTGAACACCGGGGCTTGCAGAGGAGCGGCCACCCGCGCGGCGCTTGC 55779
QY 3562 GAGAGCGAGCGACCTTGGCGCAGAGCCCGCGGCGCTGACTCAGTGGGGGCCCTT 3621
DB 55780 GAGAGCGAGCGACCTTGGCGCAGAGCCCGCGGCGCTGACTCAGTGGGGGCCCTT 55839
QY 3622 GCTGTGGCTTGAACCTTCACTGCTTCCGAGGAGAGAGCGGCCCAAGGGTCTCTG 3681
DB 55840 GCTGTGGCTTGAACCTTCACTGCTTCCGAGGAGAGAGCGGCCCAAGGGTCTCTG 55899
QY 3682 GGGGCTGAGAGCGAGGTTCAGAGCGGTGAGCGGTTCATGTCTCCGAGCTCAGAGCCG 3741
DB 55900 GGGGCTGAGAGCGAGGTTCAGAGCGGTGAGCGGTTCATGTCTCCGAGCTCAGAGCCG 55959
QY 3742 ACAAGCCGAGCATCCCGAAAGGTCCCGCGTGGCGCTGAGGAGTGGCTTGCAGCA 3801
DB 55960 ACAAGCCGAGCATCCCGAAAGGTCCCGCGTGGCGCTGAGGAGTGGCTTGCAGCA 56019
QY 3802 GGGGCTTGCAGAGAGATGATGCTTTGTTGCTCAAAAGCTGAGAGAGATCAGAGTA 3861
DB 56020 GGGGCTTGCAGAGAGATGATGCTTTGTTGCTCAAAAGCTGAGAGAGATCAGAGTA 56079

QY 3862 AATCCCCCATGTTCTCCGCGGTAAAGCCCTCTTCCCTGCGTGTCTCCCGACGCC 3921
DB 56080 AATCCCCCATGTTCTCCGCGGTAAAGCCCTCTTCCCTGCGTGTCTCCCGACGCC 56139
QY 3922 CTGGAGAGGCTGGGCTTGGGTACCTGTCTGCTTCTGCTGAGACGAGTGTGGCTGTG 3981
DB 56140 CTGGAGAGGCTGGGCTTGGGTACCTGTCTGCTTCTGCTGAGACGAGTGTGGCTGTG 56199
QY 3982 TGCTGTGCTGTGGCTGTGATCCGAGGAGCATGTGTCCTGGGACATCTGCTTGGC 4041
DB 56200 TGCTGTGCTGTGGCTGTGATCCGAGGAGCATGTGTCCTGGGACATCTGCTTGGC 56259
QY 4042 TTGCTGTGAGCCCATAGGCCCGACGCTCTCTGCTGAGCTTGAAGCCCTTGGAGTG 4101
DB 56260 TTGCTGTGAGCCCATAGGCCCGACGCTCTCTGCTGAGCTTGAAGCCCTTGGAGTG 56319
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DB 56380 CCGGACATGTGGCTGACATGCTGGGCGCCCTCGGCTGGGCGCTTCCCAATCAGCTTC 56439
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QY 4282 CATCCCATTCACCTCTCTCTTGAAGGAGGCTTCAGAGGCTCCCTTCTGGGAAGTGTATG 4341
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QY 4342 TGAGGAGTGTAGTACAGCTCTGAGGCTCTCTGCGCCCTCGGAGAGCTTGAAGCTGTG 4401
DB 56560 TGAGGAGTGTAGTACAGCTCTGAGGCTCTCTGCGCCCTCGGAGAGCTTGAAGCTGTG 56619
QY 4402 AGTGTGCGTGAAGTATTCCTTGGGCGCCCGACAGGCTTGTGCTTGGGCTGAAGCAC 4461
DB 56620 AGTGTGCGTGAAGTATTCCTTGGGCGCCCGACAGGCTTGTGCTTGGGCTGAAGCAC 56679
QY 4462 CCACTGAGAGGAGTGTCTCTTGAAGGAGGAGGAGGACATACAGGAGCGGCCACAC 4521
DB 56680 CCACTGAGAGGAGTGTCTCTTGAAGGAGGAGGAGGACATACAGGAGCGGCCACAC 56739
QY 4522 CACCGCGCCCTCAGAGCCCGCTGACCAAGCTTCTTCTGCGCCCAACCAAGCT 4578
DB 56740 CACCGCGCCCTCAGAGCCCGCTGACCAAGCTTCTTCTGCGCCCAACCAAGCT 56796

RESULT 7
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LOCUS BC019679
DEFINITION Homo sapiens, clone IMAGE:4932488, mRNA, partial cds.
ACCESSION BC019679
VERSION BC019679.1 GI:18044627
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus					
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata, Euteleostomi:					
Mammalia: Eutheria: Rodentia, Sciurognathi; Muridae; Murinae; Mus					
1 (bases 1 to 190494)					
Plumb, B.					
Direct Submission					
Submitted (12-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,					
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:					
humgvery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk					
On Jul 14, 2002 this sequence version replaced gi:2172735.					
Genome Center					
Center: Wellcome Trust Sanger Institute					
Center code: SC					
Web site: http://www.sanger.ac.uk					
Contact: humgvery@sanger.ac.uk					
Project Information					
Center project name: DM173K14					
----- Summary Statistics					
Assembly program: XGAP4; version 4.5					
Chemistry: Dye-terminator; 100% of reads					
Consensus quality: 185080 bases at least Q40					
Consensus quality: 186587 bases at least Q30					
Consensus quality: 187481 bases at least Q20					
Insert size: 188194; sum-of-contacts					
Insert size: 206960; 2.0% error; agarose-fp					
Quality coverage: 4.43x in Q20 bases; sum-of-contacts Quality					
coverage: 4.41x in Q20 bases; agarose-fp					

* NOTE: This is a 'working draft' sequence. It currently					
* consists of 24 contigs. The true order of the pieces					
* is not known and their order in this sequence record is					
* arbitrary. Gaps between the contigs are represented as					
* runs of N, but the exact sizes of the gaps are unknown.					
* This record will be updated with the finished sequence					
* as soon as it is available and the accession number will					
* be preserved.					
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5587: contig of 5587 bp in length					
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13216 23347: contig of 10132 bp in length					
23348 23447: gap of 100 bp					
23448 29152: contig of 5705 bp in length					
29153 29252: gap of 100 bp					
29253 33546: contig of 4294 bp in length					
33547 33646: gap of 100 bp					
33647 38589: contig of 4943 bp in length					
38590 38689: gap of 100 bp					
38690 47471: contig of 8782 bp in length					
47472 47571: gap of 100 bp					
47572 56726: contig of 9155 bp in length					
56727 56826: gap of 100 bp					
56827 69122: contig of 12296 bp in length					
69123 69222: gap of 100 bp					
69223 86407: contig of 17185 bp in length					
86408 86507: gap of 100 bp					
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94579 94678: gap of 100 bp					
94679 97023: contig of 2345 bp in length					
97024 97123: gap of 100 bp					
97124 103688: contig of 6565 bp in length					
103689 103788: gap of 100 bp					
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106764 106863: gap of 100 bp					
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111794 111893: gap of 100 bp					
111894 114584: contig of 2691 bp in length					
114585 114684: gap of 100 bp					
114685 120901: contig of 6217 bp in length					
120902 121001: gap of 100 bp					
121002 145630: contig of 24629 bp in length					

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	*	145731	148965:	contig of 3235	bp	in length
	*	148966	149065:	gap of	100	bp
	*	149066	161171:	contig of 12106	bp	in length
	*	161172	161271:	gap of	100	bp
	*	161272	179780:	contig of 18509	bp	in length
	*	179781	179880:	gap of	100	bp
	*	179881	187153:	contig of 7273	bp	in length
	*	187154	187254:	gap of	100	bp
	*	187254	190494:	contig of 3241	bp	in length
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			/db xref="taxon:10090"			
			/chromosome="4"			
			/clone="RP23-173X14"			
			/clone_1ib="RPc1-23"			
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			121002..145630			
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misc_feature      179881..187153
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ORIGIN

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Best Local Similarity 100.0%; Pred.No. 3.7e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1422 CACTACTTCACCTGCTGCCACACCTACTCGTGGTGCACGACTCATGTCCAG 1481
Db 143233 CACTACTTCACCTGCTGCCACACCTACTCGTGGTGCACGACTCATGTCCAG 143292
Oy 1482 TC 1483
Db 143293 TC 143294

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RESULT 12
AC120432/c
LOCUS             AC120432             67142 bp    DNA             linear      HTG 06-MAY-2002
DEFINITION       Mus musculus clone RP24-553K14, LOW-PASS SEQUENCE SAMPLING.
ACCESSION        AC120432
VERSION          AC120432.1 GI:20455766
KEYWORDS         HTG; HTGS_PHASE0.
SOURCE           Mus musculus.
ORGANISM         Mus musculus.
REFERENCE        1 (bases 1 to 67142)
AUTHORS          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
TITLE            Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL          Mus musculus, clone RP24-553K14
REFERENCE        2 (bases 1 to 67142)
AUTHORS          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
TITLE            Anderson, S., Batra, N., Bastien, V., Bloom, T., Boguslavsky, L.,
JOURNAL          Boukhalil, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
REFERENCE        Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
AUTHORS          Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S.,
TITLE            Fato, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
JOURNAL          Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
REFERENCE        Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
AUTHORS          Kanat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
TITLE            Lander, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
JOURNAL          Maclean, C., MacDonald, P., Major, U., Margulis, N., Matthews, C.,
REFERENCE        McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, J.,
AUTHORS          Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
TITLE            Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
JOURNAL          Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
REFERENCE        Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
AUTHORS          Roman, V., Rosetti, W., Roy, A., Santos, R., Schauer, S., Schuback, R.,
TITLE            Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
JOURNAL          Strauss, N., Subramanian, A., Talamas, U., Testaye, S., Theodore, J.,
REFERENCE        Topham, K., Travers, M., Travis, N., Triggillo, J., Vasilev, H.,
AUTHORS          Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
TITLE            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
JOURNAL          Direct Submission

```

TITLE
JOURNAL
Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

All repeats were identified using RepeatMasker:
Smt, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Project name: L26051
Center clone name: 553_K_14

NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
692 791: gap of 100 bp in length
792 1524: contig of 733 bp in length
1525 1624: gap of 100 bp
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3136 3235: gap of 100 bp
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3929 4028: gap of 100 bp
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4731 4830: gap of 100 bp
4831 5532: contig of 702 bp in length
5533 5632: gap of 100 bp
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6373 6472: gap of 100 bp
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9632 9731: gap of 100 bp
9732 10448: contig of 717 bp in length
10449 10548: gap of 100 bp
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11269 11368: gap of 100 bp
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12088 12187: gap of 100 bp
12188 12931: contig of 744 bp in length
12932 13031: gap of 100 bp
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13781 13880: gap of 100 bp
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* 21226 21974: contig of 749 bp in length
* 21975 22074: gap of 100 bp
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* 22784 22883: gap of 100 bp
* 22884 23584: contig of 701 bp in length
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* 23685 24409: contig of 725 bp in length
* 24410 24509: gap of 100 bp
* 24510 25220: contig of 711 bp in length
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* 26130 26849: contig of 720 bp in length
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* 38361 38460: gap of 100 bp
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Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 67142;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3015 GTGTACTAGAGGATGGAAGGCCTC 3043
Db 20050 GTGTACTAGAGGATGGAAGGCCTC 20022

RESULT 13
LOCUS HSA338904/c 621 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
ACCESSION AJ338904
VERSION AJ338904
KEYWORDS NLI-VF5R.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kutsenko,A.S., Gizaev,I.I., R.Z., Al-Amin,A.N., Wang,F., Kvashina,S.M.,
Podowski,R.M., Matukhkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
Levitsky,V.G., Kolchanov,N.A., Protodopov,A.I., Kashuba,V.I.,
Kiselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 621)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorphology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NLI-VF5R"
BASE COUNT 152 a 217 c 172 g 80 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 28; DB 9; Length 621;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 519 TTCTTGGAGGCGCAATCTGCGCGTG 546
Db 621 TTCTTGGAGGCGCAATCTGCGCGTG 594

RESULT 14
LOCUS AC023583
AC023583 176291 bp DNA linear HTG 24-AUG-2002

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DEFINITION Homo sapiens chromosome 19 clone RP11-294120 map 19, WORKING DRAFT

SEQUENCE, 38 unordered pieces.

ACCESSION AC023583.2 GI:7139848

VERSION HTG: HTS_PHASE1; HTS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 176291)

REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 19, clone RP11-294120

Unpublished

2 (bases 1 to 176291)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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AUTHORS

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REFERENCE

Center Project name: L6822
Center Clone name: 294_I-20

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 15757 bases at least Q40

Consensus quality: 165762 bases at least Q30

Consensus quality: 165979 bases at least Q20

Insert size: 172591; sum-of-contigs

Quality coverage: 4.3 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	1112:	contig of 1112 bp	in length
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3808	3907:	gap of 100 bp	
3908	5199:	contig of 1292 bp	in length
5200	5299:	gap of 100 bp	
5300	6456:	contig of 1157 bp	in length
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8374	8473:	gap of 100 bp	
8474	9630:	contig of 1157 bp	in length
9631	9730:	gap of 100 bp	
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11040	11138:	gap of 100 bp	
11140	12863:	contig of 1730 bp	in length
12870	12969:	gap of 100 bp	
12970	14713:	contig of 1744 bp	in length
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14814	16251:	contig of 1438 bp	in length
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16352	18265:	contig of 1914 bp	in length
18266	18365:	gap of 100 bp	
18366	21235:	contig of 2870 bp	in length
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23748	26775:	contig of 3028 bp	in length
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26876	29829:	contig of 2954 bp	in length
29830	29929:	gap of 100 bp	
29930	33977:	contig of 4048 bp	in length
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34078	37757:	contig of 3680 bp	in length
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42752	42851:	gap of 100 bp	
42852	47106:	contig of 4255 bp	in length
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* 91035 91134: gap of 100 bp
* 91135 96686: contig of 5552 bp in length
* 96687 96786: gap of 100 bp
* 96787 104241: contig of 7455 bp in length
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QY 3579 CGCCAGCAGCCCGGCGCGCT 3602
Db 37682 CGCCAGCAGCCCGGCGCGCT 37705

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ACCESSION AC121463
VERSION AC121463.2 GI:21909415
KEYWORDS HTG; HTGS PHASE1.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus

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REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 77863)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alshrooke,S.L., Amarunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Bimge,K., Blankenburg,K., Bonnin,D., Buck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhey,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.U., Draper,H., Dugan-Kocha,S., Durbin,K.D., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsl,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,B., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabak,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,S., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokweto,S., Oguh,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojudoxan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tameiro,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telirod,B., Thomas,N., Thomas,S., Usmani,K., Vaequez,L., Vera,V., Villalón,D., Vinson,R., Wang,S., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G., and Gibbs,R.

TITLE

Direct Submission

REFERENCE

2 (bases 1 to 77863)

AUTHORS

Worley,K.C.

TITLE

Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 77863)

REFERENCE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 19, 2002 this sequence version replaced gi:20976415.

TITLE

Center: Baylor College of Medicine

AUTHORS

Worley,K.C.

REFERENCE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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REFERENCE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Consensus quality: 19063 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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2641 2740: gap of unknown length
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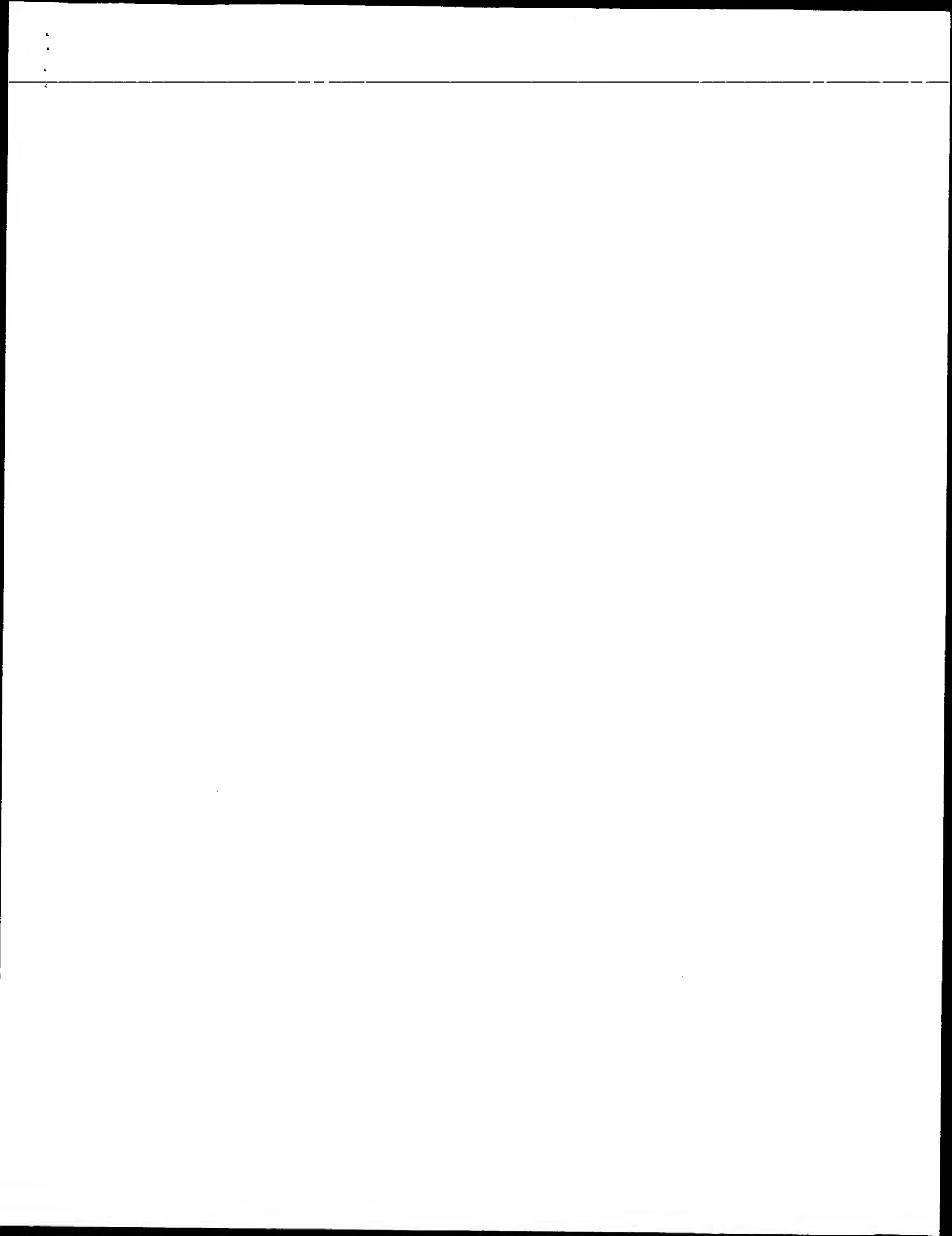
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Db 24913 GACCTGACCTGCTGCTGAC 24891

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Job time: 16606 secs



GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 18:26:44 ; Search time 1028 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1579	34.1	6551	24	ABK12390
4	60	1.3	60	24	ABN36694
5	56	1.2	233	21	AAC30759
6	44	0.9	534	24	ABK15752
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13	20	0.4	324	23	AAS91012	DNA encoding novel
14	20	0.4	426	24	ABK64733	Human benign prost
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36	20	0.4	3441	20	AA180044	Human PRO243 nuc1e
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43	20	0.4	4235	22	AAK68399	Human lung tumour
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45	20	0.4	4235	24	ABK83310	CDNA encoding clon

ALIGNMENTS

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KW	immunosuppressive; anti-inflammatory; cardiovascular; gene therapy;	
KW	enzyme therapy; cancer; neurological disorder; autoimmune disorder;	
KW	inflammatory disorder; cardiovascular disorder; ss.	
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PR	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	

XX (INCYTE GENOMICS INC.
PA Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-Young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;
XX
DR WPI: 2002-089794/12.
DR P-PSDB; ABB08205.
XX
PT New lipid metabolism enzymes useful for diagnosing, treating and
PT preventing cancer, neurological disorders, autoimmune/inflammatory
disorders, and cardiovascular disorders
XX
XX Claim 5; Page 121-122; 122pp; English.
XX
XX The sequence encodes a novel human lipid metabolism enzyme (LME-5) of
CC the invention. The invention relates to novel human LME's, and the
CC polynucleotides which identify and encode them. The enzymes of the
CC invention have cytosolic, neuroprotective, immunosuppressive,
CC anti-inflammatory, and cardiovascular activity. The polypeptides and
CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
CC metabolism enzymes are useful in the diagnosis, treatment and prevention
CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
CC cardiovascular disorders, and in the assessment of the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
CC for compounds that modulate the activity of LME. Polynucleotides encoding
CC LME may be used for somatic or germline gene therapy, to detect and
CC quantify gene expression in biopsied tissues in which expression of LME
CC may be correlated with disease, to generate a transcript image of a
CC tissue or cell type, to generate hybridization probes useful in mapping
CC the naturally occurring genomic sequence, and for screening libraries of
CC compounds in drug screening techniques. The polypeptide sequences may be
CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
CC primers derived from polynucleotide sequences encoding LME may be used to
CC detect single nucleotide polymorphisms.
XX
XX Sequence 4237 BP; 816 A; 1327 C; 1370 G; 724 T; 0 other;
SQ
Query Match 69.1%; Score 3205; DB 24; Length 4237;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1247 GGTGACATGTATGCTTGGGCTCTGACAGGCTGGCTGCGCTGTGAGGTGACGTGCTG 1306
Qy 1547 GGATGGGCCCGACCGGGAGGCCATTGTGACCAATGAGTACACTGTGCTTCAAGATCT 1606
Db 1307 GGATGGGCCCGACCGGGAGGCCATTGTGACCAATGAGTACACTGTGCTTCAAGATCT 1366
Qy 1607 CTTCAAGAGCTCATTTGAACCATCAACAAATATGCTTCAATCAAGATAGTACCCAGT 1666
Db 1367 CTTCAAGAGCTCATTTGAACCATCAACAAATATGCTTCAATCAAGATAGTACCCAGT 1426
Qy 1667 GATCTGTCATCGAATAACCATGTCAGTATCAGACAGAAAGAAATGGCCAGTATCT 1726
Db 1427 GATCTGTCATCGAATAACCATGTCAGTATCAGACAGAAAGAAATGGCCAGTATCT 1486
Qy 1727 GACTGACATCCCTTGGGAGCAAGCTGAACTGTATCATGATGAGCATGTAAGTCCACAC 1786
Db 1487 GACTGACATCCCTTGGGAGCAAGCTGAACTGTATCATGATGAGCATGTAAGTCCACAC 1546
Qy 1787 ACTCCCTCTTCCACAGATGCTCAAGGGCAAGTCTTGTGAAGGGAAAGTCTCCAGC 1846
Db 1547 ACTCCCTCTTCCACAGATGCTCAAGGGCAAGTCTTGTGAAGGGAAAGTCTCCAGC 1606
Qy 1847 CAACATCAGCAGAGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1906
Db 1607 CAACATCAGCAGAGATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1666
Qy 1907 TGACGATGACTGCAAGCTCTCTCAATGGGGATGATCCACCAATCGAAAGCTGTAGAAAA 1966
Db 1667 TGACGATGACTGCAAGCTCTCTCAATGGGGATGATCCACCAATCGAAAGCTGTAGAAAA 1726
Qy 1967 CACGCTTAAGAGAGAAATGAGATTCCTTCAACAAAGATGCAAAATTCGGGACTGTGAGGA 2026
Db 1727 CACGCTTAAGAGAGAAATGAGATTCCTTCAACAAAGATGCAAAATTCGGGACTGTGAGGA 1786
Qy 2027 CCCCACAACTTCCCTCCCTCCACACTGTCCTCCATCTGAAAGCTCGAGCGAAGAGCAA 2086
Db 1787 CCCCACAACTTCCCTCCCTCCACACTGTCCTCCATCTGAAAGCTCGAGCGAAGAGCAA 1846
Qy 2087 GGCTGAAGAGAGAGTGTGAGTGTGGGAGAGATGCGGGGCGCAGACAGCATATGCGGCT 2146
Db 1847 GGCTGAAGAGAGAGTGTGAGTGTGGGAGAGATGCGGGGCGCAGACAGCATATGCGGCT 1906
Qy 2147 CGTGTGGGAAAGCTTCCAGGGCGCAAGAAAGAGGCGAGACATGAAGAGCGGCGCGAG 2206
Db 1907 CGTGTGGGAAAGCTTCCAGGGCGCAAGAAAGAGGCGAGACATGAAGAGCGGCGCGAG 1966
Qy 2207 CGTGAAGAGAGAGATGAGGAGTCAAGACTTCCCGGAGAGCGAGAGCGGAGCGAGCCG 2266
Db 1967 CGTGAAGAGAGAGATGAGGAGTCAAGACTTCCCGGAGAGCGAGAGCGGAGCGAGCCG 2026
Qy 2267 GCGAAGAAAGACATGAAGTGTCCCGGGCCCTCTGTGACCTGTGAACTGTGAATGAACCAAGT 2326
Db 2027 GCGAAGAAAGACATGAAGTGTCCCGGGCCCTCTGTGACCTGTGAACTGTGAATGAACCAAGT 2086
Qy 2327 CGTGGCCACCAAGATGAGAGTGAAGGCGGCTCACTGTGGCAGGTGTGCTTCAAG 2386
Db 2087 CGTGGCCACCAAGATGAGAGTGAAGGCGGCTCACTGTGGCAGGTGTGCTTCAAG 2146
Qy 2387 GGAAGCAAGAGCCACCAAGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2446
Db 2147 GGAAGCAAGAGCCACCAAGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2206
Qy 2447 GGAAGCAAGTCTCCCGAGATCAACCTTCTCTCAACGTGTGAGTCAAGAACTAACAACC 2506
Db 2207 GGAAGCAAGTCTCCCGAGATCAACCTTCTCTCAACGTGTGAGTCAAGAACTAACAACC 2266
Qy 2507 GCAAGCCCTTCTGAGAGCGCGGCTGCAAAATGTTGGCTGAATCAAGTCAAGAGAGAGG 2566
Db 2267 GCAAGCCCTTCTGAGAGCGCGGCTGCAAAATGTTGGCTGAATCAAGTCAAGAGAGAGG 2326
Qy 2567 GATGCTGACAGCTGAACGAGCAAGTTCAAGCGCCAAAGGTGAGCTGCGGTACGTACAA 2626

Db 2327 GATGCTGACGTGAACCGAGCCAAAGTTTCAGCGCCAAAGTGTGCTGCGCTAGCTACTCA 2386
Qy 2627 GCTTGGGTGATGTGCGACAGGGGCTTTCAACCCCACTGGAGAGACCCCTGCTCCGGGGA 2686
Db 2387 GCTTGGGTGATGTGCGACAGGGGCTTTCAACCCCACTGGAGAGACCCCTGCTCCGGGGA 2446
Qy 2687 GCTCAAGAAAGACAGTGTGCTGCGATCATCATAGTGGCCAGAGCTTCCCAAGCCGGGGA 2746
Db 2447 GCTCAAGAAAGACAGTGTGCTGCGATCATCATAGTGGCCAGAGCTTCCCAAGCCGGGGA 2506
Qy 2747 CTTCATGCTGGGAGACCTGGAGAGATCATCGACCCCTTTGTGAGAGTGAATCATTTGG 2806
Db 2507 CTTCATGCTGGGAGACCTGGAGAGATCATCGACCCCTTTGTGAGAGTGAATCATTTGG 2566
Qy 2807 GCTTCTGTGATGTGACAGAGAGAGAGACCCCGGTGTGAGAGAGAGAGAGAGAGAGAGAG 2866
Db 2567 GCTTCTGTGATGTGACAGAGAGAGAGAGACCCCGGTGTGAGAGAGAGAGAGAGAGAGAGAG 2626
Qy 2867 CACTGGAGAGAGACCTGGATTTTCATGTGACATGCGAGAGATCGCGTGTGCTT 2926
Db 2627 CACTGGAGAGAGACCTGGATTTTCATGTGACATGCGAGAGATCGCGTGTGCTT 2686
Qy 2927 CCTGCTGTGAGACACAGATCCATCGGCGGTGACTTCAATTGCGCAGAGACGCTGCTT 2986
Db 2687 CCTGCTGTGAGACACAGATCCATCGGCGGTGACTTCAATTGCGCAGAGACGCTGCTT 2746
Qy 2987 CAGACATATATGCTGAGGCTACAGACCTGTGATCTTGAAGAGATGGAAGAGAGAGAGAGAG 3046
Db 2747 CAGACATATATGCTGAGGCTACAGACCTGTGATCTTGAAGAGATGGAAGAGAGAGAGAGAG 2806
Qy 3047 CTTCGATGATGTGAGGCTGTGATGATCATGAGGATTAAGTCAAGAGAGAGAGAGAGAGAGAG 3106
Db 2807 CTTCGATGATGTGAGGCTGTGATGATCATGAGGATTAAGTCAAGAGAGAGAGAGAGAGAGAG 2866
Qy 3107 AGGAGCTTCTCTCGAG 3166
Db 2867 AGGAGCTTCTCTCGAG 2926
Qy 3167 CCGGAG 3226
Db 2927 CCGGAG 2986
Qy 3227 GAGCAG 3286
Db 2987 GAGCAG 3046
Qy 3287 CTTCAG 3346
Db 3047 CTTCAG 3106
Qy 3347 AGCCAG 3406
Db 3107 AGCCAG 3166
Qy 3407 GAAAGAGCTGTGCGAG 3466
Db 3167 GAAAGAGCTGTGCGAG 3226
Qy 3467 GAGCGGCAATGATGAATGT 3526
Db 3227 GAGCGGCAATGATGAATGT 3286
Qy 3527 GCAAG 3586
Db 3287 GCAAG 3346
Qy 3587 GCGCCGAG 3646
Db 3347 GCGCCGAG 3406
Qy 3647 CCGGAG 3706
Db 3407 CCGGAG 3466

Qy 3707 TAGCGGCTCCATGTCTCTCGGATCTTCAGACAGCCAGACAGCCCGGAGATCCCGAAAGTTC 3766
Db 3467 TAGCGGCTCCATGTCTCTCGGATCTTCAGACAGCCAGACAGCCCGGAGATCCCGAAAGTTC 3526
Qy 3767 CCGCGGCTGCTGAG 3826
Db 3527 CCGCGGCTGCTGAG 3586
Qy 3827 CTGTGTGCTCAAAAGCTGAG 3886
Db 3587 CTGTGTGCTCAAAAGCTGAG 3646
Qy 3887 GCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3946
Db 3647 GCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3706
Qy 3947 TGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4006
Db 3707 TGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3766
Qy 4007 GTGAGCATGTCTCGGTGAGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4066
Db 3767 GTGAGCATGTCTCGGTGAGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3826
Qy 4067 CTCTGCTGAGCTTGAAG 4126
Db 3827 CTCTGCTGAGCTTGAAG 3886
Qy 4127 GGAAGAAACAGCTGCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4186
Db 3887 GGAAGAAACAGCTGCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3946
Qy 4187 GCGCCCTCGGAG 4246
Db 3947 GCGCCCTCGGAG 4006
Qy 4247 CCGTATGCTTCTCTGAG 4306
Db 4007 CCGTATGCTTCTCTGAG 4066
Qy 4307 GAGGCTCAAG 4366
Db 4067 GAGGCTCAAG 4126
Qy 4367 GTCCTGAG 4426
Db 4127 GTCCTGAG 4186
Qy 4427 GCGCCAG 4475
Db 4187 GCGCCAG 4235

RESULT 2
ABA94696
ID ABA94696 standard; cDNA; 2243 BP.
XX
AC ABA94696;
XX
DT 23-APR-2002 (first entry)
XX
DE Human lipid metabolism molecule (LMN) cDNA (ID: 2965233CB1).
XX
XX Lipid metabolism molecule; LMN; cytosolic; neuroprotective;
XX anti-convolusant; immunosuppressive; anti-inflammatory; dermatological;
XX cardiovascular; anti-HIV; antileptic; antiallergic; hypertensive; human;
XX cancer; gene therapy; protein therapy; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 321..2189
FT CDS

Db	1321	TCACCTGCTCCCAACACCACTACTCTGTGGGTGACCACTATGTGCCAGTCAACGGGTGG	1380
Qy	1492	ACATGTATGCTTGGGTGCTGTGCAGGCTGTGGCTGGCTGGGTGGAGGTGACTGTGGATG	1551
Db	1381	ACATGTATGCTTGGGTGCTGTGCAGGCTGTGGCTGGCTGGGTGGAGGTGACTGTGGATG	1440
Qy	1552	GGCCCGACGGGGAGCCCATTTGTGTACCAATGGCTTACACTCTTCCAAAGATCCTCTTCA	1611
Db	1441	GGCCCGACGGGGAGCCCATTTGTGTACCAATGGCTTACACTCTTCCAAAGATCCTCTTCA	1500
Qy	1612	AAGACGTCAATTGAAAACCATCAACAATATGCTCTTATCATAGATAGATACCAGTGTATCC	1671
Db	1501	AAGACGTCAATTGAAAACCATCAACAATATGCTCTTATCATAGATAGATACCAGTGTATCC	1560
Qy	1672	TGTCCATCGAAAAACACTGCAGTGTATCTCAGACAGAGAAAAATGGCCAGTATCTGACTG	1731
Db	1561	TGTCCATCGAAAAACACTGCAGTGTATCTCAGACAGAGAAAAATGGCCAGTATCTGACTG	1620
Qy	1732	ACATCTTTGGGGACAACTGTGGACCTGTCAATCAATGACAGTGAAGATGCCACCACTCC	1791
Db	1621	ACATCTTTGGGGACAACTGTGGACCTGTCAATCAATGACAGTGAAGATGCCACCACTCC	1680
Qy	1792	CCTCTCCACAGATCTCAAGGCGAAGACTCCTGTGATGACAGTGAAGATGCCACCACTCC	1851
Db	1681	CCTCTCCACAGATCTCAAGGCGAAGACTCCTGTGATGACAGTGAAGATGCCACCACTCC	1740
Qy	1852	TCAGCAGAGATGCGGAGAGAAAGCGAGGTGTCTGATGAGGACAGTGTATGATTAAGC	1911
Db	1741	TCAGCAGAGATGCGGAGAGAAAGCGAGGTGTCTGATGAGGACAGTGTATGATTAAGC	1800
Qy	1912	ATGACTGCAGACTCTCTCAATGGGGATGTCAATGCCAATGGAAGGTGTAGAAAAACACTG	1971
Db	1801	ATGACTGCAGACTCTCTCAATGGGGATGTCAATGCCAATGGAAGGTGTAGAAAAACACTG	1860
Qy	1972	CTAAGAGGAAACTGGAATTCCTCCTCATCAAGAAGTCGAAGATTGCGGACTGTGAGACCCCA	2031
Db	1861	CTAAGAGGAAACTGGAATTCCTCCTCATCAAGAAGTCGAAGATTGCGGACTGTGAGACCCCA	1920
Qy	2032	ACAACTTCTCCGCTTCGACACTGTGCCCATCTGTGAAAAGCTGTGAGCGAAGACAGGCTG	2091
Db	1921	ACAACTTCTCCGCTTCGACACTGTGCCCATCTGTGAAAAGCTGTGAGCGAAGAGGCTG	1980
Qy	2092	AAGAGACGTGGAATCTTGGGGAGGATGTCCGGGGCCACAGACGCAATGGCCGCTCCGTGCG	2151
Db	1981	AAGAGACGTGGAATCTTGGGGAGGATGTCCGGGGCCACAGACGCAATGGCCGCTCCGTGCG	2040
Qy	2152	TGGGAAGCTTCTCCACAGGCGCAAGAAGAGGCGACAAAGCTGAAGAAAGGCGGCGACGCTG	2211
Db	2041	TGGGAAGCTTCTCCACAGGCGCAAGAAGAGGCGACAAAGCTGAAGAAAGGCGGCGACGCTG	2100
Qy	2212	AGGAGGAGATGAGGGGTTCAGGACTCCCGGAGAGCCCAAGCCGAGGCGGACCTCCGCGAGA	2271
Db	2101	AGGAGGAGATGAGGGGTTCAGGACTCCCGGAGAGCCCAAGCCGAGGCGGACCTCCGCGAGA	2160
Qy	2272	AGA 2274	
Db	2161	AGA 2163	
RESULT 3			
ABK12390			
ID	ABK12390 standard; cDNA: 6551 BP.		
XX	ABK12390;		
XX	05-JUN-2002 (first entry)		
DE	cDNA encoding human lipid metabolism enzyme, LMM-6.		
KW	Human: lipid metabolism enzyme; LMM-6; immune system disorder;		
KW	neurological disorder; developmental disorder; cancer; nontoxic;		
KW	cell proliferative disorder; immunomodulator; neuroprotective;		
KW	cytostatic; gene; ss.		

QY 2381 CTTGAGGAGACCAAGGCCCAACGATTTCTGACAGAGAAAGCCGGCCGACGATCCTT 2440
 Db 3759 CTTGAGGAGACCAAGGCCCAACGATTTCTGACAGAGAAAGCCGGCCGACGATCCTT 3818
 QY 2441 CAACGAGCAGAGCTCCCGCATCTACCCCTCTCTACCGGTGAGACTCCAGCAACTA 2500
 Db 3819 CAACGAGCAGAGCTCCCGCATCTACCCCTCTCTACCGGTGAGACTCCAGCAACTA 3878
 QY 2501 CAACCCGAGCCTTTCTGAAACGCCGCTGCAAAATGTTGCCCTGAACCTACAGCTAGA 2560
 Db 3879 CAACCCGAGCCTTTCTGAAACGCCGCTGCAAAATGTTGCCCTGAACCTACAGCTAGA 3938
 QY 2561 GGGGCGGATGCTGAGCTGAACCGAGCCAAATGAGCCCAAGGTGGCTGGGCTAGCT 2620
 Db 3939 GGGGCGGATGCTGAGCTGAACCGAGCCAAATGAGCCCAAGGTGGCTGGGCTAGCT 3998
 QY 2621 ACTCAAGCCTGAGTGTGATGTCAGAGGCGGTGTTCAACCCCACTGGAGAGACCCCTGCG 2680
 Db 3999 ACTCAAGCCTGAGTGTGATGTCAGAGGCGGTGTTCAACCCCACTGGAGAGACCCCTGCG 4058
 QY 2681 CGGCGAGCTCAAGAGCAGCTGAGTCTCCGATCATCAATGAGCCAGCAGCTTCCAGAGCC 2740
 Db 4059 CGGCGAGCTCAAGAGCAGCTGAGTCTCCGATCATCAATGAGCCAGCAGCTTCCAGAGCC 4118
 QY 2741 GCGCGACTCAGTGTGGGAGACCGTGGGAGATCATGACCCCTTTGTGAGTGGAGAT 2800
 Db 4119 GCGCGACTCAGTGTGGGAGACCGTGGGAGATCATGACCCCTTTGTGAGTGGAGAT 4178
 QY 2801 CATTGGGCTCCCTGTGAGCTGACAGCAGAGAGCAGACCCGCGTGTGAGAGCAAGAGAGT 2860
 Db 4179 CATTGGGCTCCCTGTGAGCTGACAGCAGAGAGCAGACCCGCGTGTGAGAGCAAGAGAGT 4238
 QY 2861 CAACCCACCTGGAGAGAGACCTTGTGTTTATGTGTGACATATGCGGAGATGCGCTGCT 2920
 Db 4239 CAACCCACCTGGAGAGAGACCTTGTGTTTATGTGTGACATATGCGGAGATGCGCTGCT 4298
 QY 2921 CCGCTTCTCTGCTGAGGACCAAGATCCCAATCGGCGGTGACTTATTGGCAGAGAGACGT 2980
 Db 4299 CCGCTTCTCTGCTGAGGACCAAGATCCCAATCGGCGGTGACTTATTGGCAGAGAGACGT 4358
 QY 2981 GGCCTTCAAGCAGATGATCCAGGCTTACAGACACGTGTACTTAAAGGATGAAAGAGCC 3040
 Db 4359 GGCCTTCAAGCAGATGATCCAGGCTTACAGACACGTGTACTTAAAGGATGAAAGAGCC 4418
 QY 3041 CTCACATCTCGTGTGATGATGCTGATGATCATCAAGCGGTAAAGTCAACGAGCTCTGGG 3100
 Db 4419 CTCACATCTCGTGTGATGATGCTGATGATCATCAAGCGGTAAAGTCAACGAGCTCTGGG 4478
 QY 3101 CCTAAAGGCTCTTCTCTGAGGACCAAGGCTGCTGAGACAGTCAATGCTGTGG 3160
 Db 4479 CCTAAAGGCTCTTCTCTGAGGACCAAGGCTGCTGAGACAGTCAATGCTGTGG 4538
 QY 3161 GGGGCCCCCGGCGCCCTCGTTAGCCAGGATCTTGGCGCCACCGCCAGGCGCC 3220
 Db 4539 GGGGCCCCCGGCGCCCTCGTTAGCCAGGATCTTGGCGCCACCGCCAGGCGCC 4598
 QY 3221 GACCAAGGCTGAGAGCGGGCGGAGGGGCTTCCGAGCTGTGCTGGGTACACGGGA 3280
 Db 4599 GACCAAGGCTGAGAGCGGGCGGAGGGGCTTCCGAGCTGTGCTGGGTACACGGGA 4658
 QY 3281 CAAGGCTTCAAGGGGCTGAGAGCATGTGTGCCCCCGGCGCCAGGCTGCTCGGA 3340
 Db 4659 CAAGGCTTCAAGGGGCTGAGAGCATGTGTGCCCCCGGCGCCAGGCTGCTCGGA 4718
 QY 3341 AGCCCAAGCCGAGAGGGGCGCGGAGCGGACGCCCCGAGGTAAAGCGCAGCTGCGGT 3400
 Db 4719 AGCCCAAGCCGAGAGGGGCGCGGAGCGGACGCCCCGAGGTAAAGCGCAGCTGCGGT 4778
 QY 3401 GGCAGAGAAAGCCTGTGCGAGTGGCGGCCCCGCGGTCTCGAGAGCGGCCCGGCGCTGC 3460
 Db 4779 GGCAGAGAAAGCCTGTGCGAGTGGCGGCCCCGCGGTCTCGAGAGCGGCCCGGCGCTGC 4837

QY 3461 TGGATGCGCCGACATGATGAAGTGTGTGTGGATCTCTGCGCCGCTGAACACCGG 3520
 Db 4838 TGGATGCGCCGACATGATGAAGTGTGTGTGGATCTCTGCGCCGCTGAACACCGG 4897
 QY 3521 GGGCTGTGAGAGGAGGAGGAGCCACCCAGCCCGGGGCTGTGAGAGAGAGCAGCTTGC 3580
 Db 4898 GGGCTGTGAGAGGAGGAGGAGCCACCCAGCCCGGGGCTGTGAGAGAGAGCAGCTTGC 4957
 QY 3581 CCAGCAGCCCGGCGCCCGGCTGACTGAGTGGGAGCCCTGCTGTGTGAGCCTGA 3640
 Db 4958 CCAGCAGCCCGGCGCCCGGCTGACTGAGTGGGAGCCCTGCTGTGTGAGCCTGA 5017
 QY 3641 CGCTATCCCGGAGAGAGCAGAGAGGCTCCCAAGGCTCTGGGAGGAGGAGGCTC 3700
 Db 5018 CGCTATCCCGGAGAGAGAGGAGGCTCCCAAGGCTCTGGGAGGAGGAGGCTC 5077
 QY 3701 AGGCGGTAGAGGAGCTCAATGCTCTGAGCTGACAGAGCCAGAGCCCGGAGTCTCCGA 3760
 Db 5078 AGGCGGTAGAGGAGCTCAATGCTCTGAGCTGACAGAGCCAGAGCCCGGAGTCTCCGA 5137
 QY 3761 AAGTCCCGCGCTGAGGAGGCTGTGAGGAGCAACCGGAGGCTGTGAGAGAGAT 3820
 Db 5138 AAGTCCCGCGCTGAGGAGGCTGTGAGGAGCAACCGGAGGCTGTGAGAGAGAT 5197
 QY 3821 GAGTCCCTTGTGTTGCTCAAAAGCTGAGAGATGAGAGTAAATCCCATGTTCCCG 3880
 Db 5198 GAGTCCCTTGTGTTGCTCAAAAGCTGAGAGATGAGAGTAAATCCCATGTTCCCG 5257
 QY 3881 CG 3882
 Db 5258 CG 5259

RESULT 4
 ABN36694
 ID ABN36694 standard; DNA; 60 bp.
 XX
 AC ABN36694;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:9442.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-1B01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 9442; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 60 BP; 14 A; 15 C; 19 G; 12 T; 0 other;

Query Match 1.3%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4446 TTGGGCTGAGACGCCACTAGAGGGTGTCTCTTACCTGAGGAGGACATACAC 4505
1 TTGGGCTGAGACGCCACTAGAGGGTGTCTCTTACCTGAGGAGGACATACAC 60

RESULT 5
ID AAC30759 standard; cDNA; 233 BP.

XX AAC30759;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 34834.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

OS EPI033401-A2.

PN 06-SEP-2000.

PD 21-FEB-2000; 2000EP-0200610.

PP 26-FEB-1999; 99US-0122487.

PR (GERT) GENSET.

PA Dumas Milne Edwards J, Duclert A, Giordano J;

PI WPI; 2000-500381/45.

DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 34834; 71pp + CD-ROM, English.

XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)

of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

Sequence 233 BP; 41 A; 80 C; 72 G; 33 T; 7 other;

Query Match 1.2%; Score 56; DB 21; Length 233;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 234 GGTGTGATATGCGCTGCGCCGAGGCTACACCCCGACAGGAGACCGGGGGCC 309
DB 21 GGTGTGATATGCGCTGCGCCGAGGCTACACCCCGACAGGAGACCGGGGGCC 76

RESULT 6

ID ABK71572 standard; cDNA; 534 BP.

XX ABK71572;

DT 30-JUL-2002 (first entry)

DE Human dithp polynucleotide #38.

KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW skin; testis; thymus.

XX Homo sapiens.

OS WO200220754-A2.

PN 14-MAR-2002.

PD 29-AUG-2001; 2001WO-US27127.

PP 05-SEP-2000; 2000US-229747P.

PR 05-SEP-2000; 2000US-229748P.

PR 05-SEP-2000; 2000US-229749P.

PR 05-SEP-2000; 2000US-229750P.

PR 05-SEP-2000; 2000US-229751P.

PR 05-SEP-2000; 2000US-230583P.

PR 06-SEP-2000; 2000US-230585P.

PR 06-SEP-2000; 2000US-230586P.

PR 06-SEP-2000; 2000US-230587P.

PR 06-SEP-2000; 2000US-230588P.

PR 06-SEP-2000; 2000US-230589P.

PR 06-SEP-2000; 2000US-230590P.

PR 06-SEP-2000; 2000US-230591P.

PR 07-SEP-2000; 2000US-231163P.

PR 07-SEP-2000; 2000US-231167P.

PA (INCY-) INCYTE GENOMICS INC.

PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
 PI Momiyama MG, Bradley JL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gertin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 XX WPI: 2002-383054/41.
 DR P1PSDB: ABG59980.
 XX
 PT An isolated polynucleotide useful in diagnostics and therapeutics -
 XX
 PS Claim 1; Page 424-425; 686pp; English.
 XX
 CC The invention relates to human diagnostic and therapeutic (dthp)
 CC polynucleotides and their associated polypeptides (dthp polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis), multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
 CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
 CC ABK155-ABK1809 represent human dthp polynucleotides of the invention.
 XX
 SQ Sequence 534 BP; 125 A; 154 C; 140 G; 115 T; 0 other;
 XX
 Query Match 0.9%; Score 44; DB 24; Length 534;
 Best Local Similarity 100.0%; Pred. No. 2e-09;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Oy 1440 TCCCAACACCTACTCTGCTGCTGACCAAGCTCATGTCAGTCCAGTGC 1483
 Db 334 TCCCAACACCTACTCTGCTGCTGACCAAGCTCATGTCAGTCCAGTGC 377
 XX
 RESULT 7
 AAD33703
 ID AAD33703 standard; CDNA; 896 BP.
 XX
 AC AAD33703;
 XX
 DT 01-JUN-2002 (first entry)
 XX
 DE Human secreted protein-encoding gene 12 cDNA clone HCOMM91, SEQ ID NO:22.
 XX
 KW Human; secreted protein; immune disorder; antiallergic; antirheumatic;
 KW rheumatoid arthritis; breast neoplasia; breast cancer; antiallergic;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; trauma;
 KW Tourette syndrome; encephalitis; cytosolic; haemostatic; anaemia; mania;
 KW antiinflammatory; ophthalmological; dermatological; immunostimulatory;
 KW immunomodulatory; immunosuppressive; antibacterial; antiparasitic;
 KW gene therapy; autoimmune disease; Huntington's disease; meningitis;
 KW demyelinating disease; peripheral neuropathy; congenital malformation;
 KW spinal cord injury; peripheral neuropathy; ischemia; perception;
 KW multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia;
 KW depression; panic disorder; learning disability; ALS; feeding disorder;
 KW hyperproliferative disorder; sleep pattern; cardiovascular disorder;
 KW reproductive disorder; digestive system disorder; behavioural disorder;
 KW gene; ss.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 542..817
 FT /tag= a
 FT /product= "Human secreted protein"
 FT /transl_except= (pos:791..793, aa:Xaa)

PT /note= "Xaa equals any of the naturally occurring
 FT L-amino acids"
 FT sig_peptide 542..634
 FT /tag= b
 FT mat_peptide 635..814
 FT /tag= c
 FT /product= "Human mature secreted protein"
 XX
 XX W0200216390-A1.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-JAN-2001; 2001WO-US01435.
 XX
 XX 18-AUG-2000; 2000US-226282P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Komatsu G, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M,
 PI Ni J;
 XX
 XX WPI: 2002-304113/34.
 DR P-PSDB; AAE21202.
 XX
 PT An isolated nucleic acid molecule (1) comprising a polynucleotide which
 PT encodes a polypeptide useful in the diagnosis and treatment of
 PT disorders e.g. immune disorders -
 XX
 PS Claim 1; Page 447; 534pp; English.
 XX
 CC AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
 CC protein genes, and AAE21191-AAE21235 represent the proteins they encode.
 CC AAE21236-AAE21280 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 21 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC immune or autoimmune diseases e.g. AIDS (acquired immune deficiency
 CC syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
 CC and breast cancer, neurological diseases e.g. Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, Tourette syndrome,
 CC meningitis, demyelinating disease, peripheral neuropathies, neoplasia,
 CC trauma, congenital malformations, spinal cord injuries, toxic
 CC neuropathies induced by neurotoxins, peripheral neuropathies, multiple
 CC sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania,
 CC altered behaviours e.g. disorders in feeding, sleep patterns, balance
 CC and perception, encephalitis, disorders in cardiovascular, neural/
 CC sensory, reproductive and digestive systems, behavioural disorders and
 CC hyperproliferative disorder. The present sequence represents a human
 CC secreted protein-encoding cDNA of the invention.
 XX
 SQ Sequence 896 BP; 200 A; 213 C; 297 G; 180 T; 6 other;
 XX
 Query Match 0.5%; Score 21; DB 24; Length 896;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Oy 4561 TCTGCCCCCACCACCGCTTGC 4581
 Db 823 TCTGCCCCCACCACCGCTTGC 843
 XX
 RESULT 8
 AAQ87044/C
 ID AAQ87044 standard; CDNA; 1365 BP.
 XX
 AC AAQ87044;
 XX

```

DT 10-DEC-1995 (first entry)
XX
XX Pig interleukin-10 cDNA.
DE
XX Swine; interleukin-10; cytokine; lymphokine; protein; stem cell;
KM haematopoiesis; ss.
XX
XX Sus scrofa.
OS
XX Key Location/Qualifiers
FH CDS 73..651
FT /*tag= a
XX
XX MO9513363-A1.
XX
XX 18-MAY-1995.
XX
XX 01-NOV-1994; 94MO-US12522.
XX
XX 10-NOV-1993; 93US-0150739.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Emery DW, Le GUERN CA, Sachs DH, Leguern CA;
XX
XX WPI: 1995-194083/25.
XX
XX P-PSDB; AAR73018.
XX
XX New purified haematopoietic stem cells - isolated from swine cord
XX PT blood, used in transplantation, inducing immune tolerance and immune
XX PT system reconstitution
XX
XX PS Disclosure; Page 45; 58pp; English.
XX
XX This sequence encoding pig interleukin-10 may be expressed
XX CC recombinantly in swine cord blood haematopoietic stem cells. These
XX CC engineered stem cells may then be introduced into a recipient animal
XX CC so that the stem cells express IL-10. These recombinant cells may
XX CC be used in the induction of immunological tolerance, tissue
XX CC transplantation and reconstitution of the immune system without
XX CC having to use broad spectrum immune suppressants.
XX
XX SQ Sequence 1365 BP; 386 A; 322 C; 313 G; 344 T; 0 other;
XX
XX Query Match 0.5%; Score 21; DB 16; Length 1365;
XX Best Local Similarity 100.0%; Pred. NO. 42;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3334 CTCGGAAGCCCCAGCCAGG 3354
XX DB 1066 CTCGGAAGCCCCAGCCAGG 1046
XX
XX RESULT 9
XX AA085772/c
XX ID AA085772 standard; cDNA; 1365 BP.
XX
XX AA085772;
XX
XX 09-OCT-1995 (first entry)
XX
XX Porcine interleukin-10 (IL-10) cDNA.
XX
XX Interleukin-10; cytokine; immune response; ss.
XX
XX Sus scrofa.
XX
XX Key Location/Qualifiers
XX FH CDS 73..600
XX FT /*tag= a
XX
XX MO9506657-A.
XX

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PD 09-MAR-1995.
XX
XX 15-AUG-1994; 94MO-US09361.
XX
XX 30-AUG-1993; 93US-0114072.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Blanco GJF, Le GUERN CA, Sachs DH, Sykes M, Leguern CA;
XX
XX WPI: 1995-115396/15.
XX
XX P-PSDB; AAR71471.
XX
XX New DNA encoding porcine interleukin 10 and related vectors -
XX PT used to induce immunological tolerance, esp. for controlling
XX PT graft versus host disease.
XX
XX PS Claim 1; Page 33-35; 47pp; English.
XX
XX AA085772 excludes the poly A tail of porcine IL-10 cDNA. At the nt
XX CC level, the SQ is 82% homologous with the human IL-10 SQ, and 75%
XX CC homologous with the mouse IL-10 SQ. At the AA level the porcine
XX CC peptide is 74% homologous with human and 68% homologous with the
XX CC mouse SQ. The pig protein contains one potential N-linked
XX CC glycosylation site at Asn 130, 5 Cys residues, and 9 Met's. The calc.
XX CC mol. wt. of the porcine protein in 19,921 daltons. The pig sequence
XX CC shows a gap of four AAs in posn. 20-23, as compared with the human and
XX CC and mouse sequences.
XX
XX SQ Sequence 1365 BP; 386 A; 322 C; 313 G; 344 T; 0 other;
XX
XX Query Match 0.5%; Score 21; DB 16; Length 1365;
XX Best Local Similarity 100.0%; Pred. NO. 42;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3334 CTCGGAAGCCCCAGCCAGG 3354
XX DB 1066 CTCGGAAGCCCCAGCCAGG 1046
XX
XX RESULT 10
XX ABR84021
XX ID ABR84021 standard; cDNA; 4242 BP.
XX
XX ABR84021;
XX
XX 14-AUG-2002 (first entry)
XX
XX Human cDNA differentially expressed in granulocytic cells #592.
XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
XX KM viral infection; parasitic infection; protozoal infection;
XX KM fungal infection; sterile inflammatory disease; psoriasis;
XX KM rheumatoid arthritis; glomerulonephritis; asthma; chromoblast;
XX KM cardiac reperfusion injury; renal reperfusion injury; AIDS;
XX KM adult respiratory distress syndrome; inflammatory bowel disease;
XX KM Crohn's disease; ulcerative colitis; periodontal disease;
XX KM granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
XX
XX WO200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001MO-US30821.
XX
XX 03-OCT-2000; 2000US-237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley U;
XX

```

DR WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 592; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4242 BP; 1116 A; 1097 C; 1127 G; 902 T; 0 other;
SQ
Query Match 0.5%; Score 21; DB 24; Length 4242;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1661 CCCAGTATCCTGTCATCGA 1681
Db 1349 CCCAGTATCCTGTCATCGA 1369

RESULT 11
ABK84532
ID ABK84532 standard; CDNA; 4242 BP.
XX
XX ABK84532;
AC
XX
XX 14-AUG-2002 (first entry)
DT
XX
XX
DE Human cDNA differentially expressed in granulocytic cells #1103.
XX
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
OS
XX
XX WO200228999-A2.
PN
XX
XX 11-APR-2002.
PD
XX
XX 03-OCT-2001; 2001WO-US30821.
FF
XX
XX 03-OCT-2000; 2000US-237189P.
PR
XX
XX (GENE-) GENE LOGIC INC.
PA
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI
XX
XX WPI; 2002-435328/46.
DR
XX
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 1103; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4242 BP; 1116 A; 1097 C; 1127 G; 902 T; 0 other;
SQ
Query Match 0.5%; Score 21; DB 24; Length 4242;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1661 CCCAGTATCCTGTCATCGA 1681
Db 1349 CCCAGTATCCTGTCATCGA 1369

RESULT 12

ID ABK84127 standard; cDNA; 4519 BP

AC ABK84127;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #698.

KM Human use; granulocytic cell; DNA chip; bacterial infection;
KM viral infection; parasitic infection; protozoal infection;
KM fungal infection; sterile inflammatory disease; psoriasis;
KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
KM adult respiratory distress syndrome; inflammatory bowel disease;
KM Crohn's disease; ulcerative colitis; periodontal disease;
KM granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens

PN WO200228999-A2

PD 11-APR-2002

PF 03-OCT-2001; 2001WO-US30821

PR 03-OCT-2000; 2000US-237189P

PA (GENE-) GENE LOGIC INC.

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J, ...

WPI; 2002-435328/46

PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -

PS Claim 1; SEQ ID No 698; 114pp; English

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, Rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, AIDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC http://wipo.int/pub/published_pat_sequences.

SQ Sequence 4519 BP; 1033 A; 1314 C; 1301 G; 871 T; 0 other;

Query Match	0.5%;	Score 21;	DB 24;	Length 4519;
Best Local Similarity	100.0%;	Pred. No. 40;		
Matches 21, Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY 1436 CTCGTCACACACCTACCT 1456

Db 1136 CTCGTCACACACCTT 1156

RESULT 13

ID	standard; cDNA; 324 BP
AA591012	

AC AAS91012;
VV

DT 13-FEB-2002 (first entry)
VY

DE DNA encoding novel human diagnostic protein #26816. YX

KW Human; chromosome mapping; gene mapping; gene therapy; Lorenzian; food supplement; medical imaging; diagnostic; genetic disorder; ss

XX Homo sapiens

XX WO200175067-A2
 PN

XX
PD 11-OCT-2001

XX
PF 30-MAR-2001: 2001WO-US08631

XX
PR 31-MAR-2000: 2000US-0540217

PR 23-AUG-2000; 200005-064916 /

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT,

DR WPI; 2001-639362/73

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 26816; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 324 BP; 97 A; 61 C; 79 G; 87 T; 0 other;
Query Match 0.4%; Score 20; DB 23; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2181 GGCAGCAAGCTGAAGAAGGC 2200
DB 160 GGCAGCAAGCTGAAGAAGGC 179
RESULT 14
ABK64733/c
ID ABK64733 standard; DNA; 426 BP.
XX
AC ABK64733;
XX
DT 18-JUN-2002 (first entry)
DE Human benign prostatic hyperplasia gene #628.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
FN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI (NLSB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 339; 444p; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of genes in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for

CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 426 BP; 149 A; 78 C; 87 G; 112 T; 0 other;
Query Match 0.4%; Score 20; DB 24; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3044 CATCTTCGTGATGTGGCTG 3063
DB 234 CATCTTCGTGATGTGGCTG 215
RESULT 15
ABL66602/c
ID ABL66602 standard; DNA; 426 BP.
XX
AC ABL66602;
XX
DT 15-MAY-2002 (first entry)
DE Lung cancer related gene sequence SEQ ID NO:4939.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
FN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235846P.
PR 28-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236412P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.

PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

XX
 PA (AVAL-) AVALON PHARM.

XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;

XX
 DR MPI; 2002-188264/24.

XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -

XX
 PS Claim 1; SEQ ID 4939; 44p; English.

XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.

XX
 SQ Sequence 426 BP; 149 A; 78 C; 87 G; 112 T; 0 other;

Query Match 0.4%; Score 20; DB 24; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3044 CATTTCGTCATGTGGCTG 3063

DB 234 CATTTCGTCATGTGGCTG 215

Search completed: March 28, 2003, 22:25:35
 Job time : 1104 secs

GenCore version 5.1.4_P5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 21:31:59 ; Search time 6815 Seconds
(without alignments)
11014.832 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
Sequence: 1 tgcgcatctagaactagtg.....ggtacggggccagccccc 4635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estnu:*
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6: em_estpl:*
7: em_estro:*
8: em_hlc:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587	12.7	759	12 BG472146	BG472146 602513869
2	548	11.8	561	10 BE255177	BE255177 601151717
3	512	11.0	1016	12 BG394794	BG394794 602457129
4	473	10.2	14	BM903836	BM903836 BGENCOURT
5	365	7.9	436	12 BE908459	BE908459 601503091
6	340	7.3	663	12 BG819793	BG819793 602781835

7	293	6.3	395	10	BE244972	BE244972 TCBA3E16
8	172	3.7	801	13	BE255354	BE255354 601115369
9	156	3.4	684	13	BI756147	BI756147 603030048
10	57	1.2	839	17	AO741196	AO741196 HS_2273_A
11	38	0.8	509	12	BF463298	BF463298 UI-M-CGDP
12	38	0.8	696	10	BB430723	BB430723 BB430723
13	38	0.8	711	12	BG299246	BG299246 602395735
14	38	0.8	889	14	BQ946757	BQ946757 AGENCOURT
15	38	0.8	930	14	BQ960462	BQ960462 AGENCOURT
16	35	0.8	427	12	BE988680	BE988680 UI-M-CGDP
17	35	0.8	645	14	BO571436	BO571436 UI-M-FCO-
18	35	0.8	733	14	BM050299	BM050299 UI-M-EHDP
19	32	0.7	543	17	AZ503328	AZ503328 1M0343105
20	32	0.7	667	10	BB624082	BB624082 BB624082
21	32	0.7	702	17	AZ805180	AZ805180 2M0066013
22	32	0.7	714	12	BB652903	BB652903 BB652903
23	29	0.6	300	13	BG955666	BG955666 CM4-CT065
24	29	0.6	514	10	BB283947	BB283947 BB283947
25	29	0.6	577	14	BM932679	BM932679 UI-M-CGDP
26	29	0.6	664	10	BB642639	BB642639 BB642639
27	27	0.6	678	10	AV361753	AV361753 AV361753
28	27	0.6	226	10	BB047756	BB047756 BB047756
29	26	0.6	308	13	BG946330	BG946330 PM3-KT004
30	25	0.5	885	13	BI737630	BI737630 603358539
31	23	0.5	109	17	BH089788	BH089788 RRCI-24-3
32	23	0.5	324	13	BG945796	BG945796 PM3-KT004
33	23	0.5	624	12	BG682479	BG682479 602623577
34	22	0.5	230	10	AM889403	AM889403 RC6-NT002
35	22	0.5	233	12	BF944313	BF944313 RCS-NN116
36	22	0.5	245	12	BF804488	BF804488 OVA-C1015
37	22	0.5	276	12	F00147	F00147 HSB35B091_S
38	22	0.5	381	12	BF877125	BF877125 I13-ET011
39	22	0.5	400	13	BI816577	BI816577 1031046D0
40	22	0.5	485	14	BQ243736	BQ243736 TAE15010A
41	22	0.5	484	10	AV621575	AV621575 AV621575
42	22	0.5	497	10	BF399557	BF399557 UI-R-CA1-
43	22	0.5	512	10	AV392820	AV392820 AV392820
44	22	0.5	553	9	AA892330	AA892330 EST196133
45	22	0.5	555	17	AZ599264	AZ599264 IM0414D02

ALIGNMENTS

RESULT 1
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LOCUS 602513869F1 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:4645721 5',
DEFINITION mRNA sequence.
ACCESSION BG472146
VERSION BG472146.1 GI:13404520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 759)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM1419 row: 1 column: 18
High quality sequence stop: 683.
Location/Qualifiers
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/organism="Homo sapiens"

FEATURES

source

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/db xref="taxon:9606"
/clone="IMAGE:4645721"
/clone_1lb="NIH_MGC_1c"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT      148 a      248 c      256 g      107 t
ORIGIN

Query Match      12.7% Score 587; DB 12; Length 759;
Best Local Similarity 100.0%; Pred. No. 8e-260;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Query Match	Similarity	12.7%	Score 587	DB 12	Length 759
Best Local	Similarity	100.0%	Pred. No. 8e-260		
Matches	587	Conservative	0	Mismatches	0
				Indels	Gaps
QY 2795	GGAGATCATTTGAGCTCCCTGTGTGACTGACAGAGAGACAGACCCCGGTGATGACACAA				2854
Db 2	GGAGATCATTTGAGCTCCCTGTGTGACTGACAGAGAGAGACAGACCCCGGTGATGACACAA				61
QY 2855	CGGGTTCAACCCCACTGGAGAGAGACCTGTGTTTCAATGTGTCAATATGCCGAGATGCC				2914
Db 62	CGGGTTCAACCCCACTGGAGAGAGACCTGTGTTTCAATGTGTCAATATGCCGAGATGCC				121
QY 2915	GCTGTGCGCTTCTCTGTGTGGAGACACAGATCCATCGGAGCGTGAATTATTGGCCAGAG				2974
Db 122	GCTGTGCGCTTCTCTGTGTGGAGACACAGATCCATCGGAGCGTGAATTATTGGCCAGAG				181
QY 2975	GACCGTGGCTTTCAGACGATGATGTCAGAGCTTACAGACAGTGTACCTTAAAGAGATGGA				3034
Db 182	GACCGTGGCTTTCAGACGATGATGTCAGAGCTTACAGACAGTGTACCTTAAAGAGATGGA				241
QY 3035	AGAGCGCTCATCTTCTGTGATCATGTGGCTGTCAAGTGCATCAGGGGTAAAGTCAAGAGGC				3094
Db 242	AGAGCGCTCATCTTCTGTGATCATGTGGCTGTCAAGTGCATCAGGGGTAAAGTCAAGAGGC				301
QY 3095	TCTGGGCTTAAAGGCTCTTCTCTCGAGAGCCCAAGCCCGGCTCGCTTGAACATCATGC				3154
Db 302	TCTGGGCTTAAAGGCTCTTCTCTCGAGAGCCCAAGCCCGGCTCGCTTGAACATCATGC				361
QY 3155	TGCTGG				3214
Db 362	TGCTGG				421
QY 3215	CGCCCGACCAAGAGACCAAGAGCCCGAGCGACAGGGGCTTCCGAGACTGTCTTGGATAC				3274
Db 422	CGCCCGACCAAGAGACCAAGAGCCCGAGCGACAGGGGCTTCCGAGACTGTCTTGGATAC				481
QY 3275	ACGGGACACAGGCTTCCAAAGGGGTGGCAGACGATGTGGTCCCTCCCGGGCCCGGACTTGC				3334
Db 482	ACGGGACACAGGCTTCCAAAGGGGTGGCAGACGATGTGGTCCCTCCCGGGCCCGGACTTGC				541
QY 3335	TCCGGAAACCCCAAGCCCAAGAGAGGGCCCGGACGCGGACGAGCCCGGAG 3381				
Db 542	TCCGGAAACCCCAAGCCCAAGAGAGGGCCCGGACGCGGACGAGCCCGGAG 588				
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LOCUS	BE255177				
DEFINITION	60115717P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:335069 5',	561 bp	mRNA	linear	EST 13-JUN-2000
ACCESSION	BE255177				
VERSION	BE255177.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				

REFERENCE	1 (bases 1 to 561)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strauberg, Ph.D. rstraub@nihs.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at: image.llnl.gov
Plate: LLCML61 row: b column: 06
High quality sequence (snp): 539

FEATURES	Location/Qualifiers
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/clone_1b="NIH MGC 16"
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pOT67; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: This is a NIH_MGC library."

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	Query Match Similarity	11.8%; Score 548; DB 10; Length 561;
	Best Local Similarity	100.0%; Pred. No. 7.9e-242;
	Matches 548; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2828	GGAGCAGACCCGCGTGTGAGCGAACAGGGATTCACCCACCCTGGGAGAGACCTGTG 2887
Db	14	GGAGCAGACCCGCGTGTGAGCGAACAGGGATTCACCCACCCTGGGAGAGACCTGTG 73
QY	2888	TTTCATGTGTGACATGATCCGGAGATCCGGCTGTGTCCGCTTCTGTGTGGACCAAGATCC 2947
Db	74	TTTCATGTGTGACATGATCCGGAGATCCGGCTGTGTCCGCTTCTGTGTGGACCAAGATCC 133
QY	2948	CATCGGACGTGACTTCATTGTGCGAGAGAGAGCGTGGCCTTCAGCAGCATATGCGAGGCTA 3007
Db	134	CATCGGACGTGACTTCATTGTGCGAGAGAGCGTGGCCTTCAGCAGCATATGCGAGGCTA 193
QY	3008	CAGACACGCTGTACTTAGAAGGATGAGAAAGCGCTCATCTTGTGTCATGTGACTGTGAG 3067
Db	194	CAGACACGCTGTACTTAGAAGGATGAGAAAGCGCTCATCTTGTGTCATGTGACTGTGAG 253
QY	3068	TGACATCAGCCGTAAAGTCACAGCGAGCTCTGGGCGCTTAAAAAGGCTTCTCTCCGAGGCC 3127
Db	254	TGACATCAGCCGTAAAGTCACAGCGAGCTCTGGGCGCTTAAAAAGGCTTCTCTCCGAGGCC 313
QY	3128	AAAGCCCGGCTCGCTGAGCAGTCACTGTGCTGGGCGGACCCCGGACCCGAGCCTCCGTTAG 3187
Db	314	AAAGCCCGGCTCGCTGAGCAGTCACTGTGCTGGGCGGACCCCGGACCCGAGCCTCCGTTAG 373
QY	3188	CCAGCGGATCTCTGCGGCGCACGGCCAGCGCCCGGACCAAGAGCCAGAAACCAGGACCGAGCGGAG 3247
Db	374	CCAGCGGATCTCTGCGGCGCACGGCCAGCGCCCGGACCAAGAGCCAGAAACCAGGACCGAGCGGAG 433
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QY	3308	TGTGTGTGCCCCCGAGGACCCGAGACCTGTCTCCGAAAGGCCACAGGCCAGAGAGGGGCCCGGAG 3367
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 VERSION BG394794.1 GI:13288242
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1016)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L12M1297 row: 1 column: 08
 High quality sequence stop: 599.
 Location/Qualifiers
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: POTB; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES

source
 1. 1016
 /organism="Homo sapiens"
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 /note="Organ: eye; Vector: POTB; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 324 a 302 c 247 g 143 t
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 Best Local Similarity 99.8%; Pred. No. 3 8e-225;
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 DB 9 GAGCCATGCCAGAAAACAAGTAAGGGCTGTGGGCAATTGATGCTTACCAACTAC 68
 QY 1347 ACCAGAGCCCTGTGTGTCATCTTCAACCTGAGACCAACCATGTGACCCAGACATG 1406
 DB 69 ACCAGAGCCCTGTGTGTCATCTTCAACCTGAGACCAACCATGTGACCCAGACATG 128
 QY 1407 ACCGAGCCGTGAGCCACTACTCATCACTGTCCACAACCACTACCTGTGGGTGAC 1466
 DB 129 ACCGAGCCGTGAGCCACTACTCATCACTGTCCACAACCACTACCTGTGGGTGAC 188
 QY 1467 CAGCTCATGTCCAGTCACGGGTGACATGTATGCTTGGTCTTCGACAGCTGGCTGGC 1526
 DB 189 CAGCTCATGTCCAGTCACGGGTGACATGTATGCTTGGTCTTCGACAGCTGGCTGGC 248
 QY 1527 TGGCTGAGAGTGAATCTCTGGATGGGCGGAGGAGGAGCCATTGGCAACCATGGCTAC 1586
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 QY 1647 ATCAAGATAGTATCCAGATCCCTGTGATGAGAAACCAACGACGTGATCCAGACAG 1706
 DB 369 ATCAAGATAGTATCCAGATCCCTGTGATGAGAAACCAACGACGTGATCCAGACAG 428
 QY 1707 AAGAAATGCGCCAGTATCTGATGATCAATCTTGGGACAAAGCTGACCTGTATGATG 1766
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 DEFINITION AGENCOURT_6695882 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5492312
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 VERSION BM903836.1 GI:19353598
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1002)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L12M1214 row: d column: 09
 High quality sequence stop: 428.
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Library constructed by Life
 Technologies."

FEATURES

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 /lab_host="DH10B (phage-resistant)"
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.75 kb. Library constructed by Life
 Technologies."
 BASE COUNT 220 a 299 c 343 g 140 t
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 Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 AAAGCTGAGCGCAAGCAAGCTGAAGAGAGCTGAGTCTGGAGAGATGCTGGGGC 60
 QY 2126 CAGCAGAGCAATGCGCCCTCTGCTGTGGGAAGCTTCTCCAGGCGCAAGAAAGAGGCGAG 2185

Db	61	CAGCAGAGCCATGCGCGCTGTCGTGGGAAGCTTCTCCAGGCGCAAGAGAGGGCAG	120
OY	2186	CAAGCTGAAGAAAGCGCGCCAGCGCTGGAGGAGGAGATGAAGGTCAAGACTCCCCGGAGG	2245
Db	121	CAAGCTGAAGAAAGCGCGCCAGCGCTGGAGGAGGAGATGAAGGTCAAGACTCCCCGGAGG	180
OY	2246	CCAGAGCCGAGGGGGCGACCCGGCGAGAGAAAGACATGAAGCTGTCCCGGGCCCTCTCTCA	2305
Db	181	CCAGAGCCGAGGGGGCGACCCGGCGAGAGAAAGACATGAAGCTGTCCCGGGCCCTCTCTCA	240
OY	2306	CTGTGTGAAGTACACCAAGTCTCGTGGCCACCCACGACATAGAGATGGAAGCGCGCTCCAG	2365
Db	241	CCTGTGTGAAGTACACCAAGTCTCGTGGCCACCCACGACATAGAGATGGAAGCGCGCTCCAG	300
OY	2366	CTGGCAGGTGTGTCCTCTCAGCGAGCCAAAGGCCCAACGATTTCTGCACAGAGCGCGG	2425
Db	301	CTGGCAGGTGTGTCCTCTCAGCGAGCCAAAGGCCCAACGATTTCTGCACAGAGCGCGG	360
OY	2426	GGAGTACCTTACGCTTTCACACAGCAGAGCTTTCGGCATCTACCCCTCTCTTACCGTGT	2485
Db	361	GGAGTACCTTACGCTTTCACACAGCAGAGCTTTCGGCATCTACCCCTCTCTTACCGTGT	420
OY	2486	GGACTTCAGCACTCAACCCGAGCGCTTTCGGAACGCGGGGTGCAAAATGG	2538
Db	421	GGACTTCAGCACTCAACCCGAGCGCTTTCGGAACGCGGGGTGCAAAATGG	473

RESULTS	
BE908459	
LOCUS	
DEFINITION	436 bp mRNA linear EST 20-OCT-2000
ACCESSION	BE908459
VERSION	6015030191.1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3904894 5',
KEYWORDS	mRNA sequence.
	BE908459
	BE908459.1 GI:10403059
	EST.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	1 (bases 1 to 436)	NIH-MGC http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLM8711 row: e column: 23
High quality sequence stop: 433.

FEATURES

Location/Qualifiers
1. .436

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BASE COUNT      100 a      129 c      138 g      69 t
ORIGIN
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:3904894"
/clone_1lb="NH MGC 70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: NotI
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

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Query Match	7.9%	Score 365;	DB 12;	Length 436;
Best Local Similarity	100.0%;	Pred. No. 2.7e-157;		
Matches 365;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	937	AGTGGCTGAAGCAGACGTTTGAACGAGGCCGAACAAGAACGGGGGATGAGCAGCTTGAGCATTTG	996
Db	72	AGTGGCTGAAGCAGACGTTTGAACGAGGCCGAAGAACGGGGGATGAGCAGCTTGAGCATTTG	131
QY	997	GCGAGGTCCTGCACTGCTGCACAAGCTTCAAGTGAACCTGCCCCGCGAGAGGGGTGAAGC	1056
Db	132	GCGAGGTCCTGCACTGCTGCACAAGCTTCAAGTGAACCTGCCCCGCGAGAGGGGTGAAGC	191
QY	1057	AGAGTTTCAGGGAAAGGGGACATGATGACACCAAGGGAAGCTTGGGTTTGAAGAGTTCT	1116
Db	192	AGAGTTTCAGGGAAAGGGGACATGATGACACCAAGGGAAGCTTGGGTTTGAAGAGTTCT	251
QY	1117	GTGCGCTTCTCAAGATGATGTCCACCCCGCGGGACCTTACCTGCTCATGCTGACCTACA	1176
Db	252	GTGCGCTTCTTCAAGATGATGTCCACCCCGCGGGACCTTACCTGCTCATGCTGACCTACA	311
QY	1177	GCAACCAACAAGACCAACTGATGTCGCGCCAGCTTGCAAGCCGTTTCTTGCAAGTGAAGCAAG	1236
Db	312	GCAACCAACAAGACCAACTGATGTCGCGCCAGCTTGCAAGCCGTTTCTTGCAAGTGAAGCAAG	371
QY	1237	AGATGGGGGGGTGTGACCCCTCGAGAGCTGCAAGACATATGTGAAGCAAGTTTGAAGCCATGCC	1296
Db	372	AGATGGGGGGGTGTGACCCCTCGAGAGCTGCAAGACATATGTGAAGCAAGTTTGAAGCCATGCC	431
QY	1297	CAGAA 1301	
Db	432	CAGAA 436	

RESULT	6
BG819793	
LOCUS	663 bp mRNA linear EST Z2-MAY-2001
DEFINITION	602781835F1 NCI CGAP_Brn67 Homo sapiens CDNA IMAGE:4932488
ACCESSION	BG819793
VERSION	BG819793.1 GI:14167380
KEYWORDS	EST.
SOURCE	human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 663)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LNLN10858 Row: F Column: 09
 High quality sequence stop: 649.

FEATURES

SOURCE

Location/Qualifiers
1. .663

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4932488"
/clone_id="NCI_CGAP_Brm67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (r1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
BASE COUNT      133 a      199 c      212 g      119 t
ORIGIN

```

Query Match	7.3%	Score 340	DB 12	length 663
Best Local Similarity	-99.8%	Pred. No. 1	1e-145	
Matches 460	Conservative 0	Mismatches 0	Indels 1	Gaps 1

QY	2596	GGCGCAACGGATGATCGCGGCTACGTAACCTGAGGTCATGTGCGCAGGGCGATGTTCA	2655
Db	78	GGCGCAACGGATGATCGCGGCTACGTAACCTGAGGTCATGTGCGCAGGGCGATGTTCA	137
QY	2656	ACCCCAACTCGGAGGACCCCTTGCCCGGAGCTCAAGAGCACTGTGTTCCGGATCA	2715
Db	138	ACCCCAACTCGGAGGACCCCTTGCCCGGAGCTCAAGAGCACTGTGTTCCGGATCA	197
QY	2716	TCAGTGGCGCAGA -GCTTCCCAAGCCGCGGCACTGCATCTGTGGGGGACCGTGGGGGATC	2774
Db	198	TCAGTGGCGCAGATCTTCCCAAGCCGCGGCACTGCATCTGTGGGGGACCGTGGGGGATC	257
QY	2775	ATCGACCCCTTGTGTGAGGTGAGATCATTTGGGCTCCCTGTGGACTGCGACGAGGAGCAG	2834
Db	258	ATCGACCCCTTGTGTGAGGTGAGATCATTTGGGCTCCCTGTGGACTGCGACGAGGAGCAG	317
QY	2835	ACCCECGTGTGTGACAGCAACGGGTTCAACCCCACTGGGAGAGAACCTTGTTTTCATG	2894
Db	318	ACCCECGTGTGTGACAGCAACGGGTTCAACCCCACTGGGAGAGAACCTTGTTTTCATG	377
QY	2895	GTCGACATGTCGCGAGATCGCGCTGTGTCGACTTCTTGTCGTGGGACCAACGATCCCATCGGG	2954
Db	378	GTCGACATGTCGCGAGATCGCGCTGTGTCGACTTCTTGTCGTGGGACCAACGATCCCATCGGG	437
QY	2955	CGTGACTTCATTGGCCAGAGAACGCTGCGCTTTCAGCAGCATGATGTCAGAGCTTACAGACAC	3014
Db	438	CGTGACTTCATTGGCCAGAGAACGCTGCGCTTTCAGCAGCATGATGTCAGAGCTTACAGACAC	497
QY	3015	GTCGTAACCTGAGAGGATGGAAGAGGCTCCATCTTCGTGCA 3055	
Db	498	GTCGTAACCTGAGAGGATGGAAGAGGCTCCATCTTCGTGCA 538	

RESULT	7
LOCUS	B244972
DEFINITION	B244972 395 bp mRNA linear EST_03-OCT-2001 TCBAP31691 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1691, mRNA sequence.
ACCESSION	B244972
VERSION	B244972
KEYWORDS	EST.
SOURCE	B244972.1 GI:9096637
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 395) Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D. Pouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project Unpublished (2000)
TITLE	Contact: Dr. Judith F. Margolin
JOURNAL	Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
COMMENT	1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536 Fax: 832-825-4038 Email: clones@xcsc.org Citation: Carinci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seq primer: M13 primer.

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/tissue_type="Leukopheresis"
/cell_type="Pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB, Site_1: BamHI, Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo (dT) primer (5'GGAGGACTCGAGCGGCGGAGGAG(17)VN
3'; V=A,C,G; N=A,C,G,T) and then dg tailed. Second strand
was primed with a BamHI-dC primer
(5'AGAGAGCTCGAGTCGCGCGCGCCGATATATAT(C) 3').
Double-stranded cDNA was then digested with BamHI and SalI sites of
lambda and directionally cloned into the BamHI and SalI sites of
lambda PSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasakini, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y. High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-66, Feb 28, 1997)"

```

Query Match	6.3%	Score 293	DB 10	Length 395
Best Local Similarity	100.0%	Pred. No. 5e-124		
Matches 293	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	2257	GGGGACCCGGGCAGAAAGAACCAATGAAGCTGTCCCGGGCCCTCTCTGACCTGGAGAAAT	2316
Db	103	GGGGCACCCGGCAGAAAGAACCAATGAAGCTGTCCCGGGCCCTCTCTGACCTGGAGAAAT	162
Qy	2317	AACACCAAGTCCGTGGCCACCCACGACATAGAATGAGAGCGGCGTCCAGCTGGACGGTGT	2376
Db	163	AACACCAAGTCCGTGGCCACCCACGACATAGAATGAGAGCGGCGTCCAGCTGGACGGTGT	222
Qy	2377	CGTCTTTAGAGAGAACCAAGGCCACCAAGATTCTGACACAGAAAGCCGGGCGACGTACTAC	2436
Db	223	CGTCTTTAGAGAGAACCAAGGCCACCAAGATTCTGACACAGAAAGCCGGGCGACGTACTAC	282
Qy	2437	GCTTCAACCAAGACAGAGCTCTCCCGCATCTAACCCCTCCTCTACCGGTGAGCTCCAGCA	2496
Db	283	GCTTCAACCAAGACAGAGCTCTCCCGCATCTAACCCCTCCTCTACCGGTGAGCTCCAGCA	342
Qy	2497	ACTAAACCCGACGACCTTTGGAAGACGCGCGTGCAAAATGGTTGGCCCTGAAC	2549
Db	343	ACTAAACCCGACGACCTTTGGAAGACGCGCGTGCAAAATGGTTGGCCCTGAAC	395

RESULT 8	BE255354	801 bp	mRNA	linear	EST 13-JUL-2000
LOCUS	BE255354				
DEFINITION	BE255354	601115369P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355889 5',			
ACCESSION	BE255354				
VERSION	BE255354				
KEYWORDS	EST.	GI:9125792			
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Mumukhota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Emmalyota; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 801)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				

		/dev stage="adult"	
		/lab host="SOLR"	
		/note="Site 1: Xhol; Site 2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',	
		GAGAGAAGAGATCCCAAGACCTCTTTTTCCTTTTTTNN 3']	cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
		GAGAGAAGATTCTCGATTATTAAATTATGCCCCCCCCC 3']"	
BASE COUNT	184 a	175 c	202 g 134 t 1 others
ORIGIN			
Query Match Best Local Similarity	0.8%; 100.0%;	Score 38; Pred. No.	DB 10; 3,7e-06;
Matches	38;	Conservative	0; Indels 0; Gaps 0;
OY	1641	GCCTCATCAGAATGATGACCAGCATCGTGCCAT	1678
Dd	145	GGCTTCATCAAAGATGAGTACCAAGTAGTCGTCCAT	192
RESULT 13			
LOCUS	BG299246		
DEFINITION	603395735F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4507377 5', mRNA Sequence.		
ACCESSION	BG299246		
VERSION	BG299246.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria (to 711)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
JOURNAL	Contact: Robert Stransberg, Ph.D. Email: cgabbs@mail.nih.gov		
COMMENT	Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLM10384 row: e column: 10 High quality sequence start: 4 High quality sequence stop: 660. Location/Qualifiers 1..711 /organism="Mus musculus" /db_xref="taxon:10090" /clone_image=4507377" /clone_id="NIH_MGC_94" /libsize_type="retina" /lab_host="MDH1OB (phage-resistant)" /note="Organ: eye; Vector: pcMV-SPOr6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: This is a NIH_MGC library."		
BASE COUNT	179 a	204 c	211 g 116 t 1 others
ORIGIN			
Query Match Best Local Similarity	0.8%; 100.0%;	Score 38; Pred. No.	DB 12; 3.7e-06;
			Length 711;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2466 TACCCCTCCTCTACCCTGTGAGCTTCACCACTCA 2503
|||||
Db 310 TACCCCTCCTCTACCCTGTGAGCTTCACCACTCAA 347

RESULT 14
B0946757
LOCUS B0946757
DEFINITION AGENCOURT_8924326 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466785
ACCESSION B0946757
VERSION B0946757.1 GI:22362235
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LRAM1391 row: k column: 10
High quality sequence stop: 676.

FEATURES
source location/Qualifiers
1..889
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6466785"
/clone_id="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCW-SKOR6; Site 1: NCI;
Site_2: Salt; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

BASE COUNT 193 a 268 c 272 g 155 t 1 others

ORIGIN
Query Match 0.8%; Score 38; DB 14; Length 889;
Best Local Similarity 100.0%; Prid. No. 3..9e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2535 ATGGTTGCCCTGAAGTAACAGATCGAGGCGCATGCT 2572
|||||
Db 24 ATGGTTGCCCTGAAGTAACAGATCGAGGCGCATGCT 61

RESULT 15
B0960462
LOCUS B0960462
DEFINITION BO960462 930 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8930277 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466491
ACCESSION B0960462
VERSION B0960462.1 GI:22375940
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1390 row: 0 column: 04
High quality sequence stop: 634.
Location/Qualifiers

FEATURES

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1. 930
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6466491"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 222 a 267 c 292 g 148 t 1 others
ORIGIN

Query Match 0.8%; Score 38; DB 14; Length 930;
Best Local Similarity 100.0%; Pred.No. 3.9e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2466 TACCCCTCTCTACCGTGTGAGACTCCAGCACTACCA 2503
Db 431 TACCCCTCTCTACCGTGTGAGACTCCAGCACTACCA 468

Search completed: March 29, 2003, 08:02:21
Job time : 6873 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 13:51:40 ; Search time 38 Seconds
(without alignments)
1865.249 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379

Sequence: 1 MAPPTAGPLPGPALPEDP...ALYPMHCLRGMLPWLACGP 1207

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6379	100.0	1207	10	US-09-927-112-2
2	1738	27.2	325	10	US-09-927-112-10
3	1441	22.6	762	10	US-09-804-969-15
4	1441	22.6	762	10	US-09-908-664-2
5	1281	20.1	744	9	US-10-096-961-4
6	1279.5	20.1	736	10	US-09-800-971-2
7	1278.5	20.0	736	9	US-10-096-961-2
8	1262	19.8	744	9	US-10-096-961-5
9	1085.5	17.0	608	10	US-09-908-664-5
10	1002	15.7	567	10	US-09-835-996A-8
11	840.5	13.2	1809	10	US-09-822-635-2
12	723.5	11.3	1054	10	US-09-828-447-11
13	685.5	10.7	628	10	US-09-828-447-12
14	522.5	8.2	340	10	US-09-835-996A-19
15	515	8.1	191	10	US-09-908-664-22
16	494	7.7	170	10	US-09-908-664-13
17	458	7.2	158	10	US-09-927-112-11
18	452.5	7.1	847	10	US-09-765-298A-10
19	452	7.1	182	10	US-09-800-971-7

20	444	7.0	119	9	US-09-764-868-637	Sequence 637, App
21	444	7.0	119	9	US-09-955-999-84	Sequence 84, App1
22	426.5	6.7	153	10	US-09-822-635-5	Sequence 5, App11
23	426.5	6.7	153	10	US-09-800-971-6	Sequence 6, App11
24	426.5	6.7	153	10	US-09-927-112-7	Sequence 7, App11
25	426.5	6.7	153	10	US-09-908-664-10	Sequence 10, App1
26	426.5	6.7	153	10	US-09-908-664-19	Sequence 19, App1
27	375	5.9	201	10	US-09-867-550-1334	Sequence 1334, App
28	335	5.3	119	10	US-09-800-971-9	Sequence 9, App11
29	323.5	5.1	128	10	US-09-908-664-23	Sequence 23, App1
30	320.5	5.0	272	10	US-09-804-969-19	Sequence 19, App1
31	319.5	5.0	128	10	US-09-908-664-15	Sequence 15, App1
32	290	4.5	128	10	US-09-800-971-8	Sequence 8, App1
33	290	4.5	128	10	US-09-927-112-8	Sequence 8, App1
34	290	4.5	128	10	US-09-927-112-8	Sequence 11, App1
35	290	4.5	128	10	US-09-908-664-11	Sequence 20, App1
36	284.5	4.5	181	10	US-09-908-664-20	Sequence 14, App1
37	284.5	4.5	202	10	US-09-927-112-14	Sequence 14, App1
38	264	4.1	158	10	US-09-908-664-14	Sequence 377, App
39	264	4.1	158	10	US-09-764-870-377	Sequence 342, App
40	263.5	4.1	102	10	US-09-764-860-342	Sequence 7, App11
41	260.5	4.1	105	10	US-09-822-635-7	Sequence 357, App
42	255.5	4.0	134	10	US-09-764-870-357	Sequence 15, App1
43	249	3.9	92	10	US-09-927-112-15	Sequence 16, App1
44	228	3.6	1134	9	US-10-001-873-50	Sequence 50, App1
45	193.5	3.0	535	9	US-10-043-487-306	Sequence 306, App

ALIGNMENTS

```
RESULT 1
US-09-927-112-2
Sequence 2, Application US/09927112
Patent No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Siles-Santiago, Immaculada
TITLE OF INVENTION: 32544, a novel human phospholipase C and
FILE REFERENCE: 38155-20048.00
CURRENT FILING DATE: US/09/927,112
CURRENT APPLICATION NUMBER: US-08-10
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1207
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-112-2
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Query Match 100.0%; Score 6379; DB 10; Length 1207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAPPTAGPLPGPALPEDPDPESRWFLSANILPVERCKAMQEGMAYKLRGSKG 60
DB 1 MAPPTAGPLPGPALPEDPDPESRWFLSANILPVERCKAMQEGMAYKLRGSKG 60
OY 61 LVAFYTLDRHSIRKRPKRNEKAKISTDSIOEVSEGSOSVPRYPGSDPNCFSI 120
DB 61 LVAFYTLDRHSIRKRPKRNEKAKISTDSIOEVSEGSOSVPRYPGSDPNCFSI 120
OY 121 YHSHRESLDIVSTSEVARTWTGRLYLACISDESLARORTRDWLKOTPEADKN 180
DB 121 YHSHRESLDIVSTSEVARTWTGRLYLACISDESLARORTRDWLKOTPEADKN 180
OY 181 GDGSLISGEYLQLLHLNLNLPQRYKQMFREADTDHGTGTFEFCAFYKMSRRDL 240
DB 181 GDGSLISGEYLQLLHLNLNLPQRYKQMFREADTDHGTGTFEFCAFYKMSRRDL 240
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QY 241 YLMLTYSNKHDLDAASLOEFLQVEOKMAGVTLSESCODIIEOEPCEPKSKGLGIDG 300
DB 241 YLMLTYSNKHDLDAASLOEFLQVEOKMAGVTLSESCODIIEOEPCEPKSKGLGIDG 300
QY 301 FTTNTSRPADIDFNEHHHHVHODMTQPLSHYFTTSSHNTLVGDQLMSQSRVMYAVLQ 360
DB 301 FTTNTSRPADIDFNEHHHHVHODMTQPLSHYFTTSSHNTLVGDQLMSQSRVMYAVLQ 360
QY 361 AGCCVCVDMGDGDEPIYHGGYTLTKSLFKFDVITETIKYAFIKNEYVYLIENHGS 420
DB 361 AGCCVCVDMGDGDEPIYHGGYTLTKSLFKFDVITETIKYAFIKNEYVYLIENHGS 420
QY 421 VIOQRKMAOYLTDLDGDKLDSVSSSEDATLTPSPQMLKGIIVYKGIKIPANISEDAGEG 480
DB 421 VIOQRKMAOYLTDLDGDKLDSVSSSEDATLTPSPQMLKGIIVYKGIKIPANISEDAGEG 480
QY 481 EVSDESDADEIDDDCKLNDASTNKRKVENTAKRKLDLSIKESKIRDCEDPNFVSSTL 540
DB 481 EVSDESDADEIDDDCKLNDASTNKRKVENTAKRKLDLSIKESKIRDCEDPNFVSSTL 540
QY 541 SPFGKLGKRAKAEDEVSDESDASTNKRKVENTAKRKLDLSIKESKIRDCEDPNFVSSTL 540
DB 541 SPFGKLGKRAKAEDEVSDESDASTNKRKVENTAKRKLDLSIKESKIRDCEDPNFVSSTL 540
QY 601 SPGGQSGRATROKTKMLSRALSDLVKTKSVATHDIEEAASSMQVSSFSSTKAHQIIO 660
DB 601 SPGGQSGRATROKTKMLSRALSDLVKTKSVATHDIEEAASSMQVSSFSSTKAHQIIO 660
QY 661 QKPAQKLRNFQOOLSRITSSYSSVYDSSNNPQPFMAAGCOMALNTQSGRMQLNRAKE 720
DB 661 QKPAQKLRNFQOOLSRITSSYSSVYDSSNNPQPFMAAGCOMALNTQSGRMQLNRAKE 720
QY 721 SANGGCGVYLRKPCMCQGVFNPNSEDPPLPGOLKOLVLIISGOOLPKPRDMSLGDRCET 780
DB 721 SANGGCGVYLRKPCMCQGVFNPNSEDPPLPGOLKOLVLIISGOOLPKPRDMSLGDRCET 780
QY 781 IDPFVEVEIIGLYPCOSRQOTRYVNDNGNPNFTWETLVFMVMPETALVRLVMDHDPITG 840
DB 781 IDPFVEVEIIGLYPCOSRQOTRYVNDNGNPNFTWETLVFMVMPETALVRLVMDHDPITG 840
QY 841 RDEFIGORTLAFSSMMMPGYRHYVLEGEAEASIFVHVASPDISGKVOALGKGLFIRGKRP 900
DB 841 RDEFIGORTLAFSSMMMPGYRHYVLEGEAEASIFVHVASPDISGKVOALGKGLFIRGKRP 900
QY 901 GSLDSHAAGRPARPVSORILRTASAPTKSQKGRGFPPELVLTGTRDTGSKGVADVV 960
DB 901 GSLDSHAAGRPARPVSORILRTASAPTKSQKGRGFPPELVLTGTRDTGSKGVADVV 960
QY 961 PPGPPAPAPAPAOEGPGSGSPGKAPAAVAEKSPPRVPRVPLDGPAGMAATCMKCV 1020
DB 961 PPGPPAPAPAPAOEGPGSGSPGKAPAAVAEKSPPRVPRVPLDGPAGMAATCMKCV 1020
QY 1021 GSCAGVNTGLOREPPSPGPASRQAIRQOPRARADSLGAPCCGLDHPHAIPIGSRREAPK 1080
DB 1021 GSCAGVNTGLOREPPSPGPASRQAIRQOPRARADSLGAPCCGLDHPHAIPIGSRREAPK 1080
QY 1081 GPGARROGPGSGSSSSSPDSCGTERSPRMEGACRPGALOGMSALFAOKLEEI 1140
DB 1081 GPGARROGPGSGSSSSSPDSCGTERSPRMEGACRPGALOGMSALFAOKLEEI 1140
QY 1141 RSKSPMFAGRPDLPCVYLPHAPGAGGSPAAASAMTVSRVYLVALYPMHCLRGTL 1200
DB 1141 RSKSPMFAGRPDLPCVYLPHAPGAGGSPAAASAMTVSRVYLVALYPMHCLRGTL 1200
QY 1201 PMLACGP 1207
DB 1201 PMLACGP 1207

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; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Siles-Santiago, Inmaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-10

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```

Query Match 27.2%; Score 1738; DB 10; Length 325;
Best Local Similarity 99.7%; Pred. No. 1.2e-97;
Matches 324; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 883 KYQALGLKGLFLNGPKGSLDASHAAGRPAPPSVSORILRTASAPTKSQKGRGFPPE 942
DB 1 QVQALGLKGLFLNGPKGSLDASHAAGRPAPPSVSORILRTASAPTKSQKGRGFPPE 60
QY 943 LVLTGTRDTGSKGVADVVPPGPPAPAPAOEGPGSGSPGKAPAAVAEKSPPRVPRPV 1002
DB 61 LVLTGTRDTGSKGVADVVPPGPPAPAPAOEGPGSGSPGKAPAAVAEKSPPRVPRPV 120
QY 1003 LDGPPAGMAATCMKCVYVSCAGVNTGLOREPPSPGPASRQAIRQOPRARADSLGAP 1062
DB 121 LDGPPAGMAATCMKCVYVSCAGVNTGLOREPPSPGPASRQAIRQOPRARADSLGAP 180
QY 1063 CCGLDHPHAIPIGSRREAPKGGKAMRQGGSGSSSSSPDSCGTERSPRMEGACRPG 1122
DB 181 CCGLDHPHAIPIGSRREAPKGGKAMRQGGSGSSSSSPDSCGTERSPRMEGACRPG 240
QY 1123 GALOGMSALFAOKLEIRSKSPMFSAGKPLPCVYLPHAPGAGGSPAAASAMTVSR 1182
DB 241 GALOGMSALFAOKLEIRSKSPMFSAGKPLPCVYLPHAPGAGGSPAAASAMTVSR 300
QY 1183 VLVVALYPMHCLRGTLPLWACGP 1207
DB 301 VLVVALYPMHCLRGTLPLWACGP 325

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RESULT 3
US-09-804-969-15
; Sequence 15, Application US/09804969
; Patent No. US20020081595A1
; GENERAL INFORMATION:
; APPLICANT: Nepomichy, Boris
; APPLICANT: Donoho, Gregory
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abuh, Alejandro
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides
; FILE REFERENCE: LEX-0148-USA
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,885
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 60/189,693
; PRIOR FILING DATE: 2000-03-15

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NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 762
 TYPE: PRT
 ORGANISM: homo sapiens
 US-09-804-969-15

Query Match 22.6% Score 1441; DB 10; Length 762;
 Best Local Similarity 36.3%; Pred. No. 3.2e-79;
 Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;

45 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 102
 18 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 76
 103 VQORPDGSPDNCCFSYTHGSHRESLDVSTSEVARTWYTGRIYLMAGISDDSLARR 162
 77 LRLSLAEELPLEQGFYTHG--RPSNLDLMANVSEADIMWGLLDVLTSMD---H 131
 163 ORTRDOWLKOTFEADKNGDLSIGEVYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 222
 132 QERLDOWLSDMFORDKNDGKMSQEOVORLLHLMNVEMDQYAFSLQADT--S0SGTL 190
 223 GEEFCAFYKMMSTRDLYLMLTYSNHKNHDAASLQFLQVQKMAVTLSECDITIE 282
 191 EGEFFQVQKALTKRAVEOLFESFSADGOKLTLLFDFLOEOKERDCTSELALELID 250
 283 QERPEKNSKGLDIDGFTNTYTRPADIDFNRHNNHNDOTPLSHYFTSSHNTYLV 342
 251 RYPSDSGLRHLVLSMDGFLSTYCSKDDIDFNPACLPYDQMTOPLNHYFTSSHNTYLV 310
 343 GDLMSQSRVDMYAVYLQAGRCVDCWDGDPGEPIYHNGVTLTKILFKDVIETINKY 402
 311 GDLQSGSSVEGYIRALKRGCRCEVDVWDGSGEPVYHGHITLTSRLIFKDYAVATVAY 370
 403 AFKNEYRPIVLTSENHCYVTOOKKMAQYITDILGKLDSSVSEDAATLPSPOLMKKI 462
 371 AFQTSQYPIVLTSENHCYVTOOKKMAQYITDILGKLDSSVSEDAATLPSPOLMKKI 430
 463 LVKGRKLPANISEDAEGVSDSDADEIDDDCKLLNGDASTNRKRVENTAKRKLDLSLK 522
 431 LVKGRKLPANISEDAEGVSDSDADEIDDDCKLLNGDASTNRKRVENTAKRKLDLSLK 461
 523 ESKIRDCEDPNFNSVSTLSPSGKLGKSKAEDVESGEDAGASRRNGRLVVGFSFRKKK 582
 462 ESOFTFEPERPO-----EONLNKND-----KKKK 484
 583 GSKLKAASVEBDEGODSPGOSRGATROKTKMLSRALSDLYKTKSYA---THDIE 638
 485 SKPI-----LCPALSSLVLYLKSVSFRSFTH--S 511
 639 MEAASWQVSFSETKAHOILOQKPAOYLFRNOOLSRYPSSRYSDSSNYPQPFMNG 698
 512 KEHYHFEIISFSETAKRIKEAGNEFYOHNTWQLSRYPSGLRTDSSNYPQPFMNG 571
 699 CQVVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLPGOLKQOL 756
 572 CQVVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLPGOLKQOL 629
 757 VLRITISQOOLPKPRDMLSGRGEIIDPFVETIIGLVDCSRBTRVVDONGFNPTMET 816
 630 LIOVITISQOOLPKPRDMLSGRGEIIDPFVETIIGLVDCSRBTRVVDONGFNPTMET 686
 817 LVFVWHPETALVFLVWDDHPIGR--DFIGORTLAFSSNMKGYRHVYL--EG--MEAS 870
 687 LCFEVVLPELALMRFVYMDYDKSRNDEIGQYTLPTCMQOQYRHHILSLKDISILRPAS 746
 871 IFVAVANSIDISGKVKALGLKG 892
 747 IFVAVANSIDISGKVKALGLKG 892

RESULT 4
 US-09-908-664-2
 Sequence 2, Application US/09908664
 Patent No. US20020115178A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Meyers, Rachel
 APPLICANT: Rudolph-Owen, Laura
 APPLICANT: Tsai, Fong Yin
 TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
 TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
 FILE REFERENCE: 38155-20022.00
 CURRENT APPLICATION NUMBER: US/09/908,664
 PRIOR FILING DATE: 2001-07-17
 PRIOR APPLICATION NUMBER: US 60/218,675
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 762
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-908-664-2

Query Match 22.6% Score 1441; DB 10; Length 762;
 Best Local Similarity 36.3%; Pred. No. 3.2e-79;
 Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;

45 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 102
 18 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 76
 103 VQORPDGSPDNCCFSYTHGSHRESLDVSTSEVARTWYTGRIYLMAGISDDSLARR 162
 77 LRLSLAEELPLEQGFYTHG--RPSNLDLMANVSEADIMWGLLDVLTSMD---H 131
 163 ORTRDOWLKOTFEADKNGDLSIGEVYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 222
 132 QERLDOWLSDMFORDKNDGKMSQEOVORLLHLMNVEMDQYAFSLQADT--S0SGTL 190
 223 GEEFCAFYKMMSTRDLYLMLTYSNHKNHDAASLQFLQVQKMAVTLSECDITIE 282
 191 EGEFFQVQKALTKRAVEOLFESFSADGOKLTLLFDFLOEOKERDCTSELALELID 250
 283 QERPEKNSKGLDIDGFTNTYTRPADIDFNRHNNHNDOTPLSHYFTSSHNTYLV 342
 251 RYPSDSGLRHLVLSMDGFLSTYCSKDDIDFNPACLPYDQMTOPLNHYFTSSHNTYLV 310
 343 GDLMSQSRVDMYAVYLQAGRCVDCWDGDPGEPIYHNGVTLTKILFKDVIETINKY 402
 311 GDLQSGSSVEGYIRALKRGCRCEVDVWDGSGEPVYHGHITLTSRLIFKDYAVATVAY 370
 403 AFKNEYRPIVLTSENHCYVTOOKKMAQYITDILGKLDSSVSEDAATLPSPOLMKKI 462
 371 AFQTSQYPIVLTSENHCYVTOOKKMAQYITDILGKLDSSVSEDAATLPSPOLMKKI 430
 463 LVKGRKLPANISEDAEGVSDSDADEIDDDCKLLNGDASTNRKRVENTAKRKLDLSLK 522
 431 LVKGRKLPANISEDAEGVSDSDADEIDDDCKLLNGDASTNRKRVENTAKRKLDLSLK 461
 523 ESKIRDCEDPNFNSVSTLSPSGKLGKSKAEDVESGEDAGASRRNGRLVVGFSFRKKK 582
 462 ESOFTFEPERPO-----EONLNKND-----KKKK 484
 583 GSKLKAASVEBDEGODSPGOSRGATROKTKMLSRALSDLYKTKSYA---THDIE 638
 485 SKPI-----LCPALSSLVLYLKSVSFRSFTH--S 511
 639 MEAASWQVSFSETKAHOILOQKPAOYLFRNOOLSRYPSSRYSDSSNYPQPFMNG 698
 512 KEHYHFEIISFSETAKRIKEAGNEFYOHNTWQLSRYPSGLRTDSSNYPQPFMNG 571
 699 CQVVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLPGOLKQOL 756

Db 185 LEG-AEIEFLRLRLKRPLEIEIFHQYSGEDRVLSAPLELFE--DQEGEATLARAQOL 242

QY 281 IEQEPCEPNNKSKGLGIDGFTNTRSPAGDIFNPEHHVHODMOTOPLSHTFTSSHTY 340

Db 243 IOTVELNETAKQHEIMTLDGFMWYLLSPGALDNTHTCVQDMQPLAHYFISSSHNTY 302

QY 341 LVGDOLMSQSRVDMYAWYLQAGRCVEYDCMDPGEPIVHGHVHTLSKILFKDYIETIN 400

Db 303 LQDSQIGGSSSTEAYVRAFAQGCRCVELDCWEGPGEPIYHGHVHTLSKILFKDYIETIN 362

QY 401 KYAFIKNEYPVLLSIENHCSYIQQKMAQYLLDILGDKLDSVSSSEDATTLPSQMLKG 460

Db 363 DHAFTLSPYVLLSIENHCSYIQQKMAQYLLDILGDKLDSVSSSEDATTLPSQMLKG 422

QY 461 KILVGGKILPANIISDA-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 520

Db 423 RVLVGGKILPANIISDA-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 484

QY 521 IKESKIRDCEDPNFNSVTLSPSGKLGKRSKAEDEVESGEDAGASRRNGRLVYGSFRRK 580

Db 455 -----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 469

QY 581 KKGSKLKAASVEEGDEGDSPEGOSRGATROKTKMLSRALSDLYKTKSVATHDIE-- 638

Db 470 -----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 493

QY 639 MEAASMOYSSPSETKAHOILOKPAQYLRNNOOLSRYPSSSYRDSNYPPOFWNAG 698

Db 494 PNPAPCOVSSLSERAKKILIRAGNSFVRHNAKOLITRYPLGLRNNANSANYSPQEMNNG 553

QY 699 COMVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGGVNPNSE--DP-LPGOLKOL 756

Db 554 COLVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGGVNPNSE--DP-LPGOLKOL 609

QY 757 VLAIIISGQOLP-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 811

Db 610 SIYDLIAQOLPKNLAEKPH-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 661

QY 812 TWBETLVFVHMEPIALVRLVMDHPIG-RDFIGORTLAFSSMMPGYRHVYL-----EG 865

Db 662 RMGOTILOFOLRAPELALVRYVEDYDATSNDVGOFTLPLSLKQGYRIHILSLDGAS 721

QY 866 MEASIFVHAV 877

Db 722 LSPATLFIQIRI 733

RESULT 7

US-10-096-961-2

Sequence 2, Application US/10096961

Patent No. US2002015572A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al.

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,

TITLE OF INVENTION: NOCLETIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE

FILE REFERENCE: CL000849DIV

CURRENT APPLICATION NUMBER: US/10/096,961

PRIOR FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/232,632

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 09/738,884

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 736

TYPE: PRT

ORGANISM: Homo sapien

US-10-096-961-2

Query Match 20.0%; Score 1278.5; DB 9; Length 736;

Best Local Similarity 34.6%; Pred. No. 2e-69;

Matches 297; Conservative 129; Mismatches 273; Indels 159; Gaps 18;

QY 44 AMQGMQWVLRGSGSKGLVREYVLDHRSCLR--PSSRKNKAKISIDISQIEVSEGRQ 100

Db 11 AMLGSRKLRKSTWIKERLYRLQEDGLSV-WQORIPAPASQIHFFVGHIEAVRGHQ 69

QY 101 SEVFORYPDGSFNDNCFESIYHGSRESLDSVTSSEVARTWGLRYLMAGISDEDSLA 160

Db 70 SEGRLRF-GGAFAPARCLTIIFKGRKRNLDLAAPTAEAORWVGLTKLRARL--DAMS 125

QY 161 RQRTROMLKQOTDEADKNGDSLSIGEVYQLLKLNVMLPRVRVQKQREADTDHOG 220

Db 126 QRERL-DWIMHSYLRADSNODSKSFKELKSLIRVNVVDMNDYAYALLRECHSHNDR 184

QY 221 TLGFEFCAFYKMMSTRDYLMLTYSNHDKHDAASLQRFLOVEQKMAVTLSCODI 280

Db 185 LEG-AEIEFLRLRLKRPLEIEIFHQYSGEDRVLSAPLELFE--DQEGEATLARAQOL 242

QY 281 IEQEPCEPNNKSKGLGIDGFTNTRSPAGDIFNPEHHVHODMOTOPLSHTFTSSHTY 340

Db 243 IOTVELNETAKQHEIMTLDGFMWYLLSPGALDNTHTCVQDMQPLAHYFISSSHNTY 302

QY 341 LVGDOLMSQSRVDMYAWYLQAGRCVEYDCMDPGEPIVHGHVHTLSKILFKDYIETIN 400

Db 303 LQDSQIGGSSSTEAYVRAFAQGCRCVELDCWEGPGEPIYHGHVHTLSKILFKDYIETIN 362

QY 401 KYAFIKNEYPVLLSIENHCSYIQQKMAQYLLDILGDKLDSVSSSEDATTLPSQMLKG 460

Db 363 DHAFTLSPYVLLSIENHCSYIQQKMAQYLLDILGDKLDSVSSSEDATTLPSQMLKG 422

QY 461 KILVGGKILPANIISDA-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 520

Db 423 RVLVGGKILPANIISDA-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 484

QY 521 IKESKIRDCEDPNFNSVTLSPSGKLGKRSKAEDEVESGEDAGASRRNGRLVYGSFRRK 580

Db 455 -----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 469

QY 581 KKGSKLKAASVEEGDEGDSPEGOSRGATROKTKMLSRALSDLYKTKSVATHDIE-- 638

Db 470 -----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 493

QY 639 MEAASMOYSSPSETKAHOILOKPAQYLRNNOOLSRYPSSSYRDSNYPPOFWNAG 698

Db 494 PNPAPCOVSSLSERAKKILIRAGNSFVRHNAKOLITRYPLGLRNNANSANYSPQEMNNG 553

QY 699 COMVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGGVNPNSE--DP-LPGOLKOL 756

Db 554 COLVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGGVNPNSE--DP-LPGOLKOL 609

QY 757 VLAIIISGQOLP-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 811

Db 610 SIYDLIAQOLPKNLAEKPH-----KPRDSMLGDRGEIIPVEVEIIGLPYDCSREGOTRYVDQGFNP 661

QY 812 TWBETLVFVHMEPIALVRLVMDHPIG-RDFIGORTLAFSSMMPGYRHVYL-----EG 865

Db 662 RMGOTILOFOLRAPELALVRYVEDYDATSNDVGOFTLPLSLKQGYRIHILSLDGAS 721

QY 866 MEASIFVHAV 877

Db 722 LSPATLFIQIRI 733

RESULT 8

US-10-096-961-5

Sequence 5, Application US/10096961

Patent No. US2002015572A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al.

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,

TITLE OF INVENTION: NOCLETIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE

FILE REFERENCE: CL000849DIV

; CURRENT APPLICATION NUMBER: US/10/096,961
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/232,632
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 09/738,884
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 744
 ; TYPE: PR
 ; ORGANISM: Mus musculus
 ; US-10-096-961-5

Query Match 19.8%; Score 1262; DB 9; Length 744;
 Best Local Similarity 35.9%; Pred. No. 2e-68;
 Matches 308; Conservative 186; Mismatches 274; Indels 146; Gaps 19;

QY 44 AMBGMOMVLRGSGKGLVFFYLDHRSCTMRPSRK---NEKAKISDSIOEVSFGR 99
 DB 10 ALKGSOLKLVKSSWRREFYKLOEDCKTI-WQESRKVWRSPESQLFSTIEDIQEVRMGH 68
 QY 100 QSEVFORPDGSPDPCSFYHSHRESLIDVSTSEVARTWYGLRTIAGISDESL 159
 DB 69 RTGGLKFA-RDIPEDRCSTIVFKDQNTLDLAPSPADVOHWVGLRKI---IDRSGSM 124
 QY 160 ARBQRTDQMLKQTFDEADKNGDGLSIGEVLLHKLNVNLPQRVKOMFEAD---TD 216
 DB 125 DQROKIQ-HVHISCLRKADKNKKNKMFKEVDLKLNVQVDDSAKRIFFEDCHSD 183
 QY 217 DHQGTGFEEFCAYKMSRRLYLMLTYSNKHDLDAALORFLOVEOK-NAGVTL 274
 DB 184 ----SLEDEITETFMVLTQRAEDRAFAEAGSAGTISVEKLVYLFLOHQEEREAGPAL 239
 QY 275 ESCQDITIEFEPCEPKNSKGLIDGFTVYTRSPADIDFNPHNHVHODMOPLSHYFT 334
 DB 240 --ALSTIEREPESTAKAQROMTKGFLMYLISADGNAPSLAHKRYVYDMMOPLSHYLS 297
 QY 335 SSNHTYLVDDQLMSQSRVDMYAVLQAGCYEVDGWDGPEPIVHHGYTLTKILFKD 394
 DB 298 SSNHTYLVDDQLMSQSRVDMYAVLQAGCYEVDGWDGPEPIVHHGYTLTKILFKD 357
 QY 395 VLETTIKYAFIKNEYPVILSIENHCSVLDQKMAQYLDIDGDKLDSVSESDATTIPS 454
 DB 358 VLBATRDVAFKASPYVILSIENHCSVLDQKMAQYLDIDGDKLDSVSESDATTIPS 416
 QY 455 POMLAKGKILVGRK---LPANISDAEAGEVSDSDADEIDDDCKLNGASTNRKRYE 510
 DB 417 PQLKEKILKNGKLGGLPAGGNGPEATVDSDDEAEMDEAV-----RSQVQ 467
 QY 511 NTAKRRLSLIKESKIRCEDPNNFSVTLSPSGKLGKRSKAEEDVESGEDAGASRRNGR 570
 DB 468 H-----RPKED----- 473
 QY 571 LVVGSFRRKKKSKLKAASVEEGDQDSFGQSRGATROKTKMLSRALSDLYTK 630
 DB 474 ----KLKVPESLSDVYICK 489
 QY 631 SVATHDIMEAAS---WQVSFSETKAHQILQKPAQYLFNFNOOLSRIVSSRYVDS 687
 DB 490 SVHFGFSPTSGQAFEMASFSRSLRLQSGNSFVHNHGHLSRIYPAQMRDSS 549
 QY 688 NYNPOFPNAGCOMVALYVSEGRMLQUNRAKFAFANGCGGVLPKGCN--CQGYFNPSE 745
 DB 550 NISPEVEMNGGQVALVLFQTPGPEMDVYLGCFFDNGCGGVLPAPFLRPDITFNSRAL 609
 QY 746 DPLPOLKQVLRLIISGOQLPKPRDSMLGDRGETIDPFVEVEIIGLPYDCSRQOTVVD 805
 DB 610 TGGPMARKKLRLVMIISGOQLPKYK---NKNSIVDPKVLVEHGGQDVAASQOTAVIT 665
 QY 806 DNGFPTVEETLVFMVMTALVFLVMDPIGR-DEIGQRTIARFSSMMPGRHYYLE 864
 DB 666 NNGFPRMDTEFEVAVVADLALVRFVMEVDYSSSKNDFIGQSTIIPNNSLKQGRHVL 725

QY 865 GME-----BASIFVHAV 877
 DB 726 SKNGDLHPSATLEVKISI 743

RESULT 9

US-09-908-664-5
 ; Sequence 5, Application US/09908664
 ; Patent No. US20020115178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura

; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
 ; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 38155-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/908,664
 ; PRIOR FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: US 60/218,675
 ; PRIOR FILING DATE: 2000-07-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 608
 ; TYPE: PR
 ; ORGANISM: Homo sapiens
 ; US-09-908-664-5

Query Match 17.0%; Score 1085.5; DB 10; Length 608;
 Best Local Similarity 36.1%; Pred. No. 6.9e-58;
 Matches 257; Conservative 114; Mismatches 198; Indels 143; Gaps 15;

QY 183 GSLSIGEVLLHKLNVNLPQRVKOMFEADTDHGTGFEEFCAYKMSRRLDYL 242
 DB 17 GKINLEKORLLEKLDIRCSYTHVKQFKNDR-LKGRITIEFRAIVYIITHREIE 75
 QY 243 LMLTYSNKHKLDAASLORFLOVEOKNAGYTLSCQDITIEFEPCEPKNSKGLIDGFT 302
 DB 76 IFNTYSERKLLASNAQFLQEOVAEWSKAIATFELIOKYPIEBVRKAKHMSLEGFT 135
 QY 303 NYTRSPAGIDFNPHNHVHODMOPLSHYFTSSNHTYLVDDQLMSQSRVDMYAVLQAG 362
 DB 136 RYMSRRECLLFKNCRKRVYQDMTHPLNDYFISSNHTYLVDDQLMSQSRVDMYAVLQAG 195
 QY 363 CRCYEVNOMGDPGEPIVHHGYTLTKILFKDYIETINKYATIKNEYPVILSIENHCSYI 422
 DB 196 CRCLEIDCWGAQDEPVYVHGYTLTKILFKDYIETINKYATIKNEYPVILSIENHCSYI 255
 QY 423 QOKKMAQYLDIDGDKLDSVSESDATTLPSPOMLKGKILVGRKLPANISDAEAGEV 482
 DB 256 QQEVMDNLQATGESL-LSDMDLDPDITLSPKALKKILVANKKI----- 301
 QY 483 SDESDADEIDDDCKLNGASTNRKRYENTAKRKLDSLKESKIRCEDPNNFSVTLSP 542
 DB 302 ----GLKETHERKGS----- 314
 QY 543 SGLGRSKAEEDVESGEDAGASRRNGRLVYGSFRRKKKSKLKAASVEEGDQDSP 602
 DB 315 ----KHGNDQKEGV-----KRLPGVMLKPKKKTKRL----- 343
 QY 603 GQSGRATROKTKMLSRALSDLYTKSVATHDIMEAASNOVS-----SPSE 652
 DB 344 ----KALALSDLYITKA-----EFKSFQSRILYQGFENNSIGE 381
 QY 653 TKAHQILQKPAQYLFNFNOOLSRIVSSRYVDSNYNPOFPNAGCOMVALYVSEGRM 712
 DB 382 TQARKLSKLRLVHEIFHTKFLTRITRYPKATRADSSNENQEFWNGCOMVALYVSEGRM 441
 QY 713 LQUNRAKFAFANGCGGVLPKGCN--CQGYFNP-NSEDLPLGOLKQVLRLIISGOQLPK 769
 DB 442 MDLQNGKFLDNGSGVILKPHFLRESKSYFNPSNIEKGM-----ITLTRLISGIOLPLT 497

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Oy      770  RDSMLSGELIDFVEEVEIIGLIVDSCREOTRVVDNGCFPTKEETLVFMVHPELALY 829
Db      498  HSS--SNG---DSLVIIEVGVGPNDDKQOTRIKKNAPSFRNNEFTFIINHPELALI 552
Oy      830  RELVMDHDP-I-GRDFIGORTLAFSSMMGYRHYVL-----EGMEASIFVHV 875
Db      553  REVVEGQGLIAGNEFLGQYTLPLLCIMNKGVRRIPLFSRMGESLEPASFVYV 604

RESULT 10
US-09-835-996A-8
Sequence 8, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanec, Radoje
APPLICANT: Ren, Feiyun
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunxun
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835,996A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-8

Query Match      15.7%; Score 1002; DB 10; Length 567;
Best Local Similarity 36.1%; Pred. No. 7e-53;
Matches 227; Conservative 106; Mismatches 201; Indels 112; Gaps 13.

Oy      45  MDSGMQVNRKRGSKGLVRYVYLDEHRSCLR--RPSRKNEKAKISIDSIQEVSEGRSE 102
Db      18  MDSMPKRRKRSKWKLRIRFLQNDQMTY-WIARQARSGAKSFSDISVETIRNHDSE 76
Oy      103  VFCQRPDGSDFPNCCSFISYVSHRESIDLVSTSEVARTVWGLRYIMAGISDSDSLARR 162
Db      77  LRLSLABELPLDEGFTLVPHG-RRSNLDIMANVSEEAQIMRGLOLDLVDTYMSD-----H 131
Oy      163  QRTDQWLKQTFDEADKNGSGSLSIGVYLQDLKIKLVNPLPROGVKQMFREADFDHOGTL 222
Db      132  QERLDQNLISWFGQDGNQDGKMSFOEVQRLILMANVEMQDEYAFSLFOADT-SQSGTL 190
Oy      223  GFEFCFAFYKMSSTRBLVYLMLTVYNSHKHDLDAASLQRLQYQOKMAGVLTSCODIIE 282
Db      191  EGEEFYQYKMLTRAEVQELFEESADGQKLTLLFLEDFLEQEBOKBRDCTSETALETLID 250
Oy      283  QFEPQPERKSKGLGLIGDQFTVYTRSPAGDITFNPHHHVHVDQMDQPLSHYELTSSHNLYV 342
Db      283  QFEPQPERKSKGLGLIGDQFTVYTRSPAGDITFNPHHHVHVDQMDQPLSHYELTSSHNLYV 342

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Db	251	RYEFSDSGKLRHVPSMGOFLSYLCSKRGDIJFNPAFLPTIYDQMNQPLNHRYPICSHNTYLV	310
QY	343	GDQLMSRSDMTAMVYLQAGRCVYEDVCDMPDGEPIYHNGITYSKILKRDVIETINKY	402
Db	311	GDQLGCGSVVGYRALKRGRCVEVVMWPGSPGEPVYHGHITLSIRLKDVAATVAQY	370
QY	403	AFINNEYVULISTENHCSGYIOQKKMAQYIYDIDGLDKLDSVSESDAFTTLPSPMLKGI	462
Db	371	AFQTSDFVVLSTHCSWEOQOTMARLLETITLLEQLLSTLIDGVLPOLPSPBELRKRI	430
QY	463	LVKCKKLPANISEDSEVSDSEDAEIDDDCKLLNGDASTNKRREVENTAKRRLDLIIK	522
Db	431	LVKCKKL--TLEBDL--EVEEAEPELEE-----SETAL	461
QY	523	ESKTRDCEDPNNFVSITLSPSGKLGRKSKAEDEYSESGDAGASRRNGRLVYGSFSRRKK	582
Db	462	ESOFETEPEPO-----BONLONKO-----KKK	484
QY	583	GSKLKKAASVEBGDQSGPGQSHGATROKTKMLSPALSDLYKTKSYA---THDIE	638
Db	485	SKPI-----LCPLASIVLYLKVSFRRPFTH--S	511
QY	639	MEAASSMOVSVSEFETKAHQIILQKPAQYLRFNQOOLSTIYSSIRVDSNTNPQPF	694
Db	512	KHHYFEIISFSSEFKAKRLIKEAGNEFVHOHTROLSTRVYSGLTGSSIYNPOGY	567
RESULT 11			
US-09-822-635-2			
Sequence 2, Application US/09822635			
Patent No. US2001003931A1			
GENERAL INFORMATION:			
APPLICANT: Hunter, John J.			
APPLICANT: Meyers, Rachel A.			
TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND			
TITLE OF INVENTION: USES THEREOF			
FILE REFERENCE: 10448-035001			
CURRENT APPLICATION NUMBER: US/09/822,635			
CURRENT FILING DATE: 2001-03-30			
PRIOR APPLICATION NUMBER: US 60/193,921			
PRIOR FILING DATE: 2000-03-31			
NUMBER OF SEQ ID NOS: 9			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 2			
LENGTH: 1809			
TYPE: prt			
ORGANISM: Homo sapiens			
US-09-822-635-2			
Query Match	13.2%;	Score 840.5;	DB 10;
Best local similarity	27.4%;	Pred. No. 1.8e-42;	
Matches 268;	Conservative 139;	Mismatches 315;	Indels 257;
			Gaps 33;
QY	2	APPTAGPLPGPALPPEDP-----GPPESRWLFLSANILPVERCMGAMOGQMVKLRG	56
Db	664	SPMLAAGTSSPIRPVSSPVLSSSNKSPPSSAMSSSSNH-----GRIG	705
QY	57	GSKGIVREYFLDHRSGIRMRP-----SRKENAKAISIDISIOEYSESGROSEVFORP	108
Db	706	GMGQFOSFEMVSDSNMSFVEVELFKSFVSARKDKLDLPFYAVPCNRSG--SESAPLYT	763
QY	109	DGSDFPNCCFSIYGHSHRESLDVSTSSSEVARTWVTGLRYLMAGISDEDSLARRQRTDO	168
Db	764	NITIDENT-----SDLOPDLDLTRN-----VSDLGLF-----IKSKQSLDNORISD	807
QY	169	WLKQTFDEADKNGDGSISG-----EVIQLHLKLNVLNIPROVYOMPREADTDHOGTIGF	224
Db	808	ALMAASIVTNGTGISTESTIGIFGVGILQ--LNDPLVNC-----QC-----	845
QY	225	EEPCAFKMMSTRDYLMLMUTYSNKHDDHDAASLQFLQVEORMAGVTLSECODIIEOP	284
Db	846	EHCCTYDEILS-----IIQKF	860

QY 285 EPCPENKSKGLIGDFTNTYRSPAGDIF--NPEHHVHODMTOPLSHYFTTSSHNHYLVG 343
 DB 861 EPTSMCHQIMSEPGFARFLMDKENFANKNDESGENIKELQPLSTYITLESSHNHYLTG 920
 QY 344 DQMSOSRVMYAMVLAGRCVYDCWDGPDGEPIYHNGYITLTKLFDVETITNKYA 403
 DB 921 HOLGESSVELEYSOVLLOGRSVELDCWDGDPRIYHGHITLTKLPKEVEVEAIDRSA 980
 QY 404 FIKNEYVVIISIEHNCVSIQOKKMAQYITDILGDKL---DLSVSSSDATTLTSPQMLG 460
 DB 981 FINSDELITISIEHNCSPQOKMAELFKYVGEKLVTKLETFTDSDPMLPSDQLKR 1040
 QY 461 KILYKGGKL-----PANTISEAEEGEVED- 486
 DB 1041 KVLKKNKLLAHOTPYDILKOKAHOLASMOYQAYNGNANPRANNEEDEDDEVDYX 1100
 QY 487 ---SADEIDDD---C-KL---LNGDASTRKREVENTAKK-----LDS 519
 DB 1101 ESLSDDNILEDPREKNSCNDKLOFETNEETPKRIKADNSACKKGVYDMELCEEFYLDQ 1160
 QY 520 LIESK-----TRCEDPNNFSVSTLSPSG-KIGRKSRAEEDVESGEDAGARRNG 569
 DB 1161 NKESRQIAPELSDLYCOAVKFGPLSTLNASGSRGKERSKSI-----FGNPG 1213
 QY 570 RLTVG---SRSRRKKGSKLAKRAVEEDGODSPGOSRGATROKTKMLSRALSDLY 626
 DB 1214 RMPSPGETASTNKTSKSS---CEGIRQTWESSSP-----LNPJTSLSAII 1256
 QY 627 KYTKSVATHDIEEAAASQVSSFESETKAHQILOOKPAQYLFENQOOLSRITPSSRYDS 686
 DB 1257 RFPK-----CYHISLSINNAKRIKLCRRYSOKLTHOTACQLRTYPAATRID 1303
 QY 687 SANNPQPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLR-----GCMCOGYF 740
 DB 1304 SNNPQPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLR-----GCMCOGYF 1363
 QY 741 NPNSEDPPLPGOLKOLVLRITISGOOLPKPRDSMLDGRGIDIPFEVEELIGLPVDCSRKQ 800
 DB 1364 SPLERO-LDSMPAYSLITVSGQV--CPSSNM-----GSPCEVYVLGMPDLSCHFR 1414
 QY 801 TRVVDNGENPFWETLVFMVHPELALVRLVMDHPDGRDFIGORTLAFSSMMPGYRH 860
 DB 1415 TRPIHNTLNPWMNEQFLFHVHFEDELFLRFVAVENN--SSAVTQRIIPLKALKRGYRH 1472
 QY 861 VYL-----EGMEASIFVH 874
 DB 1473 IQLRLHNEVLEISSLFTN 1491
 RESULT 12
 US-09-828-447-11
 : Sequence 11, Application US/09828447
 : Patent No. US20020069432A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSMALDO DA
 : APPLICANT: BOHNER, HANS J.
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 : FILE REFERENCE: 16313-0037
 : CURRENT APPLICATION NUMBER: US/09/828,447
 : PRIOR FILING DATE: 2001-08-20
 : PRIOR APPLICATION NUMBER: 60/196,001
 : NUMBER OF SEQ ID NOS: 41
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 11
 : LENGTH: 1054
 : TYPE: PRT
 : ORGANISM: Physcomitrella patens
 US-09-828-447-11

Query Match 11.3%; Score 723.5; DB 10; Length 1054;
 Best Local similarity 31.6%; Pred. No. 1e-35;
 Matches 218; Conservative 103; Mismatches 273; Indels 95; Gaps 21;
 QY 230 FYKMMSTRDLYLML-----TYSNKHCHLDAASIQRFLOYEQKAGYTLSCDDIEOF 284
 DB 426 FGRKSKGDLAODLIGVFSYSEN--GKLDAGELKFLQTEGGGSKSLDAKHVELI 484
 QY 285 EPCPENKSK-----GLIGDFTNTYRSPAGDIFNPEHHVHODMTOPLSHYFTTSSH 337
 DB 485 RN-ERHKKSPFETIYSDLSKGDFFKNYLSR--DLNGVLESTVHODMTOPLSHYFTTGH 541
 QY 338 NTYLVGDLMGOSRVDYAMVLAGRCVYDCWDGPDGEPIYHNGYITLTKLFDVIE 397
 DB 542 NSYLTGNOLSSDSDVPTAALQGRVVELDMPDDKGIGKYTHGNTLTSVPAFECIK 601
 QY 398 TINKYAFIKNEYPVLTISIEHNCVSIQOKKMAQYITDILGDKLDSVSSSDATTLTSPQM 457
 DB 602 AIKANAFYSKTPVYITLEDHLSPLQALAEITLNLIGEDL--YPPSSDGFKELPSPES 660
 QY 458 LKGLILYKGRKLPANISED--AEGEVSEDSADEIDDDCKILNGDASTRKREVENTAKR 515
 DB 661 LKGLILITRP--PREYLEAAYAKSALKDE-----KILNEFKADKLDQOSTAP- 708
 QY 516 KLDLIESKTRIDCEDPNNFSVSTLSPSGKGRK---SKAEEDVESGEDAGARRNGRLV 572
 DB 709 ---VSPVEKKIAPVSEKTKSISEKDLSEKVGMLRYDSEGESADPAPASPDG--- 760
 QY 573 VGSFSRRKKGSKLAKRAVEEDGODSPGOSRGATROKTKMLSRALS--DLVYTKS 631
 DB 761 -----KKNITLADSESDDD-----NKNPEIARLTIHQSPSKG 796
 QY 632 VATHDIEEAAASQVSSFESETKAHQILOOKPAQYLFENQOOLSRITPSSRYDSNYP 691
 DB 797 TVVED-RLKVEGYVVRISLSETKLEKTEEFPELVYFQRIILRYV PAGNRVNSSNYP 855
 QY 692 QPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLRPGCMCGV-----FNNSESD 746
 DB 856 TAAMIHQAQVAMQMOGYGKELMOAHGKFRNGCGYILPKYLLDLPNGKRPFNPSA-- 913
 QY 747 PLPGOLKOLVLRITISGOOLPKPRDSMLDGRGIDIPFEVEELIGLPVDCSRKQ 806
 DB 914 --PDFTKMLIKVMTMGMDKAFPKYHFDLSPRPDFFRLVTVGRADYAAKTSYIDD 971
 QY 807 NGENPFWETLVFMVHPELALVRLVMDHPDGRDFIGORTLAFSSMMPGYRHVYLDG 865
 DB 972 -VWEPHNNEDHEFYLCPELALIRIEVRHDESDDEFGOACLPNHEITKDGRCYQM-- 1028
 QY 866 MEASIFVHVAVSDISQVKAOLGLKGLF 894
 DB 1029 -----YDKKGSYVK--GVKMLF 1043
 RESULT 13
 US-09-828-447-12
 : Sequence 12, Application US/09828447
 : Patent No. US20020069432A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSMALDO DA
 : APPLICANT: BOHNER, HANS J.
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 : FILE REFERENCE: 16313-0037
 : CURRENT APPLICATION NUMBER: US/09/828,447
 : PRIOR FILING DATE: 2001-08-20
 : PRIOR APPLICATION NUMBER: 60/196,001
 : NUMBER OF SEQ ID NOS: 41
 : SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 12
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-447-12

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Query Match      10.7%; Score 685.5; DB 10; Length 628;
Best Local Similarity 30.9%; Pred. No. 1e-33; Indels 97; Gaps 20;
Matches 200; Conservative 104; Mismatches 246;

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QY 238 RDLVLLMLTYSHNHKDLDAASIQRFLOVEOKMAGVTLSCDIIIOFEPCEPKSGILG 297
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 18 QDLVGEVFTIYSENRMSBGLKFLHTEGGVDPFLDADAKIMIRIR-DWKKSGFLAS 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 298 I-----DGFNTYRSPAGDITNPEHHVHODMOTPLSHYFTTSSHNTYLVDDQMSOR 351
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 INSDLSKEAFRRYKLMNP--DLNGVYLNHVNHOQMTQPMSHYFTTGHNSLYTGNOSSDS 134
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 352 VMNMYAVLQAGRCVYVDCWDGPDGEPYVHGGYTLTKILFKDVIETIKYAFINREYV 411
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135 DFPFALALRGRVAVVELLDLMDPDCKGMKYTGNTLTNPSPKCYATKINNAFTSEYV 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 412 ILIENHCSTVIOOKKMAQYLTDLGDKIDLSSVSESDATTLPSQMLKGLLVKGLKPA 471
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 195 CVTIEDHLTSELQGHAAEILFOILGDAL-YPPPTDALVEFSPESLKRKIIISTK---- 249
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 472 NISEDAEEGEVDESDADELIDDCCKLLNGDASTNRKRVENTAKRKLDLSIKESKIRCD 531
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 250 -----PPEKYLEAC-----STOKLAMEN--RNIVEELEKEDKLEQ--- 282
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 532 PNPFSTVLTSPSGKLGKRSKAEDVESGEDAGASRRNGRLVVGSPSRK-----KK 582
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 283 -----TTFAP-----LEENHLIGENTPELKE-----VEVLSQKEMSTPAELNSRS 323
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 583 GSKLKKAASY--EEGDEGODSPGOSRGATROKTKMLKLSRLS-DLYKTKSAV-THDE 638
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 324 PSDLGEATSTRYSKSNDCNMP-----KHKKYVALITIRLAKHAKGTSMERHQ 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 639 MEDAASSQVSFSETKHAHOILQOKPAOYLFRNQOOLSRITPSSRYVDSNINPQPTWNG 698
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 373 VD--ESVKRISLSESKLEKYEKPELALVFKIKNIRVPAANRNSNFCPTLAMNG 430
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 699 CQWVALNYQSEGRMLQINRAKFSANGCGGYLKPCCMCQGV-----FNPNSEDPPLGQLK 753
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 431 AQWVAQWNGYKGEKLMQAFKFGKNGCGGYLKPQYLLEMLPSGVDFNPPTS---PRNT 486
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 754 KQVLKRTISQQLPKPRDSMLGDRGELIIDPFVEVEIIGLVPDCSRBQTRVVDNGFPTW 813
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 487 LILIKIKVTTGLGMDKAFSKRHPDLESPDPFTTRIVGVADAKAKTKTSYV-DNSNAPHW 545
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 814 EETLVFWHPELALVRELVWDHPIDGRD-FIGORTLAFSSMMFGYR 859
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 546 NEDHEFALKCEPLALLRIEVRDHDHDDSKDEEGQTCLEPIHEVRDGYR 592
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14
US-09-835-996A-19
; Sequence 19, Application US/09835996A
; Patent NO. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Zhao, Qing
; APPLICANT: Weinman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyen
; APPLICANT: Qian, Xiaohong

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; APPLICANT: Wang, Dunhui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-19

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Query Match      8.2%; Score 522.5; DB 10; Length 340;
Best Local Similarity 37.1%; Pred. No. 3.2e-24; Indels 21; Gaps 6;
Matches 124; Conservative 53; Mismatches 136;

```

```

QY 45 MOEGQWYKLGSGKGLRFYFLDEHRSICRW--RPSRKNKANISIDSIGVSEGRQSE 102
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 18 MOEGMPKRYKRSKSKKRLRYFLQNDQMTV-WHAQANGSAKPSPSISDVETIRGHQSE 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 103 VFQYPDGSPDNCFSTIYHGSRRSLDVLSTSSVATWTYTGRLYMAIGSDSDSLAR 162
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 LIRSLAEELPLEQGTIYFHG--RRSLDLMANVSEADIMWGLQLLDVLTYSMD---H 131
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 163 QFTROWMLKQTFDEADKNDGDSIGEVYQLLHKINVLPRQRYKQMPREADTDHOGTL 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 132 QERLDQMLSDWQROKDKNDGKMSFOYORLLHLMNVEMDQYAFSLQOADT--SQSGTL 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 223 GEEFCAFKMSTRDLYLLMLTYSNKHDIIDAASLQRFLOVEOKMAGVTLSCQDITE 282
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 EGEFEVQFYKALTKRAVEVLEFESFADGQKLTLEFLDFLOEKEKEDCSEALTELID 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 283 QEPCEPKNSKGLIGDGTNTYTRSPAGDIFNPEHHVHODMOTPLSHYFTTSSHNTLY 342
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 REPSDSGRLRHLVSLMDGFLSTLCSKRGDIENPACLPIDQMTQPLNHFICSSHNTLY 310
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 343 GDOLMSQSRVDMYAVLQAGRCVYVDCWDGPDG 376
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 311 GQDLGQSSVEGY-----IRCSGGRGG 332
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RESULT 15
US-09-908-664-22
; Sequence 22, Application US/09908664
; Patent NO. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 191
; TYPE: PRT

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-908-664-22

Query Match 8.1%; Score 515; DB 10; Length 191;
Best Local Similarity 53.4%; Pred. No. 4.3e-24;
Matches 101; Conservative 29; Mismatches 51; Indels 8; Gaps 4;

QY 307 SPAGDINPEHHVHODMTQPLSHYFTSSHTYLVGDQIMS-OSRYDNTAWYLQAGCRC 365
Db 1 SPDCNVFDPPEHKQVHQDMNQPLSHYFINSSTHTYLVGNQLSGSESVEMTRQALIKGCRC 60
QY 366 VEVDCMDGPDG--EPYVHGTYLTSLKFEKDVLETTINKYAFIKNEYPVILSTENHCSTI- 422
Db 61 IELDCMDGKGDDEPILTHGHTMTLEISFKDCLEAIKEHAFVTSSEYVILSTENHCDSSTP 120
QY 423 -QOKKMAQYLTDLIGDKL--DLSSVSESDATLPSPOMLKGLIKVKKLTPANISEDAE 478
Db 121 QOQAKMAEYCKEYFGDMLFTEPLESEPLFPGKELPSPEELKRLILIKKKLKEHSESEKES 180
QY 479 EGEYSDEDS 487
Db 181 EEKKTDEET 189

Search completed: March 28, 2003, 14:00:57
Job time : 46 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: March 28, 2003, 13:48:00 ; Search time 31 Seconds
(without alignments)
1145.596 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPPTACPLPEPALPPEDPG.....ALPYMHCRLGTLPLWLAGCP 1207

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backlist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1281	20.1	744	4	US-09-738-884-4
2	1278.5	20.0	736	4	US-09-738-884-2
3	1262	19.8	744	4	US-09-738-884-5
4	985	15.4	1290	1	US-08-138-641-2
5	985	15.4	1290	1	US-08-138-133-2
6	192	3.0	2972	4	US-09-579-181-2
7	192	3.0	3118	4	US-09-579-181-1
8	189	3.0	960	4	US-09-219-849-5
9	181	2.8	1064	1	US-08-642-255-62
10	180	2.8	1057	3	US-08-931-820-1
11	179	2.8	696	3	US-08-906-865-4
12	179	2.8	696	4	US-09-129-668-4
13	177.5	2.8	252	1	US-08-642-255-61
14	176	2.8	1057	3	US-08-931-820-4
15	175.5	2.8	529	4	US-09-247-806-2
16	175.5	2.8	1442	5	US-08-316-650-12
17	175.5	2.8	1442	5	PCT-US95-02251-12
18	175	2.7	1078	4	US-08-963-825-21
19	175	2.7	1078	4	US-09-500-811-21
20	175	2.7	1078	4	US-09-570-573-21
21	175	2.7	1078	4	US-09-548-608-21
22	175	2.7	1078	4	US-08-231-193A-58
23	174	2.7	1336	2	US-08-486-273A-58
24	174	2.7	1336	3	US-08-940-086A-58
25	174	2.7	1336	4	US-08-940-035A-58
26	174	2.7	1336	4	US-08-935-105A-58
27	174	2.7	1336	4	US-09-648-797-58

28	172	2.7	595	4	US-09-219-849-48	Sequence 48, App1
29	172	2.7	595	4	US-09-219-849-50	Sequence 50, App1
30	172	2.7	822	4	US-09-219-849-49	Sequence 49, App1
31	172	2.7	1341	3	US-08-963-825-18	Sequence 18, App1
32	172	2.7	1341	4	US-09-500-811-18	Sequence 18, App1
33	172	2.7	1341	4	US-09-570-573-18	Sequence 18, App1
34	172	2.7	1341	4	US-09-548-608-18	Sequence 18, App1
35	172	2.7	1461	4	US-09-585-887-9	Sequence 9, App1
36	172	2.7	1461	4	US-09-289-578-9	Sequence 9, App1
37	170	2.7	1060	3	US-08-931-820-3	Sequence 3, App1
38	170	2.7	1418	3	US-08-963-825-20	Sequence 20, App1
39	170	2.7	1418	4	US-09-500-811-20	Sequence 20, App1
40	170	2.7	1418	4	US-09-570-573-20	Sequence 20, App1
41	170	2.7	1418	4	US-09-548-608-20	Sequence 20, App1
42	169.5	2.7	1418	4	US-09-548-608-20	Sequence 20, App1
43	169	2.6	633	1	US-08-642-255-73	Sequence 73, App1
44	168	2.6	493	4	US-08-556-978B-59	Sequence 59, App1
45	168	2.6	595	1	US-08-425-069-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-738-884-4
Sequence 4, Application US/09738884
Patent No. 6391606
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
FILE REFERENCE: C1000849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 744
TYPE: PRT
ORGANISM: Cricetus griseus
US-09-738-884-4

Query Match 20.1%; Score 1281; DB 4; Length 744;
Best Local Similarity 35.7%; Pred. No. 2.4e+90;
Matches 306; Conservative 128; Mismatches 278; Indels 144; Gaps 16;

44 AMQEGQMYKLRGSGKGLVRFYLDHRSICIRMRSRK---NEKAKISIDSIOEVSGR 99
10 ALIKGSQLKLVKSSMRREFFYKLDCKTI-WQSRKVMRSPESOLFIEDIQVRMGH 68
100 QSEVFQRYPDGSPDNCFSIYHGSRESLDVSTSEFAKRWVGLRTLMAGISDESL 159
69 RTGLKRFKA-RDIPEDRCFSIYFKDQDRLDLAPSSAQAQHWQGLRKT---IHHSGM 124
160 ARROTRDQMLKQTFEADKNGSGSLSIGEVQLQLKLWNVLPQRYKQMFREAD---TD 216
125 DQKQKLD-KHHSCLKADKNDKNNKFKELDFELKELNIOVDASARKIFPDCDSQSD 183
217 DHQGLTGFEEFCAYKMMSTRDLYLIMLTYSNKHDLDAISLQRLQYQKMAQTLES 276
184 ----SLEDEIEFFYKMLQRAEIDRVFAEASATLISVEKLVTFLQHQOREAAGPAL 239
277 CQDILQFEPCPNKSGKGLIDGFLNTRSPAGDIFNEHHVHODMOPISHYFTSS 336
240 ALSLIEREPESEFAKQROTKDGLMTLISADGSFSLAHRVYQDMQPLSHYVSS 299
337 HNTLVGDQLMSQSRVDMAMVLAQCRCEVDCMDGPDGEPIVHHGYLTSLKLFKYI 396
300 HNTLVLEDQLGPSSTAYIRALCKGRCLELDQWGPQNPDEPIYHGYFTSKLIFYDV 359
397 ETINKVAFINNEPVILISINHSVIOQKMAQYLDIIGDKLDSVSSSEDAITLPSPQ 456

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Db 360 RAIDYAFKASPYVYLLSLENHCSLEQQVVAHRLKAILGPMI-IDPILDGVTMLSPPE 418
QY 457 MLKGIILVKGKRR--LPANISEDAEEGEVSEDESDADEIDDDCKLNGDASTNRKRRENT 512
Db 419 QLKGIILVKGKRRFGLLPAGENGPEPTIDVSDDEAAEMDE----- 460
QY 513 AKRRLDLIKESKRDCEDENRNFVSSTLSPSGKLGKRSKAEDVEGEDAGASRRNGRLV 572
Db 461 -----A 461
QY 573 VGSFRRKKKSKLKAASVEEGDEGODSPGGOSRGATRQKTKMLSRALSDLVKTKTSV 632
Db 462 VRSQVOOKSKEDKLNVAPE-----LSDVAVICKSV 491
QY 633 ATIDHIEAASS---WVSSFSFETKAHQIIOKPAQYLRENOQLSRIPSSRYVDSSNY 689
Db 492 HEGGFSNPSTSGAIFYEMASFSERNRLRLIOESGNNFVRHNSHLISRIYPAGRIDSSNY 551
QY 690 NPQPFVWAGCVYALNYVOSGRLDOLNRAKFSANGCGGYLKPQGM--COGYFNPNSDDP 747
Db 552 SPVEMNNGGOYVAINFQTPGPEMDYLLGFODNGAGYVLPAPLRDPTAFNPRLTQ 611
QY 748 LRGOLKQVLRLISGOQLPKPRDSMLGDRGELIDFVEVEIIGLPVDCSRQTRVYDND 807
Db 612 GPMMAOKRLRVRVYISGOQLPKVKS---KNSIYDPKVLYEVHGVQDYASQOTAVITNN 667
QY 808 GPNPTEETLVPMVHMPETALVRLVMDHPIG-RDIGORTLAFSSMMPGYRHVYL-- 863
Db 668 GPNPMDTEFEVEVAPDLALVRFVEDYDASSKNDFTGOSTIPMNSLKOGYRHHLLSK 727
QY 864 --EGMEASIFVHAV 877
Db 728 NGDQHPSATLFFKISL 743

RESULT 2
US-09-738-884-2
; Sequence 2, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human
US-09-738-884-2

Query Match 20.0%; Score 1278.5; DB 4; Length 736;
Best Local Similarity 34.6%; Pred. No. 3.7e-90;
Matches 297; Conservative 129; Mismatches 273; Indels 159; Gaps 18;

QY 44 AMOEGMOMVTLRGSSKGLVRFYLLDEHRSCTIR---RPSRKNKAKISIDSIOEVSERQ 100
Db 11 AMLRGSRLKIRKIRTKHKEKRLYLQEDGLSV-WFORIRIPAPSOHIFVQHIAVREGHQ 69
QY 101 SEVQRYPDGSPFNCFSIYHGSHPRESLDLVGSSSEVARTWTGRLYLMAGISDESDLA 160
Db 70 SEGILRRF-GGAFPARCLTIAFGGRKNDLAPTAPEAGRWVGLTKLARL---DAMS 125
QY 161 RROTRBOMLKOTFDEADKNGDSLSIGVQLLHLKLVNLPRQRYKOMREADTDDHOG 220
Db 126 QREBL-DHWTHSYLHRADSNODSKSFKEIKSLIRVNVDMNDMYVLFLFKEDHSHNNR 184
QY 221 TLGFEFCATYKMMSTRBDLYLMLTYSNKIKDLDAASIQRFYQVAKAGVTLSECODI 280

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Db 185 LRG-AEIEFFLRLLKRPLEEIFHQYSGEDRVLSAPLEEFLE-DQEGEGATLARAQOL 242
QY 281 IBOFPCPEPNKSKGLGIDGFTNYTRSPAGDLFNEHHHHVHODMOPRISHFEIINSHNTY 340
Db 243 IQTYELNETAKQHEIMLTLDGFMVYLLSPBGRALDNTHTVCVQDMNOLPLAHYFISSSHNTY 302
QY 341 LVGDQMSQSRVDMYAMYLQAGRCVEVDCWDGPDGDEIVHGYTLTKILFKDIETIN 400
Db 303 LTDSQIGPSTSEAVVRAFAOGRCEVLDCEWGPBGEPVYHGHITLSKILFRVQAQAVR 362
QY 401 KYAFTKNEYPVLTLSIENHCSYVIOOKKMAOYLJDLILGDKLDSVSSSEBATTLPSPQMLG 460
Db 363 DEAFITSPYVLTSLIENHCSYVIOOKKMAOYLJDLILGDKLDSVSSSEBATTLPSPQMLG 422
QY 461 KILVAGKLLPANISDA-----EAGEVSDSDADEIDDDCKLNGDASTNRKRRENTAK 514
Db 423 RVLVAGKLLPAPARSBDGRLALSDREGEDDEEBEE-----VEAAQ 464
QY 515 RKLDSLKESKIRDCEDENRNFVSSTLSPSGKLGKRSKAEDVEGEDAGASRRNGRLVYG 574
Db 465 RRL----- 467
QY 575 SFSRRKKKSKLKAASVEEGDEGODSPGGOSRGATRQKTKMLSRALSDLVKTKTSVAT 634
Db 468 -----AKQISPELSALAVYCHARTL 487
QY 635 HDIE--MEASSWVSSFETKAHQIIOKPAQYLRENOQLSRIPSSRYVDSSNYNQ 692
Db 488 RTLHPAPNAQPCQVSSISERKAKKILREAGNSFVRHNAHQLRVYPLGRMNSANYSQ 547
QY 693 PFVWAGCVYALNYVOSGRLDOLNRAKFSANGCGGYLKPQGM--COGYFNPNSDDP-DP-LRG 750
Db 548 EMNNSGQVAINFQTPGPEMDYLLGFODNGAGYVLPAPLRDPTAFNPRLTQ---PDSTFDEYBG 603
QY 751 QLKQVLRLISGOQLPKPRDSMLGDRGELIDFVEVEIIGLPVDCSRQTRVYDND 805
Db 604 PPRFTLSIQVLTAAQLPKLNAEKPH-----SYDPLRIEIHGVADCARQETIDYL 655
QY 806 DNGFNPTEETLVPMVHMPETALVRLVMDHPIG-RDIGORTLAFSSMMPGYRHVYL- 863
Db 656 NNGFNPTRWGOTLQPLAPALVRLVRFVEDYDASSKNDFTGOSTIPMNSLKOGYRHHLLSK 715
QY 864 ----EGMEASIFVHAV 877
Db 716 SKDGASIPATLFIQIRI 733

RESULT 3
US-09-738-884-5
; Sequence 5, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-738-884-5

Query Match 19.8%; Score 1262; DB 4; Length 744;
Best Local Similarity 35.9%; Pred. No. 7.1e-89;
Matches 308; Conservative 128; Mismatches 274; Indels 148; Gaps 19;

QY 44 AMOEGMOMVTLRGSSKGLVRFYLLDEHRSCTIRPSPK---NEKAKISIDSIOEVSERQ 99

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Db 10 ALTKSOLLKVVSSMRERFKLQEDCKTI--WQSRKVMRSPESOLFIEDIOEVRMGH 68
QY 100 OSEVFORYPDGSFDPNCPSTIYHSHRSIDLIVTSSEVARTWYGLKYLMAIGSDESL 159
Db 69 RREGLEKFA-RDIPEDRCFSIYFKDQRTNLDLAPSPADYOHMVGGLKRI---IDRSGSM 124
QY 160 ARQRTRQOMLQOTDEADKNGDGLSIGEVQLLHKLNVLNPRQVRQMFREAD---TD 216
Db 125 DQROKIQ--HMSICLRKADKNDKMKREKVDLFKELNVQVDSYAKRIPECHSQT 183
QY 217 DHQGTIGEEPCAFYKMMSTRDLYLMLTVSNHKLDAASLQFLOVEOK--MAGVTL 274
Db 184 ----SLEDSEITFYRMLTQRAIEDRAFEAGSAETLSVEKLYTFLQHQEEFAGPAL 239
QY 275 ESCODIIEFCEPCENKSGGLGIDGFTYTTSPAGDIFNPNHHVHDOMPLSHYFT 334
Db 240 --ALSLIEREPESETAKAQRMTKQGFMLYLLSADGNASLHRRYVOMNOPSHTYLS 297
QY 335 SSHNTLVGDOLMSQSRVYMAVLQAGRCVEVDCMDPDEPIVHHGYTLTSKILEFD 394
Db 298 SSNTYLLLEDOLGSPSTATYIRALCKGRCLEDCMDSPNPEPIIHHGYTTSKILFCD 357
QY 395 VIETINKYAFIKNEYPVLLSIENHGSVIOQKMAQYLDLIDCKDLSSVSEDAITLPS 454
Db 358 VLRARIDYAFKASPYVILLSENHCSLEEQRYMAHHLRAILGPM-LDPLDGYTSLPS 416
QY 455 PQLKJKTIVKGGK---IPANISDAEAGEVEDSDEADIDDDCKLLNGASTNKRVE 510
Db 417 PEOLKEKILLKGLKGLLPAAGEGCEPATVDSDEDAEMEDYAV-----RSQVQ 467
QY 511 NTAKRKIDSLIKESKIRDCEDPNPFVSSTLSPSGKLGKRSKAEVDESGEDAGASRRNG 570
Db 468 H-----KPED----- 473
QY 571 LVVGSFSRRKKKKSKLKAASVEBQDQSPGQSGRATROKTKMKSIRALSILVKKYK 630
Db 474 -----KTLPELSDMYITCK 489
QY 631 SVATHDIEMBAAS---WQVSPSETKAHQILQKPAQYLFNQOOLSRIYPSYVDS 687
Db 490 SVHFGGSSSTSGOAFYEMASFSERLRLLOESGNSFVRHNVGHLSTRYIPAGWTDSS 549
QY 688 NYNPOFPMNAGCMVALINTYSEGRMLQLNPAKFSANCGCYVLKPCM--CQGVFNPSE 745
Db 550 NYSPEVMNCGCQVALNFOTPGRPMOVYLGCFODNCGCYVLKPAFLRDPDTFNSRAL 609
QY 746 DPLRQALKQVLRITISGOOLPRRDSMLDREIIDPEVEVELIGLPVNCSEROTFRVD 805
Db 610 TQGWMAAPKRLRWITISGOOLPVKN---NKSIVDPKYVIELHGVGDVYASROTAVIT 665
QY 806 DNGFNPTMEETLVFMVHAPETALVRLVMDHPICR--DFTGORTLAFSSMMPGRHYVLE 864
Db 666 NNGNPNMDREFEVVAVPLDALVRFVEVEDYDSSSKNDFIGOSTIPWNSLKQGRVHVL 725
QY 865 GME-----EASIVYHNAV 877
Db 726 SKNGDLHPSATLFFVKISI 743

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RESULT 4
US-08-138-641-2
Sequence 2, Application US/08138641
Patent No. 5474921

GENERAL INFORMATION:
APPLICANT: Koblán, Kenneth S.
TITLE OF INVENTION: Assay to determine inhibitors of
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway

```

STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-138-641-2

Query Match 15.4%; Score 985; DB 1; Length 1290;
Best Local Similarity 25.6%; Pred. No. 4e-67;
Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;

QY 74 INWRDSRKNKAKISID--SIQVSEGRQSEVFORYP--PDGSP--DPNCPSTIYGS--HR 126
Db 60 ITW--SRGADKIEGSDIDIREIKERPKTSRDFRYQEDPAFRPDQSHCFVILYGMERL 117
QY 127 ESDLVSTSEVARTWYGLKYLMAIGSDESL--ARQRTRQOMLQOTDEADKNGDGL 185
Db 118 KTLISLOAHSSEVDVNMWIGLWLM-----EDTLQATPLQIETMLKQFYSYDRKREPRI 172
QY 186 STGEVQLLHKLNVLNPRQVRQMFREADTDDQ--GTIGEEPCAFYK--MMSTRDLY 241
Db 173 SAKDLKNMISQVNYRPNKR--FLERLTDFEQRSGDITYGQFQVLSRLYSAQKTM 229
QY 242 LML-----TYSNHKDLDAASLQRP-----LOVQKMAGYTLESCDII 281
Db 230 LPLEETNLTGTERPELCQVSLSEFOQLLELYQGLMAVDRLOVQEFMLSFRLDREIE 289
QY 282 EGFEPCEPKSGILGIDGFTYTTSPAGDIFNPNHHV--HODMTOPLSHYFTSSHTY 340
Db 290 EPI-----FFLDELVTFLFSKENSVMNSQLDAVCPETMNPPLSHYISSHTY 338
QY 341 LVGDOLMSQSRVYMAVLQAGRCVEVDCMDPDEPIVHHGYTLTSKILFKDYIEYIN 400
Db 339 LTGDQFSSESLAVARCLRMGRCIEIDCMPDPMPIYHGHLLTKIKFSVLYHTIK 398
QY 401 KYAFIKNEYPVLLSIENHGSVIOQKMAQYLDLIDCKDLSSVSEDAITLPSOMLKG 460
Db 399 EHAFFVASEYPVLLSIDHCSIAQORMAOHFRKVLADTL-LTRPVYDIAADGLPSNOLKR 457
QY 461 KILVKGKLLPA-----NISDAEES----- 480
Db 458 KILIKHKKLAEGSAEYEPVSVMYSENDISNISKNIILVLEDPVNHVPHYVLTSSKI 517
QY 481 ---EVSDESDADEIDDDCKLLNGDASTNKRKY-----ENTARKKIDS----- 519
Db 518 YSEETSSDQGNDEDEPKASGSTELHSEKWFHGLAGRGRIARLLETXYCIETG 577
QY 520 ---LIKES-----KIRDC----- 529
Db 578 APDGSFLVRESEFVGDYTLTFWRKNGVQVQCRHSHQDAGTPKFFLTDNLVFDSDLYDLT 637
QY 530 -----E 530

```

Db 638 HYQVPLRCNEFEMRLSEPVQTNHESKEWYHASLTRAQAEHMLRVPRDGAFLVYKRN 697
 QY 531 DPNNEVSSTLSPSGK-----LGRKSK----- 551
 Db 698 EPNSTALS-PRAGKIKKHCRCVQOEGOTVMLGNSEFSLVDLISYEKHPYKMKLYRPI 756
 QY 552 -----AED-----VESG----- 559
 Db 757 NEALKEIGTAEPDYGALYEGRNPFYVEANPMTFKCAVKALFDYKAQREDELFTTSA 816
 QY 560 -----EDAGASR----- 566
 Db 817 IIVNEKODGGMWKGYGKQKQMFPSNYVEEMINPALEPEREHDENSPLGDLRGVL 876
 QY 567 -----RNGRLVYVGSFSSRRKKSGSKLTKAASVEE-----GDEGDSPGG 604
 Db 877 DVPAQOIAIRPEGKNNRFLVFSTISMPVAQMSLDVYAADSELDQWYKIREVAQIADAR 936
 QY 605 QSRGATOKTKMLKSLDLVYTKSVATHD--TEMEAASSWQVSSFSFTKAQIILQO- 661
 Db 937 LTBGKMMERR-KKIALSELVYVCRVPDEEKIGTERACYRDMSSFPETKAETVYKA 995
 QY 662 KPAQYLPNQQOOLSRIPSSYRVDSNYNPQPFMNAQCCOMVALINQSEGMQLNKAES 721
 Db 996 KKKFLQYNLQSLRITPKQORLDSNYDPLPMWICGSQLVNLFTQDPKPMQMOALFM 1055
 QY 722 ANGCGYVLPKGCQGVFNPSNEDPLPQKQKQVLRILISGOOLPKPRDSMDGGEII 781
 Db 1056 AGHCGYVLPQPMRDAEPFDPKSSIRGLPCVICIEVGARHLK-----NGGC-IV 1108
 QY 782 DPEVEEIIIGLPVDSREORVYVDDNGFNPTW-EETLVPRVNHPELALVFLVMDHPDG 840
 Db 1109 CPVEIEVACAEYDSTKQKEEYVYDNGNLNFWPAKPFHFOISNPEAFILFVYEEDEMS 1168
 QY 841 -RDFIGQRLAFSSMMPGVRHV-----YLEGMEASIFVHVAV 877
 Db 1169 DQNFLOAFEPVYKGLTKGYRAVPLKNNYSDELASLLIKIDI 1211
 RESULT 5
 US-08-138-133-2
 Sequence 2, Application US/08138133
 Patent No. 5519163
 GENERAL INFORMATION:
 APPLICANT: GIBBS, JACKSON B.
 APPLICANT: KOBLAN, KENNETH S.
 APPLICANT: MACLEOD, ANGUS M.
 APPLICANT: MERCHANT, KEVIN J.
 TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID A. MUTHARD
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: U.S.A.
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,133
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MUTHARD, DAVID A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 18938
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3903
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1290 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-138-133-2

Query Match 15.4%; Score 985; DB 1; Length 1290;
 Best Local Similarity 25.6%; Pred. No. 4e-67;
 Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;
 QY 74 IMRPSRKNKAKISID--SIGEVSEGRSEVYFORV-PDGSF--DPNCCFSYHGS--HR 126
 Db 60 ITW--SRGADKIEGSDIRKEIRKPKTSRNDRYQDPAFRPDQSCFVILGMERL 117
 QY 127 ESIDLVTSSSEVARTWVGLRLMAGISDEBSL-ARRORTDQWLKQTFDEADNKGDSL 185
 Db 118 KTLSDAISSEDEVNMKIGLWLM-----EDTLQATPLQIERMLRKQFYSVDNRREDRI 172
 QY 186 SIGEVLQILKLNVLPRQVRYKMFREADTDHQ--GTIGFEERCAFYK--NMSTRDLY 241
 Db 173 SAKDLKNNLSQVNYRVPMNR--FLRERLTPDEQRSDDITYGQFQALYKSLMYSQAQTM 229
 QY 242 LLM-----TYSNKHCHDAASLQRF-----LOVEOKNAGVTLSECODII 281
 Db 230 LPFLETNPLRIGERPELQOVSSISEFOQFLYEGELMAVDRLQVOEMLSPRLPLREIE 289
 QY 282 EQFEPCKPKNSKGLIGDIFNTYRSPAGDIFENBHNV-HQDTPOLSHFTTSSNTY 340
 Db 290 EBY-----PFLDELVTPLFESKENSVMNSQLDAVCEYNNNPLSHYVSSISHNTY 338
 QY 341 LVGDQMSQSRVDMYAVYLAQACRCVEYDCWDGDPBPIYHGHYTLTKILFKVIEFIN 400
 Db 339 LTGDQSSSESLAVARCLRMGCRCIELDCWDGDPGVYIYHGHYTLTKIKFSVLTITK 398
 QY 401 KYAFIKNEYPYLSTENHCASYIOQKKAQVYITDLGKLDLSSVSSDATTLPSPOMLKG 460
 Db 399 EHAIVASIEPYLSTIEDCSIAQORNMMAOHRKYLVDTL-LTRPVYDIAADGLSPNOLKR 457
 QY 461 KILVKKKLP-----NISDAEAG----- 480
 Db 458 KILKHKKLAGSAYEEVPTSVMSSENDISNGLIYLEDVNNHMYHYVYVLTSSKI 517
 QY 481 ---EVSDESDADEIDDCCKLNGDASTNRRV-----ENTAKRKLDS----- 519
 Db 518 YSSEISSDOGNDEEPRKASGSTELHSEKWFHCKLAGRQGRHIAERLLEYCIENG 577
 QY 520 -----LIKES-----KIRDC----- 529
 Db 578 APDGSFLVRESIEPVGYTILSPFRNGKVOCHRIHSRODAGTPKFFLTDLNLFVDSLVDLT 637
 QY 530 ----- 530
 Db 638 HYQVPLRCNEFEMRLSEPVQTNHESKEWYHASLTRAQAEHMLRVPRDGAFLVYKRN 697
 QY 531 DPNNEVSSTLSPSGK-----LGRKSK----- 551
 Db 698 EPNSTALS-PRAGKIKKHCRCVQOEGOTVMLGNSEFSLVDLISYEKHPYKMKLYRPI 756
 QY 552 -----AED-----VESG----- 559
 Db 757 NEALKEIGTAEPDYGALYEGRNPFYVEANPMTFKCAVKALFDYKAQREDELFTTSA 816
 QY 560 -----EDAGASR----- 566
 Db 817 IIVNEKODGGMWKGYGKQKQMFPSNYVEEMINPALEPEREHDENSPLGDLRGVL 876
 QY 567 -----RNGRLVYVGSFSSRRKKSGSKLTKAASVEE-----GDEGDSPGG 604

Db 877 DVPACQAIARBEGRNNRLFEVSIEMPSVAQMSLDVAADSOEELDPMVKIREVAQTADAR 936
 QY 605 QSRGATROKTKMKSRLSALSDLYTKKSAVTHD--1EMRAASWOVSSESEKKAHILLOO- 661
 Db 937 ILEGKMMERR-KKIALSELVLYCRPVPEDEKIGTRACRYRDMSSPETKAEYVKA 995
 QY 662 KRAOVLRFMOOOLSHYSSYVSDSSNYPNPFMAGCOMVALNOSGRMLQOLRAAFS 721
 Db 996 KKKKFLQIKRLOLSRITKPGQRLDSSNTDPLPMWICGSQVLAVALNQTGDKPMQMOALFM 1055
 QY 722 ANGCGGYVLKPGCMQGVFNPNSEDLPGQLKQOLVLRISGOOLPKRPSDMLGDRGELI 781
 Db 1056 AGHCGGYVLQPTMDPEAFDPDKSLRGLEPCVICIEVLAGARHLPK-----NGRG-IV 1108
 QY 782 DEFEVEITIGLVDCSREOTRYVDNGNFPNTW-EETIVFMVMPETALVRLWMDHPLG 840
 Db 1109 CFEVELEVAGAYDSTKQCTEFDVNDGLNVPAPKPFHFIQJNSPEPFLRFVVEEDMFS 1168
 QY 841 -RDEIGOPTLAFSSMMPGYRHV-----YLEGMEASIFVHVAV 877
 Db 1169 DONFLAQTAFPYKGLKTYRAVPLKNNYSDELELASLKLKIDI 1211

RESULT 6
 US-09-579-181-2
 ; Sequence 2, Application US/09579181
 ; Patent No. 6365372
 ; GENERAL INFORMATION:
 ; APPLICANT: Chivlva, John
 ; APPLICANT: Yaciuk, Peter
 ; TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
 ; FILE REFERENCE: 16153-4247
 ; CURRENT APPLICATION NUMBER: US/09/579,181
 ; CURRENT FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/136,620
 ; PRIOR FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 2972
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-579-181-2

Query Match 3.0%; Score 192; DB 4; Length 2972;
 Best Local Similarity 19.6%; Pred. No. 2, 4e-05;
 Matches 187; Conservative 121; Mismatches 326; Indels 318; Gaps 42;

QY 406 KNEYPVILSIENHCYSVIOQKMAQYLTDLIGKLDLSSVSED-ATTLSPQMLKGIIV 464
 Db 173 EEPPOVLEIKPPSAVTOQNKQPMHPDEDEDEFTANEBAEDEDITIAEQLGEGV-- 230
 QY 465 KKKLPIANISEDDEEGVS-----DEDSADEIDDDCKLNGDA 502
 Db 231 ---DHAMELSELAREGELSMELLQOYAGAYAPGSGSSEDEDEDEVANSDE-PEGV 286
 QY 503 STNRKVENTAKRLDLSILKESKTRDCEDPNNTSVSTLSPSGIKGRSKAEDEVESGEDA 562
 Db 287 EAEPPEQEDSSQS-DEY--EDRSEDEDEHSEBEETSASASESESESDAOSQSA 343
 QY 563 GASRRNGRLVYGSFSRRKKKSKIKKAAVSEGBEGODSPGQSGRG-----608
 Db 344 DEEBDDDFGEVYLLADEQSE-----ADAGSGPTPEPTTLGPKKETITDIAAAS 396
 QY 609 -----ATROKKT-----MKLSRLSLDLVYTKKSVAT 634
 Db 357 LQPKCYTLATVQKTPILPILRGQLREYQHIGDMVITWYMKKINGLILADEMGKTIQT 456
 QY 635 HDI-----EKEA-----ASSWOVSF-----SETKA-----655
 Db 457 ISLHLACEKGNMGPHLIIPTSVMLNMEMELKRCMPFSKILTYGAQKERRKLRKGWT 516
 QY 656 -----HOLLQOKPAOYLRFNQOOLSRITPSSYRVDSNYNQ-----692

Db 517 KPNAFHCITSYKLVLDODHQAFRKKMRYLILDEADQIKNFKSQRMOSLINFNSORLL 576
 QY 693 ---PFWNAGCOMVALNOSGRMLQOLRAAFSANGGCVLYLKPGCMQGVFNSESDPLP 749
 Db 577 TGTPLQSLMELMSLMFLMPLHYQSHRE-----FKMPSNPLT 615
 QY 750 GOLKQOLVLRISGOOLPKRPSDMLGDRGELIDF---VEVEI-IGLP-----VDC-- 796
 Db 616 G-----MIEGSO--EYNEGLVKRLHKLRYFLRLRAVYVVERKMPKRYEHTICRL 664
 QY 797 SREOTRYVDNGNFPNTWETLVFMVMPETALVFL-----YMDHDIIGRDFIGORT 848
 Db 665 SKRQCLYDDEMAOTTKETLATGHFMSVINITLMQLKRCVNHNPMLFDPRPVTSPTI-TPG 723
 QY 849 LAFSSMMPGYRHVYLEGMEASIFVHVAVSDISGKVRQALGLKGLFLRGKPSGLSHAA 908
 Db 724 ICFSTASIVLRATDVHPLQRIDM-----GRF-DLIGLBERVSRYEADFLPRHRL 772
 QY 909 GR-----PPRAPS-VSQKILRRTASAPTKSQKPGRR-----GFPELVIGTRDTGS 952
 Db 773 SRRVLEVAATAPDPPRRPKPKMKVNRMLQFVP---KOEGRVVVVVNNPRAPLGP-----824
 QY 953 KGVADVVYPPGPGAPAREAPAGEPG-----SGSPRGKAPAAVAKESPVRVPP 1000
 Db 825 -----VVRPPEGBELSAOPTPEGVPOVYLPAISLMSASAG-PPLIPASRPFGVLLP 876
 QY 1001 RYLDGPGPAGMAATCMKCVGSCAGVNTGQLRERPPSPGASRQAIROQPRARADSLG 1060
 Db 877 PLQPSG-----SLPOVLPSPGLVLSG---TSNPPTP-----TLSLKPPPAVRLSP 921
 QY 1061 APCCG---LDPHALPGSRREAPKPGCMKRGPGGSGMSDSSPSDPIGPEKSP-----1112
 Db 922 APPGSSSLKPLTVP-----PG-YTFPPPAATVTTTATVATTAVPAPVAPQR 971
 QY 1113 -----RMPEGACRQPGALQGEMSAIPFOKLEIRSKSPMSAG--KPL 1153
 Db 972 LILSPDMQARLPDSGEVYSIGL-----ASLQR-----PVANAGSKPL 1010

RESULT 7
 US-09-579-181-1
 ; Sequence 1, Application US/09579181
 ; Patent No. 6365372
 ; GENERAL INFORMATION:
 ; APPLICANT: Chivlva, John
 ; APPLICANT: Yaciuk, Peter
 ; TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
 ; FILE REFERENCE: 16153-4247
 ; CURRENT APPLICATION NUMBER: US/09/579,181
 ; CURRENT FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/136,620
 ; PRIOR FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3118
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-579-181-1

Query Match 3.0%; Score 192; DB 4; Length 3118;
 Best Local Similarity 19.6%; Pred. No. 2, 6e-05;
 Matches 187; Conservative 121; Mismatches 326; Indels 318; Gaps 42;

QY 406 KNEYPVILSIENHCYSVIOQKMAQYLTDLIGKLDLSSVSED-ATTLSPQMLKGIIV 464
 Db 319 EEPPOVLEIKPPSAVTOQNKQPMHPDEDEDEFTANEBAEDEDITIAEQLGEGV-- 376
 QY 465 KKKLPIANISEDDEEGVS-----DEDSADEIDDDCKLNGDA 502
 Db 377 ---DHAMELSELAREGELSMELLQOYAGAYAPGSGSSEDEDEDEVANSDE-PEGV 432

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QY 503 STNRKRENTAKRRLSLIKESKIRDCEDPNNEFVSTLSPGKIGRKAKEDEVEDGEDA 562
DB 433 EAERPPEDSSSSQ-DSV--EDRSEDEDEHESEEETSGSSASSESESEDEAQSOSA 469
QY 563 GASRRNRIVYGSFRRKRSKSLKAAASVEEDGODSDGSGS-- 608
DB 490 DEEBEDDFVEVYLLADEDSQSE--ADAGSGPPPTLGPKEITDIAAAES 542
QY 609 -----ATROKKT-----BMA--ASSWQVSSF--SETKA----- 655
DB 543 LQPKGYLATATYVTPFLLRQLRGLEYQHIGDLVTMEKLNGLADEMGLAKTLOT 602
QY 635 HDI-----HILQOKPAOYLRFNQOOLSRITYPSYVDSNNPQ----- 692
DB 663 KPNAFHVCITSYKLYLQDHOAFRRKMRVLLIDEAONINFKSQRMOSLINFNSORLL 722
QY 723 TGTPLQNSLMEIWSLHFLMPLHFVQSHRE-----FKEMSNPLT 761
DB 750 GQKKQVLIRIISGQOLPKPRDSMLDGEIIDPF--VEVEI-TGLP-----VDC-- 796
QY 762 G-----MIEGSO--EYNEGIVRLKHLVPLRLRRKVDVEKQMKYEHVIRCL 810
DB 797 SRBQTRVVDNGFNPTWEETLVFMVHMPETALVRL-----WMDHPIDIGDFGQRT 848
QY 811 SKRQCLYDDFMAQTTKTEFLATGHFMSVINILMOLKACNPNLFDPPVTSPTL-TPG 869
DB 849 LAFSSAMPGRHYVLEGEAEASIEYHVAVSDISGKYKQALGKGLFKPGKSLDSHAA 908
QY 870 ICFSTASLVLRATDVHPLQRIQM-----GRF-DLIGLEGVRSYREADTFLPRHRL 918
DB 909 GR-----PPRPS-VSORILRTASAPTSOKGR--GPELVILGTRDGS 952
QY 919 SRRVLELVATADPPRPKPKVAKMQLQVY--KQGRVTVVNNRPLDGP----- 970
DB 953 KGVADDVPPGPGAPADPAQEGPG-----SGSPRKAPAAVAEKSPVRRPP 1000
QY 971 -----VVRPPGPBELSAQTPGPVPQVLPASLWVSASPAQ--PLLPAASPPPVLLP 1022
DB 1001 RYLDGPGPAGMATCMKCVVSCAGVNTGGLOREPRPSPASRAAIRQOPRPARADSLG 1060
QY 1023 PLQPSNG-----SLPOVLPSPGLVLSG--TSRPPTP--TSLKTPPPAVRRLSP 1067
DB 1061 APCCG--LDPHALPGRSREAPKPGCAMROGPGSGMSDSSSDSPDSPGIPERSP-- 1112
QY 1068 APPGSSSLKRLVYV-----PG-YTFPPRAATTSTTTATATTAVVAPLPAPQR 1117
DB 1113 -----RMEGACRQPGALQEGMSALFQKLEIRSKSPMFSAG--KPL 1153
QY 1118 LILSPDMQARLPSPGEVYSIGOL--ASLAQR-----PVANAGSKSL 1156

```

RESULT 8
 US-09-219-849-5
 Sequence 5, Application US/09219849
 Patent No. 6150081
 GENERAL INFORMATION:
 APPLICANT: VAN HEERDE, GEORGE V.
 APPLICANT: VAN RIJN, ALEXIS C.
 APPLICANT: BOUMSTRA, JAN B.
 APPLICANT: DE WOLF, FREDERIK A.
 APPLICANT: MOOBROEK, ANDREAS
 APPLICANT: WERTEN, MARC W.T.
 APPLICANT: WIND, RICHEL D.
 APPLICANT: VAN DEN BOSCH, TANJA J.
 TITLE OF INVENTION: SILVER HAIDE EMULSIONS WITH RECOMBINANT COLLAGEN
 TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
 TITLE OF INVENTION: PREPARATION THEREOF

FILE REFERENCE: 2728-2
 CURRENT APPLICATION NUMBER: US/09/219, 849
 CURRENT FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 5
 LENGTH: 960
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 US-09-219-849-5

Query Match 3.0%; Score 189; DB 4; Length 960;
 Best Local Similarity 30.4%; Pred. No. 7.3e-06;
 Matches 90; Conservative 7; Mismatches 93; Indels 106; Gaps 19;

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QY 897 GPK-----PGSLDSHAGRP-PARPSVQRIILRTASAPTSOKPGRGRPELVLT 947
DB 736 GPKAGPAGPPGSRDPPGAPAGPPGSR-----DPCPPAGPAGPAGP--GS 783
QY 948 RDTGSGVADDVPPG--PGAPAPAPAG--PGSGSPRKAPAAVAEKSPVRRPRLV 1003
DB 784 RDPGPPGAPGPPGSRDPPG--PGAGPAGPAGPAGP--GPPAPGAPGPPGSRDPP 840
QY 1004 DGPAGPAGMATCMKCVVSCAGVNTGSLQREPRPSPASRAAIRQOPRPARADSLGAPC 1063
DB 841 GAGPAG--PPGSRDPPGAPGAPGAPGPPGSRDPP-----GAP- 877
QY 1064 GDLPHALPGRSREAPKPGCAMROGPGSGMSDSSSDSPSPGIPESPPMPPGACRQPG 1123
DB 878 --GPAAGP-SRD-PGPPGA--PGAG--PPGSRDPPGAP--GPAAGP--RDPPG 923
QY 1124 ALQEGMSALFQKLEIRSKSPMFSAGKPLPCVYLPFAPGAG--PGSPAA 1173
DB 924 P-----PGAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 944

```

RESULT 9
 US-08-642-255-62
 Sequence 62, Application US/08642255
 Patent No. 5773249
 GENERAL INFORMATION:
 APPLICANT: CAPPELLO, Joseph
 APPLICANT: FERRARI, Franco A.
 TITLE OF INVENTION: High Molecular Weight Collagen-Like
 NUMBER OF SEQUENCES: 135
 CORRESPONDENCE ADDRESS:
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/642,255
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: ROWLAND, Berttram I.
 REGISTRATION NUMBER: 20,015
 REFERENCE/DOCKET NUMBER: A55556-3/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 494-8700
 TELEFAX: (415) 494-8771
 TELEX: 910 277299 FHT UR

```

Best Local Similarity 27.2%, Pred. No. 4.2e-05;
Matches 88; Conservative 15; Mismatches 120; Indels 100; Gaps 17.

OY      889 GLKGLFLRKPKRPSDLSDSA-AGRP-PARPSYSQRLIKRTASAPLTKSOK-----PGRRGFP 941
           |||          :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
Db       663 GAKG-----EPCDGAAGKADAGCPGPAGPPAGPGPGPIGNVGAPGAKGAGSGAPGATGFP 716
OY      942 ELVLGTRDNGSKGVADVVPGRG-----PAPEAPAOEGPSSGSPRKA-----985
           |              -GACARVCGPPGPGSGNACPPGPPGAGCKEKGK-G-PREFTGPRAGHPGYVR 763
Db       717 -----GACARVCGPPGPGSGNACPPGPPGAGCKEKGK-G-PREFTGPRAGHPGYVR 763
OY      986 ---PAAVAEK-SFVRVRRPVRLDGEGPAGMATCMKCVCAGVTGTGLORER--PPSP 1039
           |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db       764 PEPFGPAGEGSGPGADGAPGAPGTPOGIA-----GGRGVGVLPGGGGERGFPLP 815
OY      1040 GPASRQAIIQQQRARAADSICAPCCGLDPHALIGRSREAPRGPMIRGPGGSMSMSSDS 1099
           |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db       816 GPSGEPC-KQGSGASGERGPP---GMGPPGLA--GPSGESGRECAPAEBSPPGRDG 867
OY      1100 SSPSPGIPERSRWEEGACRPGALGEMSAIFAQKLEIRKSQPMFSAGK-----1151
           |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db       868 SPQAKGDRGETGTGAPGAPGARVARGA-----PGPYVPACKSGDRDGTG 909
OY      1152 PLTPCYVLPHPAGMGAPGSPMAA 1174
           |             |||   |||   |||
Db       910 P-----AGPAGPYGPAGA 922

RESULT 11
US-08-906-865-4
/ Sequence 4, Application US/08906865
/ Patent No. 6040168
/ GENERAL INFORMATION:
/ APPLICANT: Greengard, Paul
/ APPLICANT: Porton, Barbara
/ APPLICANT: Kao, Hung-Teh
/ TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
/ TITLE OF INVENTION: AND USES THEREOF
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave., Continental Plaza, 4th
/ STREET: Floor
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/906,865
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 600-1-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-343-1684
/ TELEFAX: 201-487-5800
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 696 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ DESCRIPTION: /desc = "Synapsin Ia"
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:

```


ORGANISM: Homo sapiens
US-09-906-865-4

Query Match 2.8%; Score 179; DB 3; Length 696;
Best Local Similarity 21.7%; Pred. No. 2.7e-05;
Matches 152; Conservative 74; Mismatches 266; Indels 210; Gaps 36;

```

QY 574 GSFRRKKKSKLKKAASVEEGDEGDDSPGQSGRATQKTKMLSRALSDLVYTKTSSVA 633
DB 75 GFFSSLSNAVKQTTAAATAATFSEQVGGSGAGGGAASRLVLIDEPHTMAKYFKGKK 134
QY 634 TH--DIEMEAASSWQVSSSEFK--AH-----QIIQKPAOYLRENOQ 672
DB 135 IHGEIDIKVEQA-----EESDLNLVAHANGGFSVDMELNKGKVKVRSLLKPDVLLRQH 188
QY 673 QLSRIYPSSTY-----VDS--SNYN--PQPMWAGCQWALNYSQEGRML 713
DB 189 AFSMARNGDYRLSLVIGLOVAGIPSVNSLSHYNFCDKPWVF--AQMVRLLH-----K 237
QY 714 QLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKQVLRLIISGQQLKPPRDSM 773
DB 238 KLGTSEFP-----LIDQTFYPNHKEMLSSTTYVYVKKMGHAGSKGKVKVDN 284
QY 774 LGDRGEI-----IDPVE-----VEIIGLPVDCSRBQTRVYVDNGFNPTWEE 815
DB 285 QHDFODIASVVALKTYATAPEFLIDAKYDVYVKIG-----QNYKAYMRTSVSGNW-K 336
QY 816 TLVFNVAHPEIALV-RFLVWD-----HPIGRDFIGQRTLAFFSMMP 856
DB 337 TMTGSAMLEQIAMSDDRYKLTWDTCEIFGLDICAVALHKGKGRDHIE---VGGSSMP 393
QY 857 GYRHYVLEG---MEASIFVHAVSDISGKVKQALGKGLFLRGPKGSDSHAAGRPPA 913
DB 394 -----LIGDHQDEDDQILVELVYN-----KMAQALPRQRORDASPRG-GSHGQTPSPG 440
QY 914 RPSVSORILKRTASAPTKSQKPGRRGFPELVLTGRDTGS-----KGV---A 956
DB 441 ALPLGRQTSQOPAPPAQOEPPQGGPPQPGPQGRQGRPPLOQRPPGQOHLSTGLGPPA 500
QY 957 DDVVP---GGPAPAPAPAEQEG--PGSGSPRGKAPAAVAEKSPVRYRPPVLDGPGPAGM 1011
DB 501 GSPLPRLPSPTSPAPQOPASQAAPPTGGQGRQSRVAGGAPAPAPARPPA---SPSPQRO 557
QY 1012 A---ATCMKCYVG---SCAGVNTGGLQREKPPS--PGPA--SKQAA-----I 1048
DB 558 AGPPQATROTSTVSGPAPAPKASGAPPGQOQROGPPQKPPGPAPGPTROASQACGVPRTGPPT 617
QY 1049 RQOPPARADS-LGAPCCGLDPHAIPIGRSREAPKPGAMRQGGSGSSSDSSPDSPGI 1107
DB 618 TQOPRPSGPGPAGAP---KPOLAKRPSQDVPPPPATAAAGP-----PHQQLFNL 663
QY 1108 PERSPRMEGACRQPGALGEMSALEFAQKLEIRSKSPMESA 1149
DB 664 PEPAP-----PRPSLSODEV-----KAETIRSLRKSFPAS 692

```

RESULT 12
US-09-129-668-4
Sequence 4, Application US/09129668B
Patent No. 6429010

GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: US/09/129,668B
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906,865
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4
LENGTH: 696
TYPE: PRT
ORGANISM: Homo sapiens
US-09-129-668-4

Query Match 2.8%; Score 179; DB 4; Length 696;
Best Local Similarity 21.7%; Pred. No. 2.7e-05;
Matches 152; Conservative 74; Mismatches 266; Indels 210; Gaps 36;

```

QY 574 GSFRRKKKSKLKKAASVEEGDEGDDSPGQSGRATQKTKMLSRALSDLVYTKTSSVA 633
DB 75 GFFSSLSNAVKQTTAAATAATFSEQVGGSGAGGGAASRLVLIDEPHTMAKYFKGKK 134
QY 634 TH--DIEMEAASSWQVSSSEFK--AH-----QIIQKPAOYLRENOQ 672
DB 135 IHGEIDIKVEQA-----EESDLNLVAHANGGFSVDMELNKGKVKVRSLLKPDVLLRQH 188
QY 673 QLSRIYPSSTY-----VDS--SNYN--PQPMWAGCQWALNYSQEGRML 713
DB 189 AFSMARNGDYRLSLVIGLOVAGIPSVNSLSHYNFCDKPWVF--AQMVRLLH-----K 237
QY 714 QLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKQVLRLIISGQQLKPPRDSM 773
DB 238 KLGTSEFP-----LIDQTFYPNHKEMLSSTTYVYVKKMGHAGSKGKVKVDN 284
QY 774 LGDRGEI-----IDPVE-----VEIIGLPVDCSRBQTRVYVDNGFNPTWEE 815
DB 285 QHDFODIASVVALKTYATAPEFLIDAKYDVYVKIG-----QNYKAYMRTSVSGNW-K 336
QY 816 TLVFNVAHPEIALV-RFLVWD-----HPIGRDFIGQRTLAFFSMMP 856
DB 337 TMTGSAMLEQIAMSDDRYKLTWDTCEIFGLDICAVALHKGKGRDHIE---VGGSSMP 393
QY 857 GYRHYVLEG---MEASIFVHAVSDISGKVKQALGKGLFLRGPKGSDSHAAGRPPA 913
DB 394 -----LIGDHQDEDDQILVELVYN-----KMAQALPRQRORDASPRG-GSHGQTPSPG 440
QY 914 RPSVSORILKRTASAPTKSQKPGRRGFPELVLTGRDTGS-----KGV---A 956
DB 441 ALPLGRQTSQOPAPPAQOEPPQGGPPQPGPQGRQGRPPLOQRPPGQOHLSTGLGPPA 500
QY 957 DDVVP---GGPAPAPAPAEQEG--PGSGSPRGKAPAAVAEKSPVRYRPPVLDGPGPAGM 1011
DB 501 GSPLPRLPSPTSPAPQOPASQAAPPTGGQGRQSRVAGGAPAPAPARPPA---SPSPQRO 557
QY 1012 A---ATCMKCYVG---SCAGVNTGGLQREKPPS--PGPA--SKQAA-----I 1048
DB 558 AGPPQATROTSTVSGPAPAPKASGAPPGQOQROGPPQKPPGPAPGPTROASQACGVPRTGPPT 617
QY 1049 RQOPPARADS-LGAPCCGLDPHAIPIGRSREAPKPGAMRQGGSGSSSDSSPDSPGI 1107
DB 618 TQOPRPSGPGPAGAP---KPOLAKRPSQDVPPPPATAAAGP-----PHQQLFNL 663
QY 1108 PERSPRMEGACRQPGALGEMSALEFAQKLEIRSKSPMESA 1149
DB 664 PEPAP-----PRPSLSODEV-----KAETIRSLRKSFPAS 692

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RESULT 13
US-08-642-255-61
Sequence 61, Application US/08642255
Patent No. 5773249

GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBREITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-255-61

Query Match 2.8%; Score 177.5; DB 1; Length 252;
Best Local Similarity 30.3%; Pred. No. 7.4e-06;
Matches 90; Conservative 6; Mismatches 108; Indels 93; Gaps 19;

QY 897 GPK--GGSLSHAGRPAPSVSQRILNRTASAPKSKQKPGRRGPELVLTGRTDGSKG 954
DB 16 GPGABE-----PAGPPGSKGDC-----PGAPAPAGPPGSKG-----DGGPPG 55
QY 955 VADVVPPG---PGAPAPAGG---PGS---GSPRGKAPAAVAEKSPVRRPPVLDG 1005
DB 56 APGAPGPGSGDPPG--PGAPGAPGPPGSGDPPGAPGAPG-----PPGSRGD 104
QY 1006 PGAGMAATCMKCVSCAGVNTGGLQREPRPSPGASRQAALRQPRARAD--SLGAPC 1063
DB 105 PGPPGAPG-----AGPPGSRDPPGPPGAPGAPG-----PPGSGDPPGAPG 147
QY 1064 CGLDPHAIPIGRSREAPKPGFAMWQPGSGSGMSDSSPSPGIPERSPMWPGACROPQ 1123
DB 148 ---GPAAPP--SKGDDPPGA--PGAPGPPGSGDPPGPPGAPG-----PAGPPGSGDPPG 196
QY 1124 ALOGESALFAOKLEIRSKSPMFSAGKPLLPVCVLPFHAPGMAGP---GSPAAASA 1176
DB 197 PPGAPGA-----GPPGSRDPPG-----GPPGAPGAPGPPGSGDPPGPPGA 236

RESULT 14
US-08-931-820-4
Sequence 4, Application US/08931820
Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1

FILING DATE:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type III
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1055
OTHER INFORMATION: /label= Modified
OTHER INFORMATION: /note= "Ala may be Pro"

US-08-931-820-4

Query Match 2.8%; Score 176; DB 3; Length 1057;
Best Local Similarity 26.5%; Pred. No. 8.5e-05;
Matches 95; Conservative 22; Mismatches 121; Indels 120; Gaps 20;

QY 887 ALGLGLRGRKPGSLDSHAGRP---PARPSVSQRIL--RRTASAPKSKQKRRGRGF 940
DB 681 APGEKG---EGGPPG-----VAGPPGSGPAGPPGPPGQVKERKSPGGPGAPGPPGARGL 732
QY 941 PELVLTGTRDTGSKGVADVVPPG-----DGPAPAPAGPPGSGSPRGAPAPAVA 990
DB 733 P-----GPPGSGNPNPPGPPGSGPGKDGPPGAPGAPGAPGAPGAPGAPGAPGAPG 783
QY 991 EKSPVRRPPVRLDPPGAPMAATCMKCVSCAGVNTGGLQREPRP-----SPGPAS 1043
DB 784 KSPGAPGPP---GAPGGLGI-----AGI--TGAGLAPPPGPPGPPGPPGPPGPPG 825
QY 1044 RQAALRQPRARADSLGAPCCGLDPHAIPIGRSREAPK-----GPA-----WROG--PGSSG 1093
DB 826 -GVGGSCKPGANGLSGERPPGPPGGLAGTAGGEGRGDGNRGSDDLPPGRDSSPGK 884
QY 1094 SMSDSSPSPSPGIP-----ERSPRWPGACROPAL----- 1125
DB 885 D-RGENSGPAGAPGHPGPPGPPGAPGSGDPPGSGPAGAPGAPGAPGAPGAPGAPGAPG 943
QY 1126 --QGESALFAOKLEIRSKSPMFSAGKPLLPVCVLPFHAPGMAGP-----GSPAAA 1174
DB 944 GPKGEGGERGAAGIRGHRG---PPGN-----PPAPGSPGAPGAGGAGGAGGAGG 988

RESULT 15
US-09-247-806-2
Sequence 2, Application US/09247806
Patent No. 6280747
GENERAL INFORMATION:
APPLICANT: PHILIPPE, Michel
APPLICANT: GABSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
EARLIER APPLICATION NUMBER: FR 98/01614
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 529
TYPE: PRT
ORGANISM: Nephila clavipes
US-09-247-806-2

Query Match 2.8%; Score 175.5; DB 4; Length 529;

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 13:45:25 ; Search time 113 Seconds
(without alignments)
2200.875 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPPPAGLPPLPPALPPDPG.....ALYPMHCLRTLLPWLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3450	54.1	656	4	08TEH5 homo sapien
2	2343	36.7	787	4	09UPR3 mus musculu
3	1587.5	24.9	1128	11	090YCI mus musculu
4	1583.5	24.8	716	4	08WUS6 homo sapien
5	1578	24.7	1154	4	09UPR0 homo sapien
6	1524.5	23.9	997	4	015111 homo sapien
7	1517	23.8	1096	11	062688 rattus norv
8	1463	22.9	772	6	08SPR7 sus scrofa
9	1441	22.6	762	4	09BRCT7 homo sapien
10	1315.5	20.6	772	11	062711 rattus norv
11	1297	20.3	895	5	017232 caenorhabd
12	1294	20.3	771	11	063693 rattus norv
13	1289	20.2	789	4	08TEC1 homo sapien
14	1287	20.2	745	11	060450 cricetus
15	1281	20.1	757	4	08TF37 homo sapien
16	1271	19.9	745	6	029517 oryctolagus

17	1268	19.9	756	11	0921B4 mus musculu
18	1266	19.8	756	11	08R3B1 mus musculu
19	1256.5	19.7	466	4	09H9U2 homo sapien
20	1158.5	18.2	503	4	096FL6 homo sapien
21	1107	17.4	612	13	091423 catfish. ph
22	1106	17.3	677	4	09H8U0 homo sapien
23	1096	17.2	641	6	095J51 macaca fasc
24	1091.5	17.1	640	6	095J50 macaca fasc
25	1075.5	16.9	738	5	097037 hydra magni
26	1000.5	15.7	1175	11	091U21 ephydatia f
27	992.5	15.6	1283	5	097034 mus musculu
28	990	15.5	1236	5	09VXH3 drosophila
29	986	15.5	1230	5	024284 drosophila
30	965	15.1	504	4	096J70 homo sapien
31	956.5	15.0	1265	4	096975 mus musculu
32	947	14.8	537	11	09D9N4 mus musculu
33	942	14.8	1173	11	0920P5 mus musculu
34	942	14.8	1216	11	0921B3 mus musculu
35	940	14.7	1012	5	097035 hydra magni
36	939	14.7	751	5	021734 caenorhabd
37	935	14.7	1311	5	0961D5 drosophila
38	928.5	14.6	1418	5	0906B9 caenorhabd
39	925	14.5	1419	5	095X30 caenorhabd
40	925	14.5	1431	5	095X29 caenorhabd
41	920	14.4	1095	5	094G44 xenopus lae
42	915.5	14.4	1210	13	092137 caenorhabd
43	886	13.9	1183	11	089040 rattus norv
44	881.5	13.8	1211	13	091086 melagris g
45	880	13.8	1299	5	022070 caenorhabd

ALIGNMENTS

RESULT 1

ID	ORTEHS	PRELIMINARY;	PRT;	656 AA.
AC	08TEH5	01-JUN-2002 (TREMBlrel. 21, Created)		
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	FLJ00222 protein (Fragment).			
GN	FLJ00222.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Ukuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;			
RT	"The nucleotide sequence of a long cDNA clone isolated from human spleen."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AK074149; BAB84975.1; -			
PT	NON-TER			
SO	SEQUENCE			
	656 AA; 70138 MW; 1E65D386AB07FIDA CRC64;			
	Query Match			
	Best Local Similarity	54.1%;	Score 3450;	DB 4; Length 656;
	Matches	653; Conservative	2; Mismatches	1; Indels

OY	552	AEDVESGPDGASRRRLVVGSPSRKKKSKLTKRAAYEGDEGQDSPGQSRGATR	611
DB	1	AEEEMSGDAGASRRRLVVGSPSRKKKSKLTKRAAYEGDEGQDSPGQSRGATR	60
OY	612	OKTKKLSRLSDLVKTKSVATHDIEMEAASMQVSSFTKRAHQILOQPAQYLFNQ	671
DB	61	OKTKKLSRLSDLVKTKSVATHDIEMEAASMQVSSFTKRAHQILOQPAQYLFNQ	120
OY	672	QOLSTRIPSYVDSSNTNPPQFMAAGQVALVQSGRLQIQRKFSANGCGYVK	731
DB	121	QOLSTRIPSYVDSSNTNPPQFMAAGQVALVQSGRLQIQRKFSANGCGYVK	180

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QY 732 PGCMCGVFNPNSEDLPLGOLKOLVLRISGQOLPKPRDSMLGDRGEIIDPEVEYEIG 791
DB 181 PGCMCGVFNPNSEDLPLGOLKOLVLRISGQOLPKPRDSMLGDRGEIIDPEVEYEIG 240
QY 792 LPVDCSREOFVVDNNGFNPMWETLVFVWHPMPEIALVRLVMDHDPDIGNDFIGQRTIAF 851
DB 241 LPVDCSREOFVVDNNGFNPMWETLVFVWHPMPEIALVRLVMDHDPDIGNDFIGQRTIAF 300
QY 852 SSMPGGRHYVLEGESEASIFVHVAVSDISGKVOALGLGLFGRGKPGSLDSHAAR 911
DB 301 SSMPGGRHYVLEGESEASIFVHVAVSDISGKVOALGLGLFGRGKPGSLDSHAAR 360
QY 912 PARSVSQRLIRRTASAPYTSQKRGRRGPELVLTGRTDTSKGVADVVPGRGPAPEAR 971
DB 361 PARSVSQRLIRRTASAPYTSQKRGRRGPELVLTGRTDTSKGVADVVPGRGPAPEAR 420
QY 972 AOBGPGSGRGAAPAAVAKSPVVRPPLVILGPGPAGMAATCMCVGSCAGVTGGL 1031
DB 421 AOBGPGSGRGAAPAAVAKSPVVRPPLVILGPGPAGMAATCMCVGSCAGVTGGL 480
QY 1032 QRRRPPSPGASROAAIROQPARADSLGAPCCGLDPHAIIPGRSREAPKPGAMROGPG 1091
DB 481 QRRRPPSPGASROAAIROQPARADSLGAPCCGLDPHAIIPGRSREAPKPGAMROGPG 540
QY 1092 SGMSDSSDSSPSPGIPERSPRMREBACRQPGALOGEMALTRQKLEIRTSKSPMSACK 1151
DB 541 SGMSDSSDSSPSPGIPERSPRMREBACRQPGALOGEMALTRQKLEIRTSKSPMSACK 600
QY 1152 PLIPCVYLPHAPMAGPGSPAAASAMTVSPRVLYALVPMHCLKGTLLPWLACGP 1207
DB 601 PLIPCVYLPHAPMAGPGSPAAASAMTVSPRVLYALVPMHCLKGTLLPWLACGP 656

```

RESULT 2

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Q90PT3 PRELIMINARY: PRT: 787 AA.
AC 090PT3:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB KIA1069 protein (Fragment).
GN KIA1069.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE=99397452; PubMed=10470851;
RA Kiluno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.
RL DNA Res. 6:187-205(1999).
DR HSSP; AB028992; BAA83021.1; -
DR HSSP; P10688; IDJH.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PPHILIPASEC.
DR Prodom; PD001202; PL_PLC_Y; 1.
DR SMART; SM00339; C2; 1.
DR SMART; SM00148; PLCXG; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.

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DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 787 AA; 89169 MW; 28FC0355B4C0FC8D CRC64;

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Query Match 36.7%; Score 2343; DB 4; Length 787;
Best Local Similarity 61.4%; Fred. No. 1.2e-139;
Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;

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QY 239 DLYLMLTYSNHKLHDAASLORFLOEOKMAGVYLESCODITIOFEPCPNKSKGLIGI 298
DB 1 DLYLMLTYSKDKHLYTELAQFLKVEOKANNVTTDCLDITLKFEEVEENKKNVYGI 60
QY 299 DGFYVTSPPADITNPENHHVHODMTPLSHYFTSSHTNYLVGDQLMSQRYDNTAWY 358
DB 61 EGFYVTSPPADITNPENHHVHODMTPLSHYFTSSHTNYLVGDQLMSQRYDNTAWY 120
QY 359 IQAGRCVYVDCMDGPEDEPIVHHGYTLTKILFKVDYETINKAFINKNEYVLTSTENH 418
DB 121 IQAGRCVYVDCMDGPEDEPIVHHGYTLTKILFKVDYETINKAFINKNEYVLTSTENH 180
QY 419 CSYIOQKMAOYLTDILGDKLIDLSVSESDATLTPSPQMLKGLTVGKKLPANVISHDAE 478
DB 181 CSYIOQKMAOYLTDILGDKLIDLSVSESDATLTPSPQMLKGLTVGKKLPANVISHDAE 240
QY 479 EGEVSEDSADEIDDDCKL-LNGDASTNRKRYENTATARKLIDSLIKESKIRDCEDPNFVS 537
DB 241 EGEVSEDSADEIDDECKLFKLHNSGTEHQVEFIRKLESLIKESQIDKDEDPSPFV 300
QY 538 STLSPSGRLGRKS--KAEDY-ESGEDAGASRRGRVLSVFSFRKKKSKLTKKASVVE 594
DB 301 RALLKATHEGLNHLKSPDYKESG----KSHGRSLMNFGRKHKTTSRKSSTYSTD 355
QY 595 GDEGODS---PGGSRATRQKTMKLSRLSDLVYKTSVATHDIEMAASSMOVSFS 651
DB 356 EEDTQOSTGKEGGQYLRLGRRRKTMKLCRELSDLVYVNTNSVAADI-VDDGTGNVLS 414
QY 652 ETKAHLQOKPAQYLRLFNQOQLSRIPSSRYVDSYNYNQPPMNGCQMALNTYSEGR 711
DB 415 ETKAHLQOKPAQYLRLFNQOQLSRIPSSRYVDSYNYNQPPMNGCQMALNTYSEGR 474
QY 712 MGLNRAKFSANGCGYVLPKPGCMGCVFNPNSEDLPLGOLKOLVLRISGQOLPKPRD 771
DB 475 MGLNRAKFSANGCGYVLPKPGCMGCVFNPNSEDLPLGOLKOLVLRISGQOLPKPRD 534
QY 772 SMLDRGEIIDPEVEYEIGLPLVDCSREOTRVVDNNGFNPMWETLVFVWHPMPEIALVRF 831
DB 535 SMLDRGEIIDPEVEYEIGLPLVDCSREOTRVVDNNGFNPMWETLVFVWHPMPEIALVRF 594
QY 832 LVMDHDPDIGNDFIGQRTIAFSSMPGGRHYVLEGESEASIFVHVAVSDISG----- 882
DB 595 LVMDHDPDIGNDFIGQRTIAFSSMPGGRHYVLEGESEASIFVHVAVSDISG----- 654
QY 883 -----KYKQALGLGLFGRGKPGSLDSHAAGPAPRPSVSQRLIRRTASAPYTSQK 931
DB 655 STYILFLGATKRNQLOGLGKFNKRRHSSSENN--HYVKKRSIGRILIRRTASAPYTSQK 712
QY 932 SQPGRGRRPELVLTGRTDTSKGVAD 957
DB 713 GRKSKMGFOENV-EIKDSVSEATRD 737

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RESULT 3

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Q90YGI PRELIMINARY: PRT: 1128 AA.
AC 090YGI:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB Phospholipase C-12.
GN PLC12 OR PLC2 OR PLC-L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=20050058; PubMed=10581172;
 RA Otsuki M., Fukami K., Kohno T., Yokota J., Takenawa T.;
 RT "Identification and characterization of a new phospholipase C-like
 RT protein, PLC-L2.";
 RL Biochem. Biophys. Res. Commun. 266:97-103(1999).
 DR EMBL: AB033615; BA89457.1; .
 DR HSSP: P10688; 10AS.
 DR MGD: MGI:1352756; PLC12.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00169; C2; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCXc; 1.
 DR SMART: SM00149; PLCYc; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 1128 AA; 125763 MW; 8598CC59D89ADC85 CRC64;

Query Match 24.98; Score 1587.5; DB 11; Length 1128;
 Best Local Similarity 36.58; Pred. No. 1.1e-91;
 Matches 352; Conservative 168; Mismatches 280; Indels 165; Gaps 21;

OY 4 PTAGPLPGPALP-----EDPGDPSPSRMLFLSANILPYVER-----CMGAMQEG 48
 DB 88 PAAGPVRDRSGPLRRSSINDGQKRRKKTVSFSSMPTEKRTSSASDCIHSWEG 147
 OY 49 MOWKVLKSGKGLVRYLLDEHNSCIWRPSRK-NEAKAISIDISIOVSGRSEVQRX 107
 DB 148 SELKKVNSNRIRYHRYFLDLADQSLRMEPSKDKSEKAKIDIKSIRKVRGKNTDIFR-- 205
 OY 108 PDG---SFDPRCCSIYHSGHRESLDVSTSSSEVARTWTGLRYTMA-GISDEDSLARQ 163
 DB 206 SNGISEQISECKAFSVIYGENYESLDLVANSADVANIWTGLRLISYCKHTLDMLESSQ 265
 OY 164 -RTRDQWLKQTFEDADKNKGDSLSIGEVYLLHKLNVNLPQRYVKQFREA-DTDDHOGT 221
 DB 266 DNMRISWISQMFSEIDVDGLGHTLCHAVOCIRMLNPGIKTSKIELFKELHKSCKRAGT 325
 OY 222 -LGFEEFCAFYKMMSTRDYLMLMTSNHNDHLDASLOEFLQVEKMGAGVTLESODI 280
 DB 326 EITKEEFLEVHEHREIREIFELLVOFSNKEFDITKDLMMFLKEGVAINEISLEI 385
 OY 281 IEQFEPENKSGGLIGIDGFTNTYRSPAGDIFNPEHHHVDMTQPLSHYFITSSNNTY 340
 DB 386 IHKYPSEKGEQKGLSDGFTNYLMSDXYIFDEHKHVKQDMKOPLSFINSSHTY 445
 OY 341 LVGDQMSQSRVMTAMVLAQGCRCVDCWDGPRGEIVHAGTILTSKIIIFKVIENIN 400
 DB 446 LIEEDFRGSDITGYIRALKMGRSVELDVDPNEPVYVYTGHTISQIVFRSYIDILN 505
 OY 401 KFAFTKNEPVLTSTENHCSVIOQKMAQYLDILGDKLIDLSVSSSEDAITLPSPMOLG 460
 DB 506 KTAFFASEPFLICLENHSIKQKRVWQHMKKILGDKLYTSPMEE-SYLPSPDVLKG 564
 OY 461 KILVYKGLKPLANI SEDAEGEVSDSDADEIDDCCKLLNGASTNRKRYENTAKKDLST 520
 DB 565 KILIKRKLISNCS--GVGDDVTDEDEGAEM-----SORMKRENV----- 602

OY 521 IKESKIRDCEDPNNFVSVSTLSPSGKLGKSKAEDEVEDSGDAGASRRNGLVYGSFSRRK 580
 DB 603 -----EQPNHVPV----- 610
 OY 581 KKSGLKKAASVEGDEGDSGGSGSRGATROKTKMTKLSRALSDLYTKTSVATHD--IE 638
 DB 611 -----KRFOLKELSELVSTIGCSVQFKERQVS 637
 OY 639 MEAASMOVSSFSSETKAHQILQCKRPAQYLRFNQOOLSRITYSSRYVDSNYPNPQEFWAG 698
 DB 638 FQVQKTYEVCNFENYLAASKYANENPGDFVNNKRFELRVPSPARIDSSNMNPPQDFKCG 697
 OY 699 COMVALNTQSEGRMLQLNRAKFSANGCGGYLAKGCMQGY--FNPNSDEPLRQOLKKOL 756
 DB 698 COIYAMNFOTGLMMDLNVGMFRONGCYLVRPAIRKEEVSFSPSANTKDSVSPGSDQL 757
 OY 757 VLRITSGOULKRPBMSLGDGEIIPDVEVEIIGLPVDCSREOTRVYDNGFNPTEET 816
 DB 758 HIKIISGNFPPKPGS--GANGDVVDYVVEIHGIPADCAADRTRYVNONGDAPRFDGS 815
 OY 817 LVFVHMPLEIALVRLVMDHPDPIGRDFIGORTLAFSSMMPGYRHYLT-----EGMEAST 871
 DB 816 FEFQINPELNAVRFVLDVDDYIGDEFIQYTIPECIQTGYRHVPLQSLTGEVLAHNSL 875
 OY 872 EVHVAVSDISG-----KYQALGLKGLFLRQPKGSIDS-HAAGPPAPR 915
 DB 876 FVHVATITNRGGGKPKHKKGLSVKRGKREYASLFTLWIK-----TVDEFKRNAPPIRD 930
 OY 916 SVSOR 920
 DB 931 AYDLR 935

RESULT 4
 O8WUS6 PRELIMINARY; PRT; 716 AA.
 ID O8WUS6;
 AC O8WUS6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Hypothetical 75.7 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RA Stransberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019679; AAH19679.1; .
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 716 AA; 75724 MW; 148244B142852AB0 CRC64;

Query Match 24.88; Score 1583.5; DB 4; Length 716;
 Best Local Similarity 61.58; Pred. No. 1e-91;
 Matches 350; Conservative 19; Mismatches 101; Indels 99; Gaps 14;

OY 697 AGCOMVALNTQSEGRMLQLNRAKFSANGCGGYLAKPCMCQGYFNPNSDEPLRQOLKKOL 756
 DB 1 AGCOMVALNTQSEGRMLQLNRAKFSANGCGGYLAKPCMCQGYFNPNSDEPLRQOLKKOL 60
 OY 757 VLRITSGOULKRPBMSLGDGEIIPDVEVEIIGLPVDCSREOTRVYDNGFNPTEET 816

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Db 61 VLRISGQLEPKPRDSMLGDEGELIDFEVEIIGLPLVDCSREGTRVDDNGFPTDEET 120
QY 817 LVFWVHMEIATLVPLVWDHDPIDRDTGORTLAFSSMNGRYRNVLEGMEASIFVHVA 876
Db 121 LVFWVHMEIATLVPLVWDHDPIDRDTGORTLAFSSMNGRYRNVLEGMEASIFVHVA 180
QY 877 VSDISGKVKALGLKGLFGRPGSLDSHAAGRPAPRPSVSOILKRTASAPTKSQKPG 936
Db 181 VSDISGKVKALGLKGLFGRPGSLDSHAAGRPAPRPSVSOILKRTASAPTKSQKPG 240
QY 937 RRGPELVIGTRDNGSGVADDDVPPGPPAPAPAEPAOEGSGSSPRKAPAAVAEKSPVR 996
Db 241 RRGPELVIGTRDNGSGVADDDVPPGPPAPAPAEPAOEGSGSSPRKAPAAVAEKSPVR 295
QY 997 VRPP-----RVLDGPPAGMAATCMKCVGSGAGVGTGLOHERPSR-GPMSRQA 1046
Db 296 PLPLCLSETIIEBPAPAGPPPPPPA-----VFTSSO-GRPPYTPGPNANYA 342
QY 1047 AIHQAPARADSLGAPCCG-----LDPAIPIGRSR-----EAPK 1080
Db 343 SPLDEEPEPDSRPPRCNGGAGAYERAPGSGTDRSQPRTLGLPLVIRVASEGOVPT 402
QY 1081 GP-GAWR-----OGPGSGSSMSDSSSPSPGIPERS-PR 1113
Db 403 EPIGGRPLAAPPAPAVYSDATGSDPLMORLEPCGRDSSVSSSSMSDVTYDLSLPS 462
QY 1114 WPGACRO--PGALGEMGALPAQKLEIRSKSPMFSACKPLPLPCVYLPH-A-PGMAGPS 1170
Db 463 LGLGRREINAGAHMGRD-----PRHSASARPPDLPYTKSKSPNPLRATQ 511
QY 1171 ----PAASAMVYSPRVLYLVALPYWHCL 1195
Db 512 RRPIDELQPRSLAPMAGLPPRPWGL 540

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RESULT 5
Q9UPRO PRELIMINARY; PRT: 1154 AA.

AC Q9UPRO: 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DI 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE KIA1092 protein (Fragment).
CN KIA1092.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE=99397452; PubMed=10470851;
RX Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.*;
RL DNA Res. 6:197-205(1999).
DR EMBL: AB029015; BAA83044.1; -
DR HSSP: P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_Xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam: PF00158; C2; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00388; PL_PLC-X; 1.
DR Pfam: PF00387; PL_PLC-Y; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00390; BPHPLIPASEC.
DR ProDom: PD001202; PL_PLC_Y; 1.

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DR SMART: SM00239; C2; 1.  
DR SMART: SM00233; PH; 1.  
DR SMART: SM00148; PLCX; 1.  
DR SMART: SM00149; PLCYC; 1.  
DR PROSITE: PS50004; C2_DOMAIN_2; 1.  
DR PROSITE: PS50003; PH_DOMAIN; 1.  
DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.  
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.  
FT NON_TER 1  
SQ SEQUENCE 1154 AA; 128371 MW; 84BB2744ADE5A334 CRC64;

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Query Match 24.7%; Score 1578; DB 4; Length 1154;
Best Local Similarity 36.4%; Pred. No. 4,6e-91;

Matches 357; Conservative 166; Mismatches 279; Indels 180; Gaps 24;

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QY 2 APPTAGP-----LPGPA-----LPPED-PGDP-----ESRWLFSLANILPV 37
Db 97 ASPTGPRGVALAPRPSAVVCTLPRESKPGGLPRSSITKDTYOKRERKKTYSFSSMPT 156
QY 38 VER-----CMGAMGQWYKLGSGKGLVRYTLDHRSICIRWPSRK-NEKAKTID 90
Db 157 EKKISSASDCINSWEGSELKRVNSRIYHRYFLDLADMSLWEDSKDSEKADIK 216
QY 91 STOEYSEGRSEVQRYPDGSEF--PNCPSIYHSHRESLDVSTSEVARTWTGLR 147
Db 217 SIKEVTRKNTDIR--SNGISDQISEDCAFSVYIGENYTESLDLVANSADVANIWTGLR 274
QY 148 YLMA-GISDEDLARRQ-RPRDOWLKOTFEADKNGDGLSIGEVQLLHKLVNIPROR 205
Db 275 YLISGKHTLMLLESSODNMRTSWVQSEIDVDNGLHTLCAVOCINLNLPGKLTSK 334
QY 206 VKOMEREA-DTDDHOGT-LGEEFCATYKMASTRRDLYLMLTYSNKHDLAASLQREL 263
Db 335 IELKFKELHKSCKAAGTEVKEEFIEVFHELCYRPEYFLLYVQFSNKEFLDTKDMLEFL 394
QY 264 QVEQKMAVTLSCODITTEQFEPCPENKSKGLGIDGFTYNTSPAGDIPNPHHHVHD 323
Db 395 EAEQGVAHINEISETIHKYEPSEKEQEGWLSIDGFTYMLSPDCTYIDPPEHKVYCD 454
QY 324 MTOPLSHYFTTSHNTYLVGDQLMSOSRVDMYAVLQACRCVEVCMGDPDEPTVHG 383
Db 455 MKOPLSHYFTTSHNTYLVGDQLMSOSRVDMYAVLQACRCVEVCMGDPDEPTVHG 514
QY 384 YTLTKILFQVLETIINKYAFIKNEYPVLTISTHNSGVIOQKMAQYLDLDGKDLSS 443
Db 515 HTMSQVFRSVYDIINKYAFASBPFLILCLNHSSTIQOKVQVYHMKLLGDKLYTTS 574
QY 444 VSEEDATTLPSQMLGKTIYVGRKLPAITSEDAEGEYVSEDSADEIDDCKLNGDAS 503
Db 575 PNVEE-STLSPDVLKGLIKAKKLISNCS--GYEGDVTDEDEGEM----- 619
QY 504 TNKRRENTAKKRLDSLKESKIRDEDPNNSVSTLSFGKLGRKSKAEDEVESGEDAG 563
Db 620 SQMKGEN-----MEQNNVY----- 636
QY 564 ASRRNGRLVYGSFRRKKKSKLKAASYEGDEGDSGSGRGATROKTKMTXLRALS 623
Db 637 ----- 646
QY 624 DIYKTKSAVTHD--TEMAASSWOVSSEFTEKAOIILQKPAOYLIRNOOOLSRITPSS 681
Db 647 ELVYSICKSVQFEFOVSFOVORYTEWECSENEVLASKYAEENGDVYNNKRLRALVFPSP 706
QY 682 YRVDSNYPNPPFWNAGCOMVALNTOSSEBMLQLRAFPANSANGCGGYLAKGCMQGY- 739
Db 707 MRIDSSNMNPQDFWKGCGOYVAMNFOTPELMDLNIIGFRONGNGGYLRAIMKEEVSF 766
QY 740 FNPNSEDPLGOLKOLVLRITISGOQLPKPRDSMLGDEGELIDFEVEIIGLPLVDCS 799
Db 767 FSANTKDSVPGVSPDLHKLKISQGNPKPGS--GANGDVVDPPVYVYHIGITPADAO 824
QY 800 QTRVVDNNGFNPTWEETLVFWVHMEIATLVPLVWDHDPIDRDTGORTLAFSSMNGRYR 859

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Db 825 RIKTVHONGDAPITFDESEFQINLPETAMWVRYVDDDYIGDEFIQYTIPEECLOTGYR 884
 QY 860 HXYL-----EGMEASIFWNAVSDISG-----KYQALGLKGLFTRGPK 899
 Db 885 HVPLOSLTGVLAHNASLEFVAITNRGSGGPKHKGISYVKGKSKSEYASLRTLMWK--- 941
 QY 900 PGSLDS-HAAGRPAPRSVSQR 920
 Db 942 --TVDEVEKNAOPEIRDATDLR 961

RESULT 6

Q15111 PRELIMINARY; PRT; 997 AA.
 AC 015111;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Phospholipase C.
 GN PLC-L (PLC-EPSILON).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9535973; PubMed=7633416;
 RX Kohno T., Otsuka T., Takano H., Yamamoto T., Hamaguchi M., Terada M.,
 RA Yokota J.;
 RT "Identification of a novel phospholipase C family gene at chromosome
 RT 2q33 that is homozygously deleted in human small cell lung
 RT carcinoma."
 RL Hum. Mol. Genet. 4:667-674 (1995).
 DR EMBL; D42108; BAA07688.1; -;
 DR HSSP; P10688; IQAS.
 DR Interpro: IPR000008; C2.
 DR Interpro: IPR001849; PH.
 DR Interpro: IPR001192; PL_PLC.
 DR Interpro: IPR000909; PL_PLC_Xdom.
 DR Interpro: IPR001711; PL_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00360; PHPLIPASEC.
 DR PRODOM; PD001202; PL_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCY; 1.
 DR PROSITE; PS50004; C2_DOMAIN; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50007; PL_PLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PL_PLC_Y_DOMAIN; 1.
 SQ SEQUENCE 997 AA; 112955 MW; 08D3CEC28AD52B7 CRC64;

Query Match 23.9%; Score 1524.5; DB 4; Length 997;

Best Local Similarity 36.2%; Pred. No. 9e-88; Matches 348; Conservative 158; Mismatches 279; Indels 177; Gaps 20;

QY 41 CMGAGCQMOMVRLRGSGKLVFVYLDHRSCIRNRPGRN-EKAKISIDISQEVSEGR 99
 Db 13 CIFMQAGCELKAVRPNRSRYNRFLLDIDIALRWEPSEKDEKAKLISAKETRLGK 72
 QY 100 QSEVFORIPPGSPD---PNCCEFIYVSHRESIDVSTSEVAVRWVGTGLRYLMACISDE 156
 Db 73 NTELEFVN-NGLADQICEADAFSLIGENESIDLVAANSADVANNVSGRLIVSSKOP 130
 QY 157 -DSLARTORT-RDQWLKOTFEADKNGDGLSIGEVYQLHLKLVNLP-PROVAKOMEREAD 214
 Db 131 LDFMEGNQNTPRFWMLKTVKEADVDVNGIMLIDTSVEIKQLNPLTKKAKIKLKRFEIQ 190

QY 215 TDDHOGT--LGFEEPCAFKYMSTRDLYLMLTYSNKHDLDAASLQRLQVEQKACV 272
 Db 191 KSKKELITREVEEFCEAFCELCSTRPEYFLVQISKREKYLDAADMLFLEAQGYTHI 250
 QY 273 TIESCODITDEOREPPEPKSKGLGIDGTNTYTRPADIDFNENHNHOMTOPLSHYF 332
 Db 251 TEDIICIDITIRREYSEEGKQGFALIDFTQYLISECDIDPEEOKKAQMDTOPLSHY 310
 QY 333 ITSSHNTYLVGDLOSRSVDYAWYLQAGRCVWDGDPGDEPIVHGTYTLTKILF 392
 Db 311 INASHNTYLIEDQFRPADINGIYALAKMGCSVELYDSDGSDNPEILCNRRNMTTHVSF 370
 QY 393 KDYETETINKYAPLKNEYPIVLSIENHCSYIQKKAQYVITLIDGLKDLSSVSSDATT 452
 Db 371 RSVIEYINKFAFVASEYPLILGNHCSLPQOKVAAQOKKVFGNKL-YTEAPLPSESYL 429
 QY 453 PSMQMLKGLIVYKGLPLNPISDAEEGVSDSDADEIDDDCKLNGDASTNRKREVT 512
 Db 430 PSEKLRMIYVKGKRLPSD--PDVLEGEVYDSD----- 461
 QY 513 AKRKLDSLKESKIRDCEDPNNSVSTLSPSGKLGKSKAEEDVESGEDAGARRNGRLV 572
 Db 462 -----EQAQSR----- 469
 QY 573 VGSFRRKKKSKLKAASYEGDEGODSPGGSGCATQKTKMLKSLDLYKTKSV 632
 Db 470 -----MSVDYNGE-----QKIRLCRELSDLVSTICKSV 497
 QY 633 ATHDIE--MEASMSOVSSEFETKAHQLQOKPAQYLFENQOOLSRITYSSRYVDSNNY 690
 Db 498 QYRDFELSMKSONYEMCSSETEBASIAHEVEDVYNNKRLTIYSAMIDSSNIN 557
 QY 691 POPFWNAGCOMVALNTQSEGRMLQLNRAFSANGCGGYLKPCKMQGV--FNPSEDEL 748
 Db 558 PODEWNCGCQIVAMNFOGTPGPMDLHTGWFLOMGCGGYVLRPSIMDEVSYSFANKGIL 617
 QY 749 PGOLKQVLVRLITSGOOLPPRDSMLGDRGEIIDPFVEVETLIDPLVDCSEGRFVDDNG 808
 Db 618 PGVSPALHLIKITISGONFPKPGACA--KGDVDPYVICIHTIIPADCSQKRTKYQNS 675
 QY 809 FNPTEETLVFMVAMPETIALVFLVMDHDPIDRFGIORTIASFSSMMPGGRHYVLEG--- 865
 Db 676 DNPLFDEFEEFQVNLPELAMIRFVYVDDDYIGDEFIQYTIPEECLOPGYRHYPLASFVG 735
 QY 866 --MEASIFWNAVSDISG-----KYQALGLKGLFTR-----GP 898
 Db 736 DIMEHVTLEFVAITNRSGGKAKQKRSLSYVMGKRVETMLRNIGLTIDIFKIAVHP 795
 QY 899 KPGSLD-----SHAAGRPAPRSVSQRILRRASAPKRSQKPG-----RRGFP 941
 Db 796 LREALDMERNQNAIVSITKELGILPI-ASLAKQCLTLISLTLISDNTPTPSVLMKDSFP 854
 QY 942 EL 943
 Db 855 YL 856

RESULT 7

Q62688 PRELIMINARY; PRT; 1096 AA.

AC 062688;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE 130KDa-Ins(1,4,5)P3 binding protein.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=MISTAR; TISSUE=BRAIN;
 RX MEDLINE=96132642; PubMed=8546702;

Query Match 23.8%; Score 1517; DB 11; Length 1096;
Best Local Similarity 36.1%; Pred. No. 3.1e-87;
Matches 349; Conservative 161; Mismatches 278; Indels 180; Gaps 22

QY	41	CMAGOEOMQVYLROGSGSGLVFEYUULDERNSGTRRRPRSRKN-EKAKISIDISOEVSSEGR	99
Db	112	CIFMAGCELMKAVRNPNRSKRYNFEFLDHDLOALREBPKKLEKAKIDISAKIETRIK	171
QY	100	QSEVFQRPYDGSF---PNCSEYIHGSHRESIDIVSTSEVAFVWGTGRILMAGISDE	156
Db	172	NETFPRN--NGLADQICECDAFSLIHGENYSEIDLVDANADVANIWGSRLRVLSKOP	229
QY	157	-DSIARROFT-RDOWLKQTFEADKNGDSSLSTGEVULDLHKLNVNLPRQRYKOFREAD	214
Db	230	LDFMGNQMTPRPMWIKTYFEADVDGNGIMLEDTSVELIKOLNPTLJKSKIRLKFKEIQ	289
QY	215	TDDHOGT-LGFEECAFYKMMSTRDYLILMLTYSNHNDHDAASIQOFLOEYKMACV	272
Db	290	KSKEKLTFRVTEEBCEARCELCTREYVFLVQJSKNEYDADMLFEVEGCVIH	349
QY	273	TLESODITIEQEPCEPKSKGLCIDGFTNTYTRSPAGDIFENRHHVODTOPLSHYE	332
Db	350	TEDMCLDITIRRELSERDROKGFIAIDFPTOYLSPEDCIFDPEQKVAADWOTPOLSHYU	409
QY	333	ITSSHNTYLVGDOIMOSRVMYAWVLQAGRCVAVDQWDBRDPGRVYHNGYTLTSKLIF	392
Db	410	INASNTYLTIEQFRGPRADINKYVALMAGCRSTELVDSDGPDEPILCANNMMALISF	469
QY	393	KDVIETINKVAFINNEYPVILSTENHCSVIOOKKMAQYLTJLIDCKIDLSS-VSEDAIT	451
Db	470	RSYLVEIVINKFAVASEYPLICTIGHCSLPGQRYVWQMKRVFQNKLYTEAPLISE--SY	527
QY	452	LPSOMLKGILVYGKLPANISDEDAEBGEVSDSDADEIDDDCKLNGASTNRKRYEN	511
Db	528	LPSPKALKHMLIVKGLKLPDS--ESBLLCEVTYDDB	560
QY	512	TAKRKLDSLIESKIRDOCEPDNNFVSITLSPSGKLGKRSKAEEVYEGEAGASRRNGRL	571
Db	561	-----EEAEKMSRR-----	568
QY	572	VWGSFRRAKKKGSKLKAASVEGDEGODSPGSGSRGATROKTKMTKLSRALISDLYVTKKS	631
Db	569	VSGDYN-----GEOKHIWLCRELSDLVSTCKS	595
QY	632	VATHDIE--MEAASSWQVSSFETKAIQIILQKPAQYLRFNRNOOLSTIYSSYRVDSNNY	669

RESULT 8		
Q8SPR7		
ID	Q8SPR7	PRELIMINARY;
AC	Q8SPR7;	PRT; 772 AA.
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)	
DE	Phospholipase C delta 4.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Smith T.P.L.;	
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF098759; AAC01221; ..	
SO	SEQUENCE 772 AA; 88075 MW; 86E5706A7427548 CRC64;	

Query Match	22.9%	Score 1463;	DB 6;	Length 772;
Best Local Similarity	38.9%	Pred. No. 4, 8e-84;		
Matches 339;	Conservative 140;	Mismatches 264;	Indels 128;	Gaps 21;
QY	35	LPVVERCMAGOMGVMLRGSGKLVFFVYLDERRSCIRMPRRKNNKAK--ISIDSI	92	
Db	16	LPINQDLT-IMQGMIMRRYRSKWKKLRYLRQDDGMVY-PMARAGGRAPPSISIV	73	
QY	93	QEVSEKGESEVQCRYPDGSFDPNCCSIIYHSHRESLDVYSSEVAKRYWTGLRYLMAG	152	
Db	74	EIVRGHSEELLRNLA-EFLPLEDQFTYVHGRRSLMDLVANNSVEBAQVMOGLOLDYAPF	132	
QY	153	ISDEDSLARQRTQDWLKFQTEDEADKNGDSLISGEVQLQHLKILVNLPRQVROMFE	212	
Db	133	VTNMD----QQRRLQWLSDFWQFRGDKNGDMSPGEVQRLLHMLNVEDQDHARQLQUT	188	
QY	213	APLDHOGHGLFEFEECAFKMMSTYRDLLMLLTYSNKHDLDAASLQFLQVEQKMGV	272	
Db	189	ADT-SQSGTLSEEEVEVERYSKLTAKAEVQAELENNSSQOKLTLEFVDFLOEQRKER	247	
QY	273	TLESQDIIIEQEPCKENKSKGLIGIDFTYNTYRSPADIFENPELHNHOOTPLSHYF	332	
Db	248	ASDLAELFLDRHEDPSDGLRHYVLSLQFLATSLCKDDIDINPCLPIYQDWPOLNHYF	307	
QY	333	ITSSNNTLVNDQMLMSGRVDMYAMVLDQAGRCVEVDCWDPDGEPIVHNHYTTLSTKLIF	392	

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Db 308 INSSHTYLVGDQCGSSVEGYIRAKRCRCVEVDIMDGNPVEVYHGTILSRIFE 367
Qy 393 KDIYETINKYAFIKNEYPIYLISIEHNCVYIQKKAQYLTDLGKLDLSSVSSDATT 452
Db 368 KDVAALIAQYARQTSYDYPVILLENHCSEWQEMAHNLTLEIGDLSLTLDGOLPTOL 427
Qy 453 PPSQMLKGLIKYKGLKPLANISDAEVEGSDSDADEIDDDCKLNLNGASVNRKRVEMT 512
Db 428 PSEPELRKRLVKGKTL-RTLEEDLEEEDEEPESE-----LEG-----EDE 468
Qy 513 AKRKLDSLRKESKIRDCEDPNNEFVSTLSPSGKLGRRKRAEDVESEGDAGASRRNGRLV 572
Db 469 AELELEAGEF-----SEPOE-----LSPRSK----- 489
Qy 573 VGSFSRRKKSKRLKKAASVEEGDEGDSFGGSGRGATROKTKMTKLSRLSLDYKTKSY 632
Db 490 -----DKKKVKAT-----LCPLSALVLYLKAV 513
Qy 633 ATHDI--EMFAASSMOVSSPSETKAHQILOQKPAQYLRFNQOOLSRIPSSYRVDSNNY 690
Db 514 SFSFSAHSRHHYRFYEISFSSEAKASLKESGNEFYQHNTWOLSKRYRPGGLTDSNTN 573
Qy 691 POPFWNAGCOMVALNTOSEGRMLQLNRAKESANGCGYVLKPGCM--CQGVNPNSEDP 748
Db 574 POEFWNNAGCOMVAMNMQTAGLEMDLDCGLFRONAGCGYVLKPDFLRDAQGSFHP--ERP 631
Qy 749 PGOLKQOLVRIISGOOLPFRPDSMLGDRBEIIPFVEVEIIGLPVDCSEQOTRYVDNG 808
Db 632 SPSKAQTLTLOVTSGOOLPVRDSE--KEGSIVDPLVRFVLEFVGRPTAQRHETSYENNG 688
Qy 809 FNPTWEETLVFMVHMPETALVRFVMDHPDPIGR-DFIQGRTLAFFSSMMPGYRHVYL--E 864
Db 689 FNPWGTGTCRVLVPELALLRFVYKDYDKMSRNDYGOYTLTPWNCMOQGYRHITLISKD 748
Qy 865 G--MEASIVFAVSDISGKVKQALGKL 893
Db 749 GISLHPASIFVHICIRE-----GIEGV 770

RESULT 9
Q9BRCT PRELIMINARY; PRT; 762 AA.
ID Q9BRCT
AC Q9BRCT
DT 01-JUN-2001 (Tremblere, 17, Created)
DT 01-JUN-2001 (Tremblere, 17, Last sequence update)
DT 01-JUN-2002 (Tremblere, 21, Last annotation update)
DE Hypothetical 87.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006355; AA06355.1;
DR HSSP: P10688; IQAS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_Xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00388; PL_PLC-X; 1.
DR Pfam: PF00387; PL_PLC-Y; 1.
DR PRINTS: PR00390; PHPLIPASSEC.
DR ProDom: PD001202; PL_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00554; EPH; 3.

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DR SMART: SM00239; PH; 1.
DR SMART: SM00148; PLCXC; 1.
DR SMART: SM00149; PLCYC; 1.
DR PROSITE: PS50004; EF_HAND; UNKNOWN_2.
DR PROSITE: PS50018; EF_HAND; UNKNOWN_2.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS50007; PLIP_X_DOMAIN; 1.
DR PROSITE: PS50008; PLIP_Y_DOMAIN; 1.
DR Hypothetical protein.
SQ SEQUENCE 762 AA; 87585 MW; 544BE5CE2AE3FE CRC64;

Query Match 22.6%, Score 1441; DB 4; Length 762;
Best Local Similarity 38.3%; Pred. No. 1,2e-82;
Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;

Qy 45 MGEQOMVYLRGSGKGLVFEYVLDENRCIRW--RPSRKNKAKISIDISQIEVSEGRSE 102
Db 18 MGEQMPKRRKRSKSKKRLRYFLQNDGMTV-WHAQAAGSAKPSFSISDVETIRNGHSE 76
Qy 103 VFQRPDGSFDPNCCFSIYHGSRESLVLSTSEVARTVYGLRYLMAGISDEDSLARR 162
Db 77 LRLSLAEELPLRQGFIVPHG--RRSLDLMANSVEAQTMMKGLQLDVLYTSMQ---H 131
Qy 163 QRTROMLKOTDEADKNKNGSLSTIGEVLQHLKTLVNLPRQVRKMPREADPTDHQGL 222
Db 132 QERLDQWLSDFQRCGNKODGKMSFOEVRLLHLMVENDQYAFSLQADT--SOSGTL 190
Qy 223 GFEEFCAFYKMMSTRDYLMLLYSNHRDHLDAASLQFLQVEQKMGAVTLESQDITE 282
Db 191 EGEEFYQFQKALTKRAVEQELFESFADQKLTLEFLDFLQBEQKERCSTELALELD 250
Qy 283 QEPCEPKNSKGLIGDGFNTNTRPAGDIFNENHHVHODMTOPIRSHFITSSHTYLV 342
Db 251 RYEPSDQKRLHVLSDMGDTLYLCSKDGDFNACLPYQDMTOPIRSHFITSSHTYLV 310
Qy 343 GDOLMSQSRVDMYAWILOAGRCVEYDVCMDGPDGEPIVHNGYVLSKLLFKDYETINKY 402
Db 311 GDOLCGOSSVEGIRALKRCRCVEYDVMGPGGEVYVHGTILSRILEKDVAVTAQY 370
Qy 403 AFIKNEYPIYLISIEHNCVYIQKKAQYLTDLGKLDLSSVSEATLTPSQMLKGL 462
Db 371 AFQTSIDYPIVLSLETHCSWEQOOTMAHNLTEILGEOQLSTLDGVLPTOLPSEPELRRI 430
Qy 463 LVYKGLKPLANISDAEVEGSDSDADEIDDDCKLNLNGASTNRKRVEMTAKRKLDSL 522
Db 431 LVYKGLK--TLEEDL--EYEEBAEPELE-----SELA 461
Qy 523 ESKTRDCEDPNNEFVSTLSPSGKLGRRKRAEDVESEGDAGASRRNGRLVYFSRKKK 582
Db 462 ESQFETEPDQ-----EONLQND-----KKKK 484
Qy 583 GSKLKAASVEEGDEGDSFGGSGRGATROKTKMTKLSRLSLDYKTKSYA---THDIE 638
Db 485 SKPI-----LCPLASLVIYLYKVSFSFTH--S 511
Qy 639 MEAASSMOVSSPSETKAHQILOQKPAQYLRFNQOOLSRIPSSYRVDSNNYVNPQFWNAG 698
Db 512 KEHHEFYISFSSETKAKRLKEAGNEFYQHTQLSRYVPSGLRTDSNVNPOELMANNAG 571
Qy 699 COMVALNTOSEGRMLQLNRAKESANGCGYVLKPGCM--CQGVNPNSEDPPLGQOLKOL 756
Db 572 COMVAMNMQTAGLEMDLDCGHFRONGCGGYLKPDLFRDQSSHP--EKPISPFKQTL 629
Qy 757 VLRITSGOOLPKPRDSMLGDRGEIIPFVEVEIIGLPVDCSREGOTRYVDNGFNPTWEET 816
Db 630 LIOVTSGOOLPKRVKDT--KEGSIVDPLVYKQIFGVRLDRAQRTNVNENNGFNPYGOY 686
Qy 817 LVFVHMPETALVRFVMDHPDPIGR-DFIQGRTLAFFSSMMPGYRHVYL--EG--MEAS 870
Db 687 LCFRLVPELAMLRFVYVYDKMSRNDYGOYTLTPWNCMOQGYRHITLISKDGLSRPAS 746
Qy 871 IFVHVAVSDISGKVKQALGKL 892

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Db	250	DREPENGRLLRVLSKDFEISLYLCSADGNTFNPCLEIYYDMQPLSHIYINSSNHTYL	309
Qy	342	VGQLMSGRVDNMTAVMLDAGRCVYEVDCWDGPDDEPIVHGHTLTKILFKDIETINK	401
Db	310	LGDFGCGSSGVBGYIRALKRCGRCEVDTMPDGPDEPVYHGRITLSRIELFKDVLATLQ	369
Qy	402	YAFIKNEYVILSIENHCSVJIDQKKWADYLDIDIGDKILDSSEADATLIPSPOMLKG	461
Db	370	YAFQSSDYDYLILSDNHCTWEDQKMAHLLAILGEQLSLSTLEEQLIDIMPSEQLRGK	429
Qy	462	ILYGGKTL-PANISDAEAGEVSDESDADEIDDDCKLINGDASTNRKRVENTAKRKLSL	520
Db	430	ILYVGKRLTLIEVYSDKEEELERDEGSDLD-----PASAEID--	468
Qy	521	IKESKIRDOECPNNNSVSTLSPSGIKRKKAEDVDSGEDAGASRRNGRLVYGSESRKK	580
Db	469	-----MOSQPSBOAS-----GNKSKNK	487
Qy	581	KKSGSLKRAASVEEGDEGQDSPGQSRGATROKTKMLSRALSDLYKTKSVA-----THD	636
Db	488	KK-----FLQSSSTTLICDLBALVLYLTATAPFCSETH-	520
Qy	637	IMEAASSWOYSSSETKAHQILQCKRAQYLRFNQOQLSRITPSSYRVDSNNIPQPFNN	696
Db	521	-SKENYTHYIDISSSESSEKAKMLIREAGENEFQHNARQLCRVYPSGLRTSSNNIPQEHNN	579
Qy	697	AGCCQWALNTYSECBRMQLNRAKFSNAGGGCYLTKPCGM--CGGVNPNSEDLPLGQLRK	754
Db	580	VGCCWVAMNNMOTASSAADICDGLFRQNGSGVYLKPFELNDTQSSFNPMK---PVSILYK	635
Qy	755	Q--LYLRISGQLPKPRDSMLDGRGELIDPFVEVEITIGLPVDCSEQOTRVYDNGENPT	812
Db	636	AQILVVOYISGQRLPKYDKT---KETTVDPPLRVELXGVDEPTKQETSYENNGINPY	692
Qy	813	WEETLVFVNHPELALRFLVMDHPDGR-DFIGQRTLAFSSMMGCRYHYVL-----RCM	866
Db	693	WGEFFYQIQVPELAMLRFEVYKDYSTRSNNEFIGYTLPTCMKKGIRHVSILSKDQSTL	752
Qy	867	EEASIFVHAVSD 879	
Db	753	HPASIFVYTCMQE 765	
RESULT 11			
017232			
ID	017232	PRELIMINARY;	PRT; 895 AA.
AC	017232;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last annotation update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	hypothetical i01.3 kDa protein.		
GN	K10F12.3.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;		
OC	Rhabditidae; Pelodierinae; Caenorhabditis.		
OX	NBIL_TaxID=6239;		
RA	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		
RA	MEDLINE=9069613; PubMed=9851916;		
RA	None;		
RT	*Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium.*;		
RL	Science 283:2012-2018(1998).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN-BRISTOL N2;		
RA	Wohlmann P., Beck C.;		
RT	*The sequence of C. elegans cosmid K10F12.*;		
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		

Query Match	20.3%;	Score 1297;	DB 5;	Length 895;
Best Local Similarity	35.0%;	Pred. No. 1.8e-73;		
Matches 310;	Conservative 138;	Mismatches 266;	Indels 172;	Gaps 23

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QY 38 YERCHAMQEGMOMYKLRGSGKGLVFFYLLDEHRSGIMRPP--SRKKEKKISIDSIOEVS 96
Db 46 VSDCMNYMOTGSDVFLRGKINROFRFFESLADLUSTYNTPTPKAKKHARIAIDELREIR 105
QY 97 EGROSEVFORYPDGSF--DPMCCFSIYHGSRESIDLVSSTSEVARTWYGLRYIMAGI 153
Db 106 LKGNTELL--RSSDEVFTDQIECLFSITLYGDNETYELLDLASSGDANIIMVGTMLTSMNK 164
QY 154 SD--EDSLARRORTROOMLKOTFPEADKRNKGDSISTEVLQLLKLVNLP--PROVKOMFRE 212
Db 165 YECKPSSSOFATLRERWIESVFDEFPTKKKGHIDEOTAFAKALIHNSRISHRLLTYMKKE 224
QY 213 ADTDDHOGTIGFPE-----PDAFYKMSSTRDLYLMLTYSNHKHDLDAASLQRF 262
Db 225 V-----TIGABESERKGLEKSHFVDLYKEIGTRREVYILAMRYAN--KYLSCQDLRLF 276
QY 263 LQVEOKMAGVTLBSCODIIBQEPCEPNKSGLLGIDGFTNTRSPAGDIFNEHHHYQ 322
Db 277 LFEHQGVAVTJDNCFELTBOYEPCSEARENNMTVDGFSFLFSPDCCGFVDNHRVYTM 336
QY 323 DMTQPLSHYTTSSHNHTYLVGDQLMGSRRDMMAWLYOACRCVEYVCMQ-----GPDGEP 378
Db 337 DMQOPFERYETISSRKSYLVEDOL--GPSSDGSSEALKRRCRLEFEDIMPDNEADGETEP 395
QY 379 IVHHGYLVLEKILFQVDYIEFKNKAFYFKNEYPVLLSIENHCSYLOQKMAOYLTDLLGDK 438
Db 396 MWQNGOJAITEKITISSLARIIRERAFERSRPPLLKYSVHCSTDMQKVAAMLITYHIGTR 455
QY 439 LDL---SSVSEDAITLPSPOMLKGLKLVYKTKRPAINISDEAGEGVEDSDEIDEIDDC 495
Db 456 LYLFRKNDPTWDDKRNCPPTPWFDEPNRLLIYGRKLD--NPDUTSGEVSEED--DSL--- 506
QY 496 KILMGDASTNKKREVENTAKRKLDSLIESKIRIODED-----PNNFVSYTLSPSGKLGKRS 550
Db 507 -----ASTTR--KSKRQLQCKELSDLVPEVFNNYKTLN----- 537
QY 551 KAEEDVES--GEDAGASRRNGRLVYGSFSRRKKGSKLKAASVEBQDEQDSPGQSR 607
Db 538 ----DLSTAGSTYMSRKN----- 554
QY 608 GATROKTKMKLSRLSDLVYTKTSVATHIDIMEAASSWQVSSEFTKRAHOLLQKPAOYL 667
Db 555 -----LASVSTETCLRIMHTYATFEG 575

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RESULT	12	
063693		
ID	063693	PRELIMINARY;
AC	063693:	PRT; 771 AA.
DT	01-NOV-1996	(TREMBlrel. 01. Created)
DT	01-NOV-1996	(TREMBlrel. 01. Last sequence update)
DT	01-JUN-2002	(TREMBlrel. 21. Last annotation update)
DE	Phospholipase C delta4.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxId=10116;	

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RT      "A new phospholipase C delta 4 is induced at s-phase of the cell cycle
and appears in the nucleus.",
RL      J. Biol. Chem. 271:355-360(1996).
DR      HESP; D50455; BAA09046.1; -.
DR      HSSP; P10688; IOAS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR002048; EF-hand.
DR      InterPro; IPR001849; PH.
DR      InterPro; IPR001192; PI_PLC.
DR      InterPro; IPR000909; PI_PLC_xdom.
DR      InterPro; IPR001711; PI_PLC_Y.
DR      Pfam; PF00168; C2_1.
DR      Pfam; PF00036; ethand; 2.
DR      Pfam; PF00169; PH; 1.
DR      Pfam; PF00388; PI-PLC-X; 1.
DR      Pfam; PF00387; PI-PLC-Y; 1.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00390; PHPHILIPASEC.
DR      ProDom; PDO01202; PI_PLC_Y; 1.
DR      SMART; SM00239; C2_1.
DR      SMART; SM00054; EFh; 2.
DR      SMART; SM00233; PH; 1.
DR      SMART; SM00148; PLCXG; 1.
DR      SMART; SM00149; PLCYG; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 1.
DR      PROSITE; PS50018; EF_HAND; UNKNOWN_1.
DR      PROSITE; PS50003; PH_DOMAIN; 1.
DR      PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR      PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ      SSQDUNCE   771 AA; 88862 MW; FPFBD64AB8B6E4FF CRC64;
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Query Match	20.3%	Score 1294;	DB 11;	length 771;
Best Local Similarity	36.8%	Pred. No. 2.3e-734;		
Matches 311;	Conservative 134;	Mismatches 280;	Indels 126;	Gaps 21;
QY	45	MOEOMNYKLGSGKGLVREYLL-DEHRSCTIRRPSPKNNKKAISIDSIOEVSEGSQSEY	103	
DB	18	MOKTPMKNKVTYKSWKRLRFRLODDMTWVHGHNLEISKPPFFSISDVYRIKKQDDEL	77	

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OY 104 FORPDGSPDNCCSFYHSGHRESLDVSTSEVARTWTLRYIMAGISDEDLSARR-162
DB 78 L-RYLVEEPLEGGFTYFNRRRLDLYANVSEAOYWMAGDOLY-----DLVAMN 130
OY 163 -QRTDQKQKTFDEADKNGSGSISGEVTLQHLKLVNLPKRVKQMFREADTDHOGT 221
DB 131 YOBOLDQMLREMFQOQADNODSRMSFREAORLLMLNVEEMEEVAFSLFQADY-SQSN 189
OY 222 LGFEFCAFYKMSSTRDLYLMLTYSNHKNHDLAASLQRLQYQOKKAGVLESCDIT 281
DB 190 LDSEFQVYFALNKRFEIEBELFENFSDDOKLLEFVDPLEBQKESHOSDOLAKLI 249
OY 282 EOPFCEPMNSKGLLGIDFTNTRSPAGDIFENBHNVHODMOPLSHYFTSSHTYL 341
DB 250 DRYPSENGRLRLRYLSKDGFLSYCSADGNIFNPDCLPIYODMQLPSHYINSHTYL 309
OY 342 VGDDLMOSRDMYAWYLQAGRCVEVDCWDGPDGERIVHNGITLTKLFDVETINK 401
DB 310 LGDPPGCOSSVEGTRALKRCRCVCEVWDGPDGEFVYHGRITLSRILFKDVLATLQ 369
OY 402 YAFIKNEYPVLSIENHCSYIOOKM-AQYLTDLIGDKLLSSVSESDATLPSQMLKG 460
DB 370 YAFQSSDYPLILSDNCTMEQKTLAHLIALIGBOL-LSTLLEQDIDMFSPE-LRG 427
OY 461 KILYKGGKL-PANISEAEGEVSDSDADEIDDDCKLNGASTNKRKVENTAKRKIDS 519
DB 428 KILYKGGKLITIEVESDEKEEELKDEGSDLD-----PASAELO-467
OY 520 LINESKIRDCEDPNFVSFLSPSGKLGKRSKAEDEVEGEDAGASRRNRLVYGSFSR 579
DB 468 -----MOSPESEBOAS-----GKMSKN 485
OY 580 KKGSKLAKAASVEBDEGODSPGOSRGATROKTKMLSRALSGLVYKYSVA---TH 635
DB 486 KKK-----FLQSSSTIILCPDLASALVYLRLAPFCSFTH 519
OY 636 DIMEAASMOVSSFSEKHAQILQOKPAOYLRFNQQOISRIYPSRYRDSSTYNPOPW 695
DB 520 --SKENHYHIDISFSESRAKNIIRAGNEFVONHAKOLCRVYPSGLRDSSTYNPOEHW 577
OY 696 MAGCOVALNYESGMLOLNRAKFSANGCGGYVLKPGCM--COGVFNSESDPLPGQLK 753
DB 578 NMGCOVANNMOTAGSAMIDCGLFRONGSGGYVLKPEFLRDTQSSFNMK-----PVSLY 633
OY 754 KO--LYLRLISGQOLKPRDSMLGDBGELIIDPVEVEITGLVYDQSRQDRTVVDNGFNP 811
DB 634 KQOILVVOYISGOKLPKVDKT---KETTIVDPLVRELYGVDEDTKQOETSYVENNGINP 690
OY 812 TWEETLVFVNHPELALVFEVLWDHPDPIGR-DFIGORTLAFSSMMPGRHYVL-----EG 865
DB 691 YMGFTFYFQIOVPELAMLRFYVKDYSRTSRNNFICQYITLPTCMKHGRHVSLSKDGS 750
OY 866 MEASIFVAVASD 879
DB 751 LHPASHFYVTCMOE 764

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RESULT 13

OBTCT

ID PRELIMINARY; PRT; 789 AA.

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AC OBTCT;
DB 01-JUN-2002 (TREMELREL 21, Created)
DB 01-JUN-2002 (TREMELREL 21, Last sequence update)
DB 01-JUN-2002 (TREMELREL 21, Last annotation update)
DB CUNA FLJ23660 f1s, clone HEP00931.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

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RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoigal T., Sugano S.;
RT "NEO human cDNA sequencing project."
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK074240; BAB85029.1;
SQ SEQUENCE 789 AA; 89258 MW; C6901404D2C9D070 CRC64;

```

Query Match 20.2%; Score 1289; DB 4; Length 789;
 Best Local Similarity 34.2%; Pred. No. 4.9e-73;
 Matches 309; Conservative 136; Mismatches 290; Indels 168; Gaps 22;

```

OY 1 MAPRTGRLPGALPREDGPRPESNMLFLSANILPYVERCKG-----AMOGMOMV 52
DB 26 VAPAPA--LPSPTSDGCKRRGLRAL-----KKMGLTEDEDDVAMLRGSLRL 72
OY 53 KLGSGSKGLVREYUYLEHNSCIRW--RPSRKNKAKISIDSBESVSGROSEVOPRPD 109
DB 73 KIRSRTHKERLYRLQEDGLSV-WFORRIPRPSOHIFVGHTEAVKRGHSEGLRRP-G 130
OY 110 GSPDPCCSYHSGHRESLDVSTSEVARTWTLRYIMAGISDEDLSARRQRTPDW 169
DB 131 GAFAPARCLTTFKGRKRLDLAAPTAEAOFRVYGLTKRLARL---DAMGQRELL-DHW 186
OY 170 LKOTFDEADKNGSGSISGEVTLQHLKLVNLPKRVKQMFREADTDHOGTLCPEERCA 229
DB 187 IHSYLHRADSNODSKMSFKELSLRLMNVNDMDYALFLKECDHSDNRLRG-AETEE 245
OY 230 FYKMSSTRDLYLMLTYSNHKNHDLAASLQRLQYQOKKAGVLESCDITFEOPECE 289
DB 246 FLRLRLKRLPELEIFRQSGEDRVLSAPLELEFLE-DGEGGATLARAQOLIQYTELNET 304
OY 290 NKSGLIGIDGFTNTRSPAGDIFENBHNVHODMOPLSHYFTSSHTNYLVGDOLMSQ 349
DB 305 AKQHEMLTLDGFPMATLSPGALDNTHTCVFOMNPLAFYFTSSHTNYLTSQIGCP 364
OY 360 SRVDMYANVLOAGRCVCEVDCWDGPDGERIVHNGITLTKLFDVETINKYAFIKNEY 409
DB 365 SSTEAVYRAFAQGCRCVCEVDCWEGPGEVYHGHITLSKLFEDVQVARDNAFTLSPT 424
OY 410 PYLSIENHCSYIOOKKAOYLTDLIDDKLDSVSESDATLPSQMLKGLLVKGRKL 469
DB 425 PYLSIENHCSYIOOKKAOYLTDLIDDKLDSVSESDATLPSQMLKGLLVKGRKL 484
OY 470 PANISEAEGEVSDSDADEIDDDCKLNGASTNKRKVENTAKRKRLDLSIESKIROC 529
DB 485 PAARSEGOR--ALSDREEEEDDE-----507
OY 530 EDPNNFVSFLSPSGKLGKRSKAEDEVEGEDAGASRRNRLVYGSFSRKKKSKLAKA 589
DB 508 -----EEREVE-----AAQORRLAK-----522
OY 590 ASVEEGDEGODSPGOSRGATROKTKMLSRALSGLVYKYSVAITHDIE--MEASSMOV 647
DB 523 -----QISPELSALVYCHARTRLRLPAPNAPPCQV 555
OY 648 SPSFSEKHAQILQOKPAOYLRFNQQOISRIYPSRYRDSSTYNPOPWMAAGCOMVALNO 707
DB 556 SLSSEKRAKILREAGNSFRRHNAKRLITRYPLGLMANSNANSYPOQMMNSGCOLVALNO 615
OY 708 SEGKMLOLNAKKSANGCGGYVLKPGCMCOGVFNPNSE--DP-LPGQLKQOLVRLISGOO 765
DB 616 TPGYEMDLNAGRPLVNGOCGYVLKPAQLRQ---PDSTFDPPEYRPPRTTSLIOVLTAAQ 671
OY 766 LP-----KPRDSMLGDBGELIIDPVEVEITGLVYDQSRQDRTVVDNGNPNWETLVFM 820
DB 672 LPLKNEKPH-----SLVDPVLEIIEHGVADARQETTYVNLNGNPNWPGOTLQFO 723
OY 821 VNHPELALVFEVLWDHPDPIGR-RDFIGORTLAFSSMMPGRHYVL-----EGMEASIFVH 874
DB 724 LRAPLELALVFEVYEDYDASPNDVQGFLLPLSSLKQGRHRIHLSKQASLSLPTLTIO 783
OY 875 VAV 877

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DB 784 IRI 786

RESULT 14

060450 PRELIMINARY; PRT: 745 AA.

AC 060450: 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

RT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Phospholipase C-delta1 (Fragment).

OS Cricetulus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Cricetulus.

ON NCBI_TaxID=10029;

OX [1]

RP SEQUENCE FROM N.A.

RA Leonis M.A., Silbert D.F.;

RT "Organization of the Hamster Phospholipase C-delta1 Gene: Differential

RT Loss of Separate Alleles of the Phospholipase C-delta1 Gene in Two

RT Fibroblast Mutants Lacking Phospholipase C-delta1."

RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: U50566; AAA93481.1; JOINED.

DR EMBL: U50565; AAA93481.1; JOINED.

DR HSSP: P10688; IMA1.

DR InterPro: IPR000008; C2.

DR InterPro: IPR002048; EF-hand.

DR InterPro: IPR001849; PH.

DR InterPro: IPR001192; PL-PLC.

DR InterPro: IPR000909; PL-PLC_xdom.

DR Pfam: PF00168; C2; 1.

DR Pfam: PF00036; ehand; 2.

DR Pfam: PF00169; PH; 1.

DR Pfam: PF00386; PL-PLC-X; 1.

DR Pfam: PF00387; PL-PLC-Y; 1.

DR PRINTS: PR00360; C2DOMAIN.

DR PRINTS: PR00390; PHPLIPASEC.

DR Prodom: PD001202; PL-PLC_Y; 1.

DR SMART: SM00239; C2; 1.

DR SMART: SM00233; PH; 1.

DR SMART: SM00146; PLCX; 1.

DR SMART: SM00149; PLCY; 1.

DR PROSITE: PS50004; C2_DOMAIN_2; 1.

DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.

DR PROSITE: PS50003; PH_DOMAIN; 1.

DR PROSITE: PS50007; PLPLC_X_DOMAIN; 1.

DR PROSITE: PS50008; PLPLC_Y_DOMAIN; 1.

FT NON_TER

SQ SEQUENCE 745 AA; 84638 MW; BE13C729C41C705E CRC64;

Query Match 20.2%; Score 1287; DB 11; Length 745;

Best Local Similarity 35.8%; Pred. No. 6.1e-73;

Matches 307; Conservative 128; Mismatches 279; Indels 144; Gaps 16;

DB 44 AMOEGMOMVLRGSGKGLVYLDHRSICIRWPSRK-----NEKAKISIDISIQVSEGR 99

DB 10 ALGKQLKAVKSSWRRETFYKLOEDCKT--WQSRKYMREPSQLSIEDIQVSRCH 68

QY 100 GSEVFORVYDGSFDPNCFSTIYHGHRESLDIVTSSEVARTWTVGLRYLMAGISDEDSL 159

DB 69 RREGLEKFA-RDIPEDRCSTIYFKDQRNTLDLAPSSADAQHWVGLRKI---IHSSGM 124

QY 160 ARRRRTROWLKQTFDEAKNGDGSISIGEVQLHKLNVNLPORRYOMFREAD---TD 216

DB 125 DQRQKIQ-HWISCLKKAKKNKNKNEFKELDKELNTQVDSDYARKIFRECHSQTD 183

QY 217 DHQGTGFEFECAFYKMMSTRDLVLLMLTYSNHRDHLDAASIQFIQVQCMAGVTLES 276

DB 184 -----SLEDEIEITFYKMLTQRAEIDRVFAAGSAETLSVEKLVTFLOHQGEAAGPAL 239

QY 277 CODIIEPEPCENKSKGLGIDGFTYNTSPADINPEHHHVQDMOTPLSHYFTSS 336

DB 240 ALSTIEREPESETAKAOROMTKDGLFMYLLSADGSASFSLAHRRVYQMDPPLSHYLVSS 299

QY 337 HNTLVGDLQMSOSRVMYAMVLAQGCRCVEYDQDQDPEPTVHNGYTLSTLLEFDVY 396

DB 300 HNTVLEQDLTGPSTSTYIRALCKGRCLDQDQDPEPTVHNGYTLSTLLEFDVY 359

QY 397 ETINKYAFIKNEYVVIISINHCSTVIOKKMAQYLTDLGDKLDSVSSSEDAATLPSQ 456

DB 360 RAIDYAFKASPVYVILSTENHCSTLEDOQVYARLKAILPML-LDQPLDGYMSLPSPE 418

QY 457 MKCKIILYKGGK---LPANISDAEAGEVSDSDADEIDDCKLNGASTNKKRYENT 512

DB 419 QLKRIILKCKFGGLLPAGGENGETTVDVSDDEDAEMEDE----- 460

QY 513 AKRKLDSLKESKIRDCDEPNPFVSSTLSPGKRGKSKAEDEVEDSAGARRNRLV 572

DB 461 -----A 461

QY 573 VGSFRRKKKSKLKAAYEEGDEGODSPGQSGATRQKTKLSRALSDLVKTKSV 632

DB 462 VRSQVQKSKEDKLNVAPE-----LSDMYIKSV 491

QY 633 ATHDIEEAASS---WOVSFSETKAHQIILQQAQYLRNQQLSHYSSSYRVDSSNY 689

DB 492 HFGGFSNPSTSGAIFYEMASFSERNRRLILQESGNNVRHNVSHLSRTYPAGRRDSSN 551

QY 690 NPQPFVNAQCMVALNOSSEBMLQLNRAKFSANGGCVYKLRPCM--CGVFPNSED 747

DB 552 SPVENMNGCQIYALNFOPTPEPENVYLGRQDAGAGYVLRKFLDPPATFAPRALQ 611

QY 748 LPQGLKQLVRIISGOQLPKPRDSMLGRGEIIDPEVEEILPLPDCSREGQTRVVDN 807

DB 612 GPWMAQKRLRVRVSGQLPKRVNKS-----KMSYDPAVYIEVHGVDVASRQATVTTN 667

QY 808 GPNPTEETLVFMYMBEIALVRFVWDHDTGR-DPIGQRTLAFFSSMPGQYRRVYL--- 863

DB 668 GFNPMDTEFEFEVAVDPLAVRFVEDYDASSKNDEIGOSTIYWNLSLQGYRHVHLSK 727

QY 864 --EGMEASIFVHVAVSD 879

DB 728 NGDHPKATLVKISLQD 745

RESULT 15

QY 08TF37 PRELIMINARY; PRT: 757 AA.

AC 08TF37: 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

RT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE KIA1964 protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

ON NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RA TISSUE-BRAIN;

RX MEDLINE=21842142; PubMed=11853319;

RT "Prediction of the coding sequences of unidentified human genes. XXII.

RT The complete sequences of 50 new cDNA clones which code for large

RT proteins."

RL DNA Res. 8:319-327(2001).

DR EMBL: AB075844; BAB85550.1; -.

FT NON_TER

SQ SEQUENCE 757 AA; 85776 MW; 1CA68FF03779055 CRC64;

Query Match 20.1%; Score 1281; DB 4; Length 757;

Best Local Similarity 34.1%; Pred. No. 1.5e-72;

Matches 305; Conservative 135; Mismatches 288; Indels 166; Gaps 21;

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QY 10 PGPALPPEDPPDPDESRKLFISANILPYVERCMG-----AMQEGMAYKLRGSGKL 61
Db 1 PSPFPSPDGGTKRPGLRAL-----KMGTEDEVDYRAMLRGSRKIRSRTHWK 49
QY 62 VRFYYLIDHEHRCIRW---RPSRKNKEAKISIDISIOEVSEGRSEVFORYPDGSFPDNCCE 118
Db 50 ERLYRLQEDGLSV-WFORIRIPRPSQHIFVQHIFAVREGHSEGLRRF-GGAFAPARCL 107
QY 119 SIYHSHRESLIDVSTSEVARTWVTLGRYLMAGISDESLARQRTDQWLKQTFDEAD 178
Db 108 TIAFKGRKKNIDLAAPFAEEAQRWRGTLTKLRRL--DAMSQRERL-DHWIHSYLHRAD 163
QY 179 KNGGGSLSIGEVLOLHLKLNPNLRQRYKQMFREADTDHOGTIGFEFCAFYKAMSTR 238
Db 164 SNQSKMSFEKIKSLIRWNVNDMDMYALLFKEDHSNNDRLRG-AEIEFLRLRLKRP 222
QY 239 DLYLMLTYSNHKKDHIDAASLQRFLOVEOKMAGVTLSECODIIEQFEPCPENKSKGLGI 298
Db 223 ELEELFHQYSGEDVLSAPLELLEFLE-DQGEAGTLARAQOOLIQYELNETAKOHEIMTL 281
QY 299 DGFNTYTRSPAGDIFNPEHHVHODMTOPLSHYFTSSHNTYLVGDQIMQSRYDMYAV 358
Db 282 DGFMYTLLSPGALDMDHTVCVFDMMNQPLAHYFISSSHNTYLTDSQIGPSSTEAYVRA 341
QY 359 LQAGRCREVCVCMGDPGSEPTVHHGYTLTKLRFKDYETINKYAFINKREYVILSTENH 418
Db 342 PAQGRKCVELDCWEGPGEFVYHGHYTLTKILRDVQAVRDHAFVTLSPYVILSTENH 401
QY 419 CSVIOOKKMAQYITNDILGDKLDLSSVSEDAITLPSQMLKGLIKGLIPANISEDAE 478
Db 402 CGLEQQAAMAHNLCTIIGDMLVTQALDSPNEELPSPEQLKGRVLYKCKKLPAARSEDR 461
QY 479 EGEVSEDSADEIDDCCKLNGDASTNRKRVENTAKRKDSLKESKIRDCEDPNNESVS 538
Db 462 --ALSDREEEEDDE----- 475
QY 539 TLPSPGKIGRSKAEEDVESGEDAGASRRNGRLVGSFSRRKKGSKLKAASVEEGDEG 598
Db 476 -----EEEVE---AAQRRLAK----- 490
QY 599 QDSPGGSRGATRQKTKMKSRLSALSDLVKTYKSVATHDIE--MEAASSWQVSSESETRAH 656
Db 491 -----QISPELSALAVYCHATRLRLTHPAPNAPQPCQVYSSLSEKAK 532
QY 657 QIILOKPAQYIARFNOQOLSRIFSSYRVDSSNYPQPFWMAGCOMVALNYOSEGRMLQLN 716
Db 533 KLIREAGNSFVRHNAQRLTRYPLGLRMSNANYSPQEMWNSGCOLVALNFPQTPGYEMDLN 592
QY 717 RAKFSANGCGGYVLKPCGCMCGVFNPNSE-DP-LPGOLKQVLRIITISGOQLP-----KP 769
Db 593 AGRLVNGCGCYVAKPACLRQ---PDSTFPEYRPPRTYLSIOVLTAAOOLPKLNAEKP 648
QY 770 RDSMLGDRGELIIDFEVEELIIGLPVDCSREQTRVVDNGCFNPWEETLVFMVHMEIALV 829
Db 649 H-----SIVDELVIIEIHGVADACARQETDYLVNNGFNPRWGQTLQFOLRAPELALV 700
QY 830 RELVMDHPYIG-RDFTIGORTLAFSSMMPGYRHYVL-----EGMEASIFVHYAV 877
Db 701 RFVVEYDYDATSPNDEVGQFTLPLISLKGYRHHLLSKDGASLSPATLLEIQIRI 754
```

Search completed: March 28, 2003, 13:51:32
Job time : 122 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:39:49 ; Search time 29 Seconds
(without alignments)
1726.273 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPPTAGPLPGPALPEDPG.....ALYPWHCLRGTLPLPWACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1738	27.2	Y450_HUMAN	Q75038 homo sapien
2	1285	20.1	P1D1_HUMAN	P51178 homo sapien
3	1258	19.7	P1D1_RAT	P10688 rattus norv
4	1235.5	19.4	P1G1_BOVIN	P10895 bos taurus
5	1009	15.8	P1G1_HUMAN	P08487 bos taurus
6	999.5	15.7	P1B4_HUMAN	Q15147 homo sapien
7	997.5	15.6	P1G1_HUMAN	P19174 homo sapien
8	996.5	15.6	P1B4_RAT	Q99407 rattus norv
9	985	15.4	P1G1_RAT	P10686 rattus norv
10	968.5	15.2	P1G2_HUMAN	P24135 rattus norv
11	950.5	14.9	P1G2_HUMAN	P16885 homo sapien
12	945.5	14.8	P1G1_DROME	P25455 drosophila
13	945	14.8	P1B1_RAT	P10687 rattus norv
14	937.5	14.7	P1B4_BOVIN	Q07722 bos taurus
15	937	14.7	P1B1_HUMAN	Q99466 homo sapien
16	936	14.7	P1B1_BOVIN	P10894 bos taurus
17	925	14.5	P1PA_DICDI	Q02158 dictyosteli
18	920	14.4	P1PA_DROME	P13217 drosophila
19	908.5	14.2	P1B2_HUMAN	Q00722 homo sapien
20	900	14.1	P1P3_HUMAN	Q01970 homo sapien
21	865.5	13.6	P1C1_SCHPO	P40977 schizosacch
22	863	13.5	P1P3_MOUSE	P51433 mus musculu
23	682.5	10.7	P1C1_YEAST	P33483 saccharomyc
24	677	10.6	P1C1_CANAL	Q13433 candida alb
25	225.5	3.5	P1G1_MOUSE	Q62077 mus musculu
26	202	3.2	P1F8_PRIVKA	P33479 pseudorabie
27	201.5	3.0	P1F8_HUMAN	Q07092 homo sapien
28	194.5	3.0	P1H1_EBV	P03181 Epstein-Bar
29	185.5	2.9	P1Y1_BOVIN	P17599 bos taurus
30	185.5	2.9	P1E18_PRIVF	P11675 pseudorabie
31	184.5	2.9	P1A1_YEAST	P32521 saccharomyc
32	184.5	2.9	P1A1_RABIT	P55787 oryctolagus
33	184.5	2.9	P1A1_HUMAN	P17600 homo sapien

34	184.5	2.9	1685	1	CA54_HUMAN	P29400 homo sapien
35	181.5	2.8	1163	1	T222_HUMAN	Q92618 homo sapien
36	180	2.8	1464	1	CA11_HUMAN	P02452 homo sapien
37	179	2.8	1464	1	CA13_MOUSE	P08951 mus musculu
38	178.5	2.8	704	1	SYN1_RAT	P09951 rattus norv
39	178	2.8	625	1	DUS8_HUMAN	Q13202 homo sapien
40	177.5	2.8	2845	1	APC_MOUSE	Q61315 mus musculu
41	177.5	2.8	2944	1	CA17_HUMAN	Q02388 homo sapien
42	176.5	2.8	1388	1	CA1E_HUMAN	P39059 homo sapien
43	176.5	2.8	1453	1	CA11_CHICK	P02457 gallus gall
44	176	2.8	1466	1	CA13_HUMAN	P02461 homo sapien
45	175.5	2.8	1459	1	CA12_MOUSE	P28481 mus musculu

ALIGNMENTS

RESULT 1

ID Y450_HUMAN STANDARD; PRT; 425 AA.

AC 075038;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein KIAA0450.

GN KIAA0450.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98116662; PubMed=9455484;

RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,

RA Nakajima D., Nomura N., Ohara O.;

RT "Characterization of cDNA clones in size-fractionated cDNA libraries from human brain.";

RL DNA Res. 4:345-349(1997).

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CC EMBL: AB007919; BAA32295.1; -

DR Hypothetical protein.

KW HYPOTHEMETICAL 425 AA; 43842 MW; 2A6D733CA149E665 CRC64;

SQ SEQUENCE

Query Match 27.2%; Score 1738; DB 1; Length 425;

Best Local Similarity 99.7%; Pred. No. 7.5e-78;

Matches 324; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	883	KVKQALGKGLFLGPKPGSLDSHAAGRPAPRSVSRILIRRTASAPTKQKGRGFP	942
DB	101	QVKQALGKGLFLGPKPGSLDSHAAGRPAPRSVSRILIRRTASAPTKQKGRGFP	160
QY	943	LVLTGTRDGSAGVADVPVPGPGAPAPAPAEOPGSGSPGKAPAAVAEKSPPVAPRPV	1002
DB	161	LVLTGTRDGSAGVADVPVPGPGAPAPAPAEOPGSGSPGKAPAAVAEKSPPVAPRPV	220
QY	1003	LDGPGAPGMAATCKKCVVSCAGVNTGLOREPPSPGASROAIIQOPRAADSI GAP	1062
DB	221	LDGPGAPGMAATCKKCVVSCAGVNTGLOREPPSPGASROAIIQOPRAADSI GAP	280
QY	1063	CCGGLDPAHAPRSREAPRGAPAPAPAEOPGSGSPGKAPAAVAEKSPPVAPRPV	1122
DB	281	CCGGLDPAHAPRSREAPRGAPAPAPAEOPGSGSPGKAPAAVAEKSPPVAPRPV	340
QY	1123	GALGEGMSALPAOKLEIRSKSPMSAGKPLLPVVLPHAPGMAAGPSPAASAMTSPR	1182

DB 341 CALGEMSALEFRQKLEETRSSPMSACKPLPCVILPHABGMAGPGSPAASAMTVSPR 400
 OY 1183 VLVLVALYPWHCLRTGLLPWILACGP 1207
 DB 401 VLVLVALYPWHCLRTGLLPWILACGP 425

RESULT 2
 ID PID1_HUMAN STANDARD; PRT; 756 AA.
 AC P51178;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-II).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Aorta;
 RX MEDLINE=95197554; PubMed=7890667;
 RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
 RA Lomaney J.W., King K.;
 RT Cloning and identification of amino acid residues of human
 RT phospholipase C delta 1 essential for catalysis.";
 RL J. Biol. Chem. 270:5495-5505(1995).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC CATALYZED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC or send an email to license@sib-sib.ch).
 DR EMBL: U09117; AAA73567.1;
 DR HSSP: P10688; IMAT.
 DR GeneW: HGNC:9060; PLCD1.
 DR MIM: 602142;
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; P1-PLC.
 DR InterPro: IPR000909; P1-PLC_Xdom.
 DR InterPro: IPR001711; P1-PLC_Y.
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 DR PRINTS: PR00388; P1-PLC-X; 1.
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 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; P1-PLC_Y; 1.
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 DR PROSITE: PS00004; C2_DOMAIN_2; 1.
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 FT DOMAIN 21
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 FT DOMAIN 296 440 EF-HAND 2 (POTENTIAL).
 FT DOMAIN 492 609 DOMAIN X.
 FT DOMAIN 616 720 DOMAIN Y.
 FT ACT_SITE 311 311 C2 DOMAIN.
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Query Match 20.1%; Score 1285; DB 1; Length 756;
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OY 44 AMQEGKQVYKLRGSGKGLVREYIDHRSCLRWPSRK-----NEKAKISIDISQVSEGR 99
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 OY 100 OSEVFORV-----PDGSPDNCCFSYHSHESLDVTSSEVARTVYTLGYLMAGISD 155
 DB 80 KTEGLEKTRADYVE-----DRCESTVFQDORNTDLIPSPADQHWVLGIHKT---IHH 131
 OY 156 EDLSARRQRTDQWLKQTFDEADKNGDGLSIEVYLQHLNVLNLRQVKKQMFREED 214
 DB 132 SSGMQQRKLO-HWISCLRADKKNKKNKFKELQNTLKEKLNQVDSYARKFFRECDH 190
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 OY 273 TLESCDIIQEFPEPEKSKGILGIDFTYTSRPAQDIPNPHHVDQMTQPLSHYF 332
 DB 247 GPALALSLIEVYEPSETTKAQRQTKGDFLMTLLSADGSAFSLAHRRVYQDMGQPLSHYL 306
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 OY 393 KDVETIKKVFATKNEYVYLITENHCSYVQKMAQYLDIADKL---DLSVSEDA 449
 DB 367 CDVLRAIRDAFKAQPYPVVILSTENHCTLRQQRVMAHLHAIQMLNRPIDGVTN--- 423
 OY 450 TLPSPQWLKGLILVKKKILPANTISEDAEAGE-----VSDESDADEIDDCKLINGASTN 505
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 OY 506 RKRENTAKRRLDLISKIRQCEDPNPFVSVTLSPSGKLGKSKRAEEDVESGEDAGAS 565
 DB 474 KSRVQHKP-----KEDKLR----- 487
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 DB 488 -----LAQELSDM 495
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 DB 496 VIYCKSVHFGGFSPTGPGQAFYEMASFSENNRALLRLDSGNGFNVAHNGHLSTRIPAW 555
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OY 801 TRVVDDNGENPTWETLVEVWHPMDALVAFVHDDPLGR-DEFGRIPLAESSMMPGR 855
DB 672 TAVITNNGFNFMWDTPEFAFEVVPDIALRELVEDYDASKNDFTIGOSTIPUNSLKQGR 731
OY 860 HVYL-----EGMEASIFVHVAUSD 879
DB 732 HVHLSMKNQGHPSATLFFVATISLQD 756

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DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta 1
DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III),
DE PLCD1.
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RA MEDLINE=68270495; PubMed=3390863;
RX Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.";
RL Cell 54:161-169(1988).
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RA MEDLINE=92202192; PubMed=1313009;
RX Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
RN 13
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 12-130.
RA MEDLINE=96107342; PubMed=8521504;
RX Ferguson K.M., Lemmon M.A., Schlessinger J., Sigler P.B.;
RT "Structure of the high affinity complex of inositol triphosphate
RT with a phospholipase C pleckstrin homology domain.";
RL Cell 83:1037-1046(1995).
RN 14
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 205-756.
RA MEDLINE=96378790; PubMed=8784353;
RX Grobler J.A., Essen L.-O., Williams R.L., Hurley J.H.;
RT "C2 domain conformational changes in phospholipase C-delta 1.";
RL Nat. Struct. Biol. 3:788-795(1996).
RN 15
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 133-756.
RA MEDLINE=96186808; PubMed=8602259;
RX Essen L.-O., Perisic O., Cheung R., Katan M., Williams R.L.;
RT "Crystal structure of a mammalian phospholipidase-specific
RT phospholipase C delta.";
RL Nature 380:595-602(1996).
RN 16
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 133-756.
RA MEDLINE=97215812; PubMed=9062102;
RX Essen L.-O., Perisic O., Lynch D.E., Katan M., Williams R.L.;
RT "A ternary metal binding site in the C2 domain of phospholipidase-
RT specific phospholipase C-delta1.";
RL Biochemistry 36:2753-2762(1997).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.

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CC -1- COFACTOR: Calcium.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC P1C AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR PDB; 1DJG; 07-JUL-97.
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DR PDB; 1DJI; 07-JUL-97.
DR PDB; 1DJW; 23-JUL-97.
DR PDB; 1DJX; 07-JUL-97.
DR PDB; 1DJY; 07-JUL-97.
DR PDB; 1DJZ; 07-JUL-97.
DR PDB; 2ISD; 07-JUL-97.
DR PDB; 1MAI; 08-NOV-96.
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DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
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KW
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FT DOMAIN 21 130 PH.
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FT CA_BLIND 189 200 EF-HAND 2 (POTENTIAL).
FT DOMAIN 296 440 DOMAIN X.
FT DOMAIN 492 609 DOMAIN Y.
FT DOMAIN 630 720 C2 DOMAIN.
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Query Match 19.7%; Score 1258; DB 1; Length 756;
Best Local Similarity 35.8%; Pred. No. 3, 2e-54;
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RX MEDLINE=88270495; Pubmed=3390863;
RA Sun P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.";
RL Cell 54:161-169(1988).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: Calcium.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLG AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
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 RX MEDLINE=88156963; PubMed=2831461;
 RA Stahl M.L., Ferenz C.R., Kelleher K.L., Kitz R.W., Knopf J.L.;
 RT "Sequence similarity of phospholipase C with the non-catalytic region
 of src.";
 RL Nature 333:269-272(1988).
 RN [2]
 RP PHOSPHORYLATION SITES.

RX MEDLINE=90154080; PubMed=1689310;
 RA Kim J.W., Shim S.S., Kim D.H., Nishibe S., Whal M.I., Carpenter G.,
 RA Rhee S.G.;
 RT "Tyrosine residues in bovine phospholipase C-gamma phosphorylated by
 the epidermal growth factor receptor in vitro.";
 RL J. Biol. Chem. 265:3940-3943(1990).
 RN [3]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE=90154081; PubMed=1689311;
 RA Whal M.I., Nishibe S., Kim J.W., Kim H.K., Rhee S.G., Carpenter G.;
 RT "Identification of two epidermal growth factor-sensitive tyrosine
 phosphorylation sites of phospholipase C-gamma in intact HSC-1
 cells.";
 RL J. Biol. Chem. 265:3944-3948(1990).
 RN [4]
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 RX MEDLINE=91208680; PubMed=1708307;
 RA Kim H.K., Kim J.W., Zilberstein A., Margolis B., Kim J.G.,
 RA Schlessinger J., Rhee S.G.;
 RT "PDGF stimulation of inositol phospholipid hydrolysis requires
 PLC-gamma 1 phosphorylation on tyrosine residues 783 and 1254.";
 RL Cell 65:435-441(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 663-759,
 RX MEDLINE=94236690; PubMed=8181064;
 RA Pascal S.M., Singer A.V., Gish G., Yamazaki T., Shoelson S.E.,
 RA Pawson T., Kay L.E., Forman-Kay J.D.;
 RT "Nuclear magnetic resonance structure of an SH2 domain of
 phospholipase C-gamma 1 complexed with a high affinity binding
 peptide.";
 RL Cell 77:461-472(1994).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-3D-myo-inositol 4,5-
 bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
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 or send an email to license@isb-sdb.ch).
 CC EMBL: Y00301; CAA68406.1; -.
 CC PIR: S00666; S00666.
 DR PDB: 2PID; 26-JAN-95.
 DR PDB: 2PIE; 26-JAN-95.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
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 DR InterPro: IPR000909; PI_PLC_Xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
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 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 2.

DR pfam; PF00018; SH3; 1.
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 DR pfam; PF00388; PI-PLC-X; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRODOM; PD000066; SH3; 1.
 DR PRODOM; PD000093; SH2; 2.
 DR PRODOM; PD001202; PI-PLC-Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00233; PH; 2.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCY; 1.
 DR SMART; SM00326; SH2; 2.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS50001; SH2; 2.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 DR PROSITE; PS50004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KM Hydrolase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 Repeat; Calcium-binding; Phosphorylation; 3D-structure.
 FT DOMAIN 27 142
 FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT ACT_SITE 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION.
 FT MOD_RES 783 783 PHOSPHORYLATION.
 FT MOD_RES 1254 1254 PHOSPHORYLATION.
 SEQUENCE 1291 AA; 148312 MW; 9F31C7DMA3F8EA77 CRC64;

Query Match 15.8%; Score 1009; DB 1; Length 1291;
 Best Local Similarity 26.1%; Pred. No. 7.8e-42;
 Matches 308; Conservative 151; Mismatches 317; Indels 404; Gaps 35;

QY 74 IMRPSRKNEKAKISIDSIQEVSEGRSEVFORV-PDGSF--DPNCCFSYHGS--HRES 128
 DB 60 ITWSRGADRIEIGAIDIREIKETIRPGRSHDFRQEDPAFRPDQSHCFVILYGMFRLKT 119
 QY 129 LILVSTSEVARTWVGLKYLMAGISDEDSL-ARRQRRDQMLKOTFDEADKNGGSLSI 187
 DB 120 LSLQATSEDEVMMIRGLTWLW----EDTLOAATPIQIERLIRKQFYSVVRNRDRISA 174
 QY 188 GEVQLLRLNLNLRPRORYKQMFREADTDDHGT--LGFEEFCAYK--MMSTRDLYLL 243
 DB 175 KDLKNNLSQVNRVYPMNR---FLRRLTDLRQRTSDITYGQPAQLYRSLMTSAQTTMDLP 231
 QY 244 MLTYS---NRKDHDAASLQRF-----LOVEKMGAGVTLSCDITEQ 283
 DB 232 FLEALRALRAGERPELCRYSLEPFOFLLEYQELMAVYRLQVQERMLSFLLDPLREIEEP 291
 QY 284 FEPCEPNKSKGLIGDGTNTSRPAGDIENPENNHYAD-MTQPLSLRTTSSHTNYLV 342
 DB 292 Y-----FLDEVTYTLFSKENSIMNSQDEVCPTDNNPFLSHYMISSHTNYLT 340
 QY 343 GDOLMSQSRVDMATVAVLQAGRCVVDWDPDGEPIVHSGYTLTSKILFQVETETNKY 402
 DB 341 GDQFSESSLEAYARCLRMGRCRTELDQMDPBDGMPVIVHGHITLTKKKSDEVJLTTKEH 400
 QY 403 AFIRKRYVILSIENHGVYIOOKKAAQYLLDILDKDLSSVSSSDATTLPSPOLMKGI 462
 DB 403 AFIRKRYVILSIENHGVYIOOKKAAQYLLDILDKDLSSVSSSDATTLPSPOLMKGI 462

DB 401 AFVASEPYVILSTEDHCSIAGQNRNMAQYFKKVLGDTL-LTKPYDIAADGLSPNOLKRI 459
 QY 463 LVKCKKLP-----NISDAEAG----- 480
 DB 460 LHKKTLAAGSAVEEYPTSVMYSENDISNISKGLIYLEDYPVNHBMYPHYVLTSSKIY 519
 QY 481 -EYSDSDADEIDDOCKTLNG--DASTNKRY-----ENYAKKIDS----- 519
 DB 520 SEETSSDQNEDEBEERKEASGSTEJHSNKKWPHKGLAGRGDRHIAERLLTEYCLETGAP 579
 QY 520 ---LIKES-----KIRDC----- 529
 DB 580 DGSFLVRESETPVGYTLTFMWENKGVQCHRIHSRODAGTPKFFLLDNLVPSLIDLTHY 639
 QY 530 ----- 532
 DB 640 QQVPLRCNEFEMRLSEPVQTNHBSKEMVYHASTLRQAQEHMLKVPDGAFLVKRRNEP 699
 QY 533 NNEYSV----- 538
 DB 700 NSYALSPFAEGKIKHCRCVQEGQYMLGNSEFDSLVDLIISYEKHPLYRKMKLRYPIINEE 759
 QY 539 -----TSPS-GKL--GR-----KSKAEE 554
 DB 760 ALEKIGTAEPPDYGALYEGRNPFGEYVEANPMPTFKCAVYKALDYKAQREDELFTKSAIIQ 819
 QY 555 DYSEGE-----DAGASR----- 566
 DB 820 NVEKQGGMMRGDYGKKQMLFSPNLYEEMVSPALBPEREHLDENSPLGLRGVLDVP 879
 QY 567 -----RNGRLVYGSFRKKKSKLKAASVE-----GDEGQDSPPGQSR 607
 DB 880 AQQLAVREGKNNRLFYFSISMASVAKSLDYAADSOEILDQWYKKTREVAQQTADARLITE 939
 QY 608 CATROKTKMKLSRALISDLVYTKSVATHD--TEMEAASSMOWSSFSSTKAHQLIQ--KPA 664
 DB 940 GKMMER--KKIALSEILVYVCRPVPEDEEKIGTERACYRDMSSFPETKAKKYNNKAKG 998
 QY 665 QYLRNQCQSLRIYPSRYVDSNYPNPFMNAQCCQVAVNTYQSEGMLDNLNRAKPSANG 724
 DB 999 KFLQYNRLQLSRIYPKQORLDSSTYDPLPMYICGSQLVAINFOTPDPMOMNALFLAG 1058
 QY 725 GCGYVLKPCGCGGVFNPNSEDPGLQKQVLYRLIISGQOLPKPRDSMLGDRGEITDP 784
 DB 1059 HCGYVLQPSVARDPAFDPFKSSLRGLEPCALICIEVGANHLK-----NGNG-IYCPF 1111
 QY 785 VEVEIGLPPVDCSREQTRVYDNDNGFNPTW--EETLYEVWHPMETALVFLWMDHPIG-RD 842
 DB 1112 VEIEVAGAEYDSIKQKTEFYVVDNGLNVPWPAKPFHQISNPEFAFLRFVYVEEDMFSQDN 1171
 QY 843 FIGQRTLAFSMMPGYRHV-----YLEGMEASIFVAV 877
 DB 1172 FLAQATFPVKGKLTGYRAVPLKNNYSGLLALSLVAKIDV 1211

RESULT 6
 ID PIR4_HUMAN STANDARD; PRT: 1175 AA.
 AC Q15147; Q9U02; Q9B0W5; Q9B0W6; Q9B0W8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=96079091; PubMed=8530101;

RA Alvarez R.A., Ghalayini A.J., Xu P., Hardcastle A., Bhattacharya S.,
 RA Rao P.N., Petteinati M.J., Anderson R.E., Beehr W.;
 RT "cDNA sequence and gene locus of the human retinal phosphoinositide-
 RT specific phospholipase C-beta 4 (PLCB4).";
 RL Genomics 29:53-61(1995).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Houlden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvalho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachle L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Stalston J.E.,
 RA Swan R.M., Symmore N., Taylor R., Tee L., Thomas D.M., Thotape A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:863-871(2001).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1, 2 (shown here) and
 CC 3; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 DR EMBL, AL031652; CA21068.1; -
 DR EMBL, AL023805; CAC34525.1; -
 DR EMBL, AL023805; CAC34527.1; -
 DR EMBL, AL023805; CAC34528.1; -
 DR EMBL, LA1349; AAB02027.1; -
 DR HSSP: PI0688; IDJX.
 DR Genew: HGNC:9059; PLCB4.
 DR MIM: 600810; -
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI_PLC_Y; 1.
 DR Pfam: PF00388; PI_PLC-X; 3.

DR PRINTS: PR00390; PPHPLIPASEC.
 DR Prodom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00148; PLCXc; 1.
 DR SMART: SM00149; PLCXc; 1.
 DR PROSITE: PS50004; C2_DOMAIN2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 313 463
 FT DOMAIN 565 681
 FT DOMAIN 688 786
 FT ACT_SITE 328 328
 FT ACT_SITE 375 375
 FT VARSPIC 1 153
 FT VARSPIC 154 167
 FT VARSPIC 1 268
 FT CONFLICT 447 447
 FT CONFLICT 757 757
 FT CONFLICT 787 787
 FT CONFLICT 840 840
 FT CONFLICT 902 902
 SQ SEQUENCE 1175 AA; 134463 MM; AB208B99EF57357 CRC64;
 Query Match 15.7%; Score 999.5; DB 1; Length 1175;
 Best Local Similarity 29.2%; Pred. No. 2e-41;
 Matches 295; Conservative 131; Mismatches 308; Indels 275; Gaps 32;
 99 ROSEVFORYPDGS--FDNRCCSIIH-----LVTSSEVARTWTGRLTMAGIS 122
 18 OGAVFDRYEESFVEFPCNLEKVDGFFLTWRSEGEQVLECSLINSRGAIPDP 77
 123 -----GSHRESLD-----LVTSSEVARTWTGRLTMAGIS 154
 78 KILALEANGKSENDLEGRIVCYCGTDLYNISTFYVAENREYKQVEGRSIIHNR 137
 155 DEDSLARRQRTDQWIKQTFDEADYNGDSLSIG-----VLQILKLANVL 201
 138 -ANNVSPMTCLEKHHMKLAF--MTNTGKIPVRSITRTFASGKTEKYVFAKLKL--GL 191
 202 PRQRKQMRREDTDDHQT--LGFERPCAFYKMSGRDLYLMLTYSNHK--DHDAASL 259
 192 P-----SGKNDIEPTLAFSEKFEYELTKICPRDIDELFKINGDKTDYLYQL 242
 260 QRELYEQKMAQVT-----LESCDIIQEFEPENKSGKLGIDGFTYTRSPAGD 311
 243 VSTLNHQDPRNLNELLFFYDAKRAMQIIEYEPEDLKKGLISDQFCRYLMSDNA 302
 312 IFNPEHHVQDPTOPLSHYFTTSSHNITLVGDOLMSQSRVDMYAMVLOAGRCYEVDCW 371
 303 PVLIDRLLEYQEMDHLAFYFSSHNITLVGKQFGSKSVEMRYVLLAGRCVELDCW 362
 372 D--GPGSEPVHNGYLLTKILFKVDIETLNKAFIKNYEPIYLSIENHCSYIQQKMAQ 429
 363 DKGGEQEPITNGKAMCTDILFKDYIAIKETAFYTSSEYPIYLSFENHCSKYQYQKMK 422
 430 YLTDIIGD--KLDLSVSSSEDATTLPSQMLKGLLVGKKL----- 469
 423 YCDIDFGDILLKQALSHPLEPRALPSPNDLKRKILINKRKLKPEVEKKOLEALRSMKE 482
 470 -----PANTSEDAERGEVSDSDAIDDDCKL--LNGDASTNKKRRENTAKKRLDSL 520
 483 AGESASPANILEDNEEIEISADQEEBAHFKEFGNELSDDDIGHKEAVANSYKGLGVTV 542
 521 IKESKIRDCDPNNFVSTLSPSGKLGKRSKAKEDVESGDCASRNGLVYGSPSRK 580
 543 -----EDEQAMASRYV----- 555
 581 KKGSKLKAASVEGDEGQDPSGQSRGATROKTKMLSRALSDLVYTKSVATHDIEK- 639
 556 -----GA-----TNIIHPLYSTMIYNVQAPVFOGCFHVA 583

DR SMART; SM00149; PLCYC; 1.
 DR SMART; SM00252; SH2; 2.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00001; SH2; 2.
 DR PROSITE; PS00002; SH3; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 2.
 DR PROSITE; PS00004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS00007; PIP2C_X_DOMAIN; 1.
 DR PROSITE; PS00008; PIP2C_Y_DOMAIN; 1.
 DR Hydrolyase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KW Repeat; Calcium-binding; Phosphorylation; 3D-structure; Polymorphism.
 FT DOMAIN 27 142
 FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 530 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT ACT_SITE 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 813 813 I -> T (IN DBSNP:753381).
 FT VARIANT 813 813 FETID-VAR 011908.
 SQ SEQUENCE 1290 AA; 148531 MW; AE05ABE2A18EDDAC CRC64;
 Query Match 15.6%; Score 997.5; DB 1; Length 1290;
 Best Local Similarity 25.1%; Pred. No. 2.8e-41;
 Matches 306; Conservative 157; Mismatches 331; Indels 423; Gaps 35;

QY 74 IRMRPSKNEKAKISIDSDVSGRSEVFOR-PGSE--DPNCFSTYHGS--HRES 128
 DB 60 ITWRSAGDKLEGADIREIKREIRPKGTSRDFRQEDPARPPOSCEVLLYGEEFLKT 119
 QY 129 LDIUSTSEVARTWVTLGLRLMAGISDEDSI-ARRQRTROMLKQRTDEADKNGDSL 187
 DB 120 LSLQATSEDEVNMWIKLITWLM-----EDTLQAPTLPIQIERMLRKQYSDVRNREBISA 174
 QY 188 GEVLQHLKLVNLPORVQMFREADTDHOGTLGFEFCAYK--WMSTRDLVLLML 245
 DB 175 KDLKMLNQVYRVNKRFLRE-RLTDLQRSGDITYGFAQLYRSLMYSAGKTMDLPTL 233
 QY 246 TYS---NHKDHLDASLQRF-----LQYEQKAGVTLESODITIQE 285
 DB 234 EASFLRAGERPELCRVSLPEFOFLDLYOGELMAVDRLQVOEFMLSFRLDPLREIEEY 292
 QY 286 PCPENKSKGLGIDGFTNYTRSPAGDIFNPENHHVHOD-MTQPLSHYFITSNHTYLVGD 344
 DB 293 -----FLLDEFYTLFLEKSNVSNWNSLDLAVCDPTMNNPISHWISSNHTYLVGD 342
 QY 345 QLMQSRYDVAWVLQAGRCVEVDCDGPDEPIVHHGYTLTKILFKVYIETINKYAF 404
 DB 343 QFSSSELEAVARCLRMGCRCIEIDCDGPGMGPVYIHHGTLTKIKFSDVLTATIKKHA 402
 QY 405 IKNEPVLTLENHCSYVQOKKMOYLTLGDLIDLSVSSSEDAATLPSOMLKGKTIY 464
 DB 403 VASEPVLTLEDHCSTIAQONMAOYFRKVLGDTL-LTKPEVISAQGLPSPNQLKRLILI 461
 QY 465 KGKTL-----PAN-----ISE 475
 DB 462 KHKRLAESAYEVPYTSWMSYENDISNGKNGILYLEDPVNHEWPHYFVLTSSKIYSE 521
 QY 476 DA-----EGEVSDSDSADIEDDCKLNGDASTNKKRVENTAKRLDS----- 519
 DB 522 ETSSDOGNEDEEPREKVSSTELSHNEKWFHGLGAGHDG-RHIAERLLTEYCIETGAPD 580
 QY 520 ---LIKES-----KIRDC----- 529

DB 581 GSELVRESETEVVDYTLTSMNGKVOHCRHISRODAGTPKFFLNDLVPSLDLITRYO 640
 QY 530 -----BDPN 533
 DB 641 QVPLACNEFEMLSEPPVOTNAHESKEWYHSLTRQAQEHMLKVPDGAFLVKRNEPN 700
 QY 534 NFSVS----- 538
 DB 701 SYAISFRAGKIKHCRVOEGQTVMLGNSPDSLVDLISYEKHPYKMKLRYPINEEA 760
 QY 539 -----TSPS-GKL--GR-----SKSAED 555
 DB 761 LEKIGTAEPDYGALYGRNPGPYVEANMPPTPKCAVKALFDYKQAREDELFFIKSAIQN 820
 QY 556 VESGE-----DAGASR----- 566
 DB 821 VEKQGGMMRGVGGKQKQMFPSNYVEKVNPVLEPEREHLIDENSPGLDLRGVLPVA 880
 QY 567 -----RNGRLVYGFSPSRKKKSKLKAASVE-----GDEGDSFGGSGRG 608
 DB 881 COIARPEEKNRNLFFVFSISMAVSALVADSOEELQDMVKKIRVQTAARLREG 940
 QY 609 ATRQKTMLSRALSDLYTKSVATHD--IEMEAASSWVSSFSETRAHQILOQ-KPAQ 665
 DB 941 KIMERN-KKIALELSELVYVCPRVPEDEKIGTERACTRDNSSFPETAEKYVNAKAKGK 999
 QY 666 YLRFNQOQLSRTPSSRYVDSNTYNPQPPNAGCOMVALNTOSEGRMLQNLNKAESANGG 725
 DB 1000 FLQYNRLQSLRYPRKQORLSDSNYDPLPMWICGSLVALNFQTPPKPMQMNALPMTGRH 1059
 QY 726 CGYVLKPGCMCGVFRPNSEDEPLPGOLKQVLYRIISQOLPKPRDSMLGDSGELIDPFV 785
 DB 1060 CGGVLPSTMRDEAFEPDKSSLRGEPCAISIEVLAGAHLK-----NGHG-TVCPFV 1112
 QY 786 EVELIGLPDSCREQTRVYDNGNFPTM--EETLVPMVHPEALYVFLVMDHPDG-RDF 843
 DB 1113 EIEVAAAEVDSIKQKTEFVVDGNLNPVPAKPFHQISNPEAFALRFVYEDMDSDQNF 1172
 QY 844 IGORTLAFSSMPCYRNV-----YLEGMEASIEYHNAV----- 877
 DB 1173 LAQATFPVGLKGYRAVPLKNNYSDEBLASLILKIDIFPAKENGDLSPFSGTSLRENG 1232
 QY 878 SDISCKVKAALGLKLF 894
 DB 1233 SDASGQLFHGRAREGSF 1249

RESULT 8
 PIB4_RAT
 ID PIB4_RAT STRAND: PRT; 1175 AA.
 AC Q9QW07; Q920G6; O88356;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=9401267; Pubmed=8407970;
 RA Lee C.-W., Park D.J., Lee K.-H., Kim C.G., Rhee S.G.;
 RT "Purification, molecular cloning, and sequencing of phospholipase C-
 beta 4".
 RU J. Biol. Chem. 268:21318-21327(1993).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=9343926; Pubmed=7688223;

RA Kim M.J., Bakh Y.Y., Min D.S., Lee S.U., Ryu S.H., Suh P.G.;
 RT "Cloning of cDNA encoding rat phospholipase C-beta 4, a new member of
 RT the phospholipase C.";
 RL Biochem. Biophys. Res. Commun. 194:706-712(1993).
 RN [3]
 RP SEQUENCE OF 447-1175 FROM N.A. (ISOFORM C).
 RC TISSUE-BRAIN;
 RX MEDLINE-99132015; PubMed-9931434;
 RA Adamski F.M., Tjames K.M., Shieh B.H.;
 RT "A unique isoform of phospholipase C-beta4 highly expressed in the
 RT cerebellum and eye.";
 RL Biochim. Biophys. Acta 1444:55-60(1999).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYME. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L15556; AAK13557.1; -
 DR EMBL; U57836; AAD10403.1; -
 DR EMBL; AF031370; AAC98145.1; -
 DR EMBL; AF027571; AAC24984.1; -
 DR HSSP; P10688; IDUX.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_Xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00387; PI_PLC_Y; 1.
 DR Pfam; PF00388; PI_PLC_X; 1.
 DR PRINTS; PR00390; PPHILIPASEC.
 DR PRODOM; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 KW Hydrolyase; lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing;
 FT DOMAIN 313 463
 FT DOMAIN 565 681
 FT DOMAIN 688 786
 FT ACT_SITE 328 328
 FT ACT_SITE 375 375
 FT VARSPLIC 1013 1022
 FT VARSPLIC 1023 1175
 FT VARSPLIC 1154 1175
 FT CONFLICT 255 255
 FT CONFLICT 308 308
 FT CONFLICT 417 417
 FT CONFLICT 470 470
 FT CONFLICT 504 504
 FT CONFLICT 545 546
 EQ -> M (IN REF. 2).
 R -> E (IN REF. 2).
 Q -> E (IN REF. 2).
 E -> K (IN REF. 2).
 A -> AA (IN REF. 1).
 EQ -> DE (IN REF. 2).

FT CONFLICT 734 734 I -> L (IN REF. 2).
 FT CONFLICT 741 741 R -> H (IN REF. 2).
 FT CONFLICT 764 764 D -> M (IN REF. 2).
 FT CONFLICT 766 776 L -> N (IN REF. 2).
 FT CONFLICT 828 828 F -> Y (IN REF. 1).
 FT CONFLICT 843 843 S -> V (IN REF. 2).
 FT CONFLICT 852 852 Q -> M (IN REF. 3).
 FT CONFLICT 916 916 Q -> T (IN REF. 3).
 FT CONFLICT 1024 1024 W -> C (IN REF. 3).
 FT CONFLICT 1043 1043 L -> M (IN REF. 3).
 FT CONFLICT 1057 1057 A -> V (IN REF. 3).
 FT CONFLICT 1067 1067 L -> V (IN REF. 3).
 FT CONFLICT 1084 1084 S -> C (IN REF. 3).
 SQ SEQUENCE 1175 AA; 134496 MW; 7379C6B85B8FCED CRC64;
 Query Match 15.6%; Score 996.5; DB 1; Length 1175;
 Best Local Similarity 29.3%; Pred. No. 2.8e-41;
 Matches 294; Conservative 135; Mismatches 310; Indels 265; Gaps 31;
 QY 99 ROSEFORPPDS--FDRPCRSYH-----122
 DB 18 QGAVFDRYEESFVEFPCLEKVDGFFLTWSEKGVLECSLINSIRLAIPDP 77
 QY 123 -----GSHRESLD-----122
 DB 78 KILALESGKSENDLEGRILCYGSGTDLVNIQFTYVAENPEITKQWESLRIHNR 137
 QY 155 DEDSIARRQRTDQWLKQTFDEADKNGDSLSE-----VLQILRLVNL 201
 DB 138 -ANNVSPTCLKHKMKLAF--LNTSGKIPVNSITPTFASGTEKVIQALNEL--GL 191
 QY 202 PQQRKQMRREADPDHGGTIGFEFECFAFKMSTRRLYLMTYSNHK-DHIDAASIQ 260
 DB 132 PGRKDEIEPAFT-----YEFYELQKICPRDIEDLEFKKINGDKTYLTVQLV 243
 QY 261 RFLQVEQKMAVY-----LESCDIIQEFCEPKSKGLIGDFTYTRSPAGDI 312
 DB 244 SELNHRQDPRLNETLFFPYDAKRAMQIIEYEPDEELKKKGLSSGFCYILMSDENAP 303
 QY 313 FNPENHHVDMOTPLSHYFTTSSHNITLVGDQLMSQSDMYAMVLOAGRCVEYDCWD 372
 DB 304 VFLDLLEYQEDHPLAFYLTSSHNITLVGRGKGSVMEYQVYLACRCVEILCMD 363
 QY 373 --GPDSEPIVHGVTLSKILFKVDIETINKAFITKNEYPIYLSIENHGCVIOOKMAQY 430
 DB 364 GKGEQDEPIITHGKAMCTDILFKVIOAKETAVTSEYPIYLSFENHCKYQOYOMSKY 423
 QY 431 LTDLIGD--KLDISSVSEDDATLTPSPQMLKGIIVKGRKL-----469
 DB 424 CEDLFQDILKQALESHPLEGRILLPSPNDLKRILIKNRKLPKEVEKKOLEALSKMGEA 483
 QY 470 -----PANISEDAGEVSDSDAIEDDOCKL--LNGASITRKRYENTARKLDSL 521
 DB 484 GESAAPSLIEDDNEEFESADQEEHAPKPKGNELISADFSKREAVASVKKGLVTV- 542
 QY 522 KESKIRDCEDPNPNVSSTLSPSGKLGRRKRAEDEVGSDGAGASRRGRGLVYGSFRRKK 581
 DB 543 -----EDBQAMMASYKYV-----555
 QY 582 KGSILKRAAAYEBEDBGDSDGSGSGATNOKTKMLISRLSDLVYTVTSVATHDEM-- 639
 DB 556 -----GA-----TYNIHPLYSIMINVAQVFKQGFHVAE 584
 QY 640 EAASSQVSSFSSTKAHQIIOQKPAQVILRENOOLSTIYSSRYDVSSYNTNPQFPNAC 699
 DB 585 ERNIHYMSSFNESVIGIYKTAHLEFVNNTKROMSRITPKGRVSSYNTNPDIENNAC 644
 QY 700 QMVALNTQSEGRMLQLNRAKFSANGGCVYLKPGCMQ--GVENPNSEPLPGQULKQLV 757
 DB 645 QMVSILNTQTDLMQNLNGKFEYNGSGVYLKDPFRRDRPTDFSEFPVGVINATOS 704
 QY 758 LRITSGQLKPKPDSMLGDEGLIIDPVEVEIIGLPVDCSRQ--TRVVDNGCFNPTW-E 814
 DB 758 LRITSGQLKPKPDSMLGDEGLIIDPVEVEIIGLPVDCSRQ--TRVVDNGCFNPTW-E 814

Db 705 VQVLSGQ-----FLSDK--IGTYVEVDYMGLEPTDIRKEFRTVMNNGLNPNVNE 754
 QY 815 ETLVTF-MVNMPELALVRLVMDHPDIGNRFGIORLTAFSMMGRHYVL--EGMEEAS- 870
 Db 755 ESFVEKRVLLPDLAVLRIVYDNN--NKLQGRLLPLDGLQNGRNLHSLRNGCKPLSL 811
 QY 871 --TFVAVV-----VSDISGVKQALGLKGLFLR-----GKPGSL 903
 Db 812 PTFECNIVLKTYPDFGDIYDALSPKKFLLSTTEKRAQDLRMGTETSDIADVPEDTSK 871
 QY 904 DSHAAGRPAPPSV---SQRILRTASAPTKSOKPGRKGPPELV 944
 Db 872 NDKKGRANPAKANVTPOSSSELPTTTAALSGQEAKKGI-ELI 914
 RESULT 9
 ID PIG1_RAT STANDARD; PRT; 1290 AA.
 AC P10686;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II)
 DE (PLC-148).
 GN PLCG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88289733; PubMed-2840660;
 RA Sub P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Inositol phospholipid-specific phospholipase C: complete cDNA and
 RT protein sequences and sequence homology to tyrosine kinase-related
 RT oncogene products."
 RT Proc. Natl. Acad. Sci. U.S.A. 85:5419-5423(1988).
 RL -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PFM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
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DR InterPro: IPR001192; PI-PLC.
 DR InterPro: IPR000909; PI-PLC_xdom.
 DR InterPro: IPR001711; PI-PLC_Y.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 2.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 2.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 2.
 DR ProDom: PD001202; PI-PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00235; PH; 2.
 DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCY; 1.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS0001; SH2; 2.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KM Hydrolyase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KM Repeat; Calcium-binding; Phosphorylation.
 FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT DOMAIN 1075 1177 C2 DOMAIN.
 FT ACT_SITE 1075 1177 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 SO SEQUENCE 1290 AA; 148547 MW; BB3240C27972CE3B CRC64;
 Query Match 15.4%; Score 985; DB 1; Length 1290;
 Best Local Similarity 25.6%; Pred. No. 1,1e-40;
 Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;
 QY 74 IIRPSPKRNKAKISID--SIOEVSERGESEYQRY-PDGSF--DPNCCFSIYHGS--HR 126
 Db 60 ITW--SGNADKIGSIDIRKEIRKTSRDRQDEPAPFDDSHCFVILYGEFRL 117
 QY 127 ESDLVSTSESVARVWTGRLTYMAGISDEDSL-ARKRPRDQWLKOTDEADKNDGSL 185
 Db 118 KTLSTLQTSDEVMNMVTKLTLWLM-----EDTLQAATPLQIEFMKQFYSDVREDEDI 172
 QY 186 SIGVYLQLLKLNWVNPORVQKQMFREADRDHDO--GTIAFEFCAFYK--MMSTRRDY 241
 Db 173 SAKDLKMLSCVNTRYVNMNR---FLRRLTDFDRSGDIIYGFPAQLYRSLAMSACKTMD 229
 QY 242 LLMLT---TYSNHRDLDAASLQRF-----LQVEKMGAVTLESQDII 281
 Db 230 LPFLFTNLTLRGERPELCQVSLSEFQGLLEYGELMAVDRQLVQEFMLSLFDPLREIE 289
 QY 282 EQFPCPCPKSKGLGIDGTNTNTRSPAGDIFNPENHNH--HQMTOPLSHYFTTSSHNRY 340
 Db 290 EPY-----FFLDELVTFLFSKENSVMNSQDAVCPETMNNPLSHYWTSSSHNTY 338

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QY 341 LVGQDLMGQSVMTAVYLAQGCRCVCEVDCMDGDPGEIVHGGYTLTKLIFKDIETIN 400
DB 339 LTGQFSSSESLTAVYACRLRMGCRICIEIDCDGDPGMVYIYHGHITLTKIFSDVLT 398
QY 401 KYAFITKNEYPVITLSTENHCSTVLOOKKMAOYLTDLGDKLDLSSVSSSDATLTPSPMLKG 460
DB 399 EHAIVASBPYITLSTEDHCSTLAORNNMAOHFRKVLGDTL-LTRKVDIAADGLSPNOLKR 457
QY 461 KILVKGKLLA-----NISDAEAG----- 480
DB 458 KILKHKRLKLAGSAVEEPTSVMTSENDISNISKNGILTYLEDPVNHHEVHYVLSKSI 517
QY 481 ---EVSEDSADEIDDCCKLLNGASTNRKRV-----ENTAKKLDL----- 519
DB 518 YVSEETSDGQDEDEEPEKRAASGSTEIHSSEKKEHGLAGRGDRHIAERILTEYCIENG 577
QY 520 -----LIKES-----KIRDC----- 529
DB 578 APDGSFLVRESEFVGDYTLTFMRNGKVQCHRHRSQDAGTPKFLTLNLVFDLTLIT 637
QY 530 -----E----- 530
DB 638 HYQOVLPLRCNEFEMRLSEPVPTNAHSEKEMVHASLTRAQAEHMLKRVPRDGAFLVRKN 697
QY 531 DPNNEFVSTLSPSGK-----LGRSK----- 551
DB 698 EPPSYALS-FRACKIKCHVQOEGQVLMGENSEPDLVLSIYERKHPLYRKMLRYP 756
QY 552 -----AEDD-----VESG----- 559
DB 757 NEBALEKIGTAEPDYGALYGRNPGFYVEANPMTFCVAKALFDYKAQREDELFTTKSA 816
QY 560 -----EDAGAR----- 566
DB 817 IIONVEKODGMWRG DYGGKKQIMPPSNYVEEMINPAILEPEREHIDENSPLGDLRLGYL 876
QY 567 -----RNGRLVYGSFRRKKKSKLKAASVE-----GDEGDSPPG 604
DB 877 DVPACQIARPECKNNRLTFVFSISMPSVAMQSLDVAADQDELDQVKKIRVQAQADAR 936
QY 605 QSGGATROKKTMYLSDLYKTKYSVATHD--IEMEAASSVOVSSSETRAHOITLQO- 661
DB 937 LIEGKMEERR-KKIALELESELVYVCRPFDEKIGTERACRYDMSSEPTKAEKYVNA 995
QY 662 KPAQVLRFNQOOLSRITPSSYRVDSSNYNPOPFMANQOMVALINQSEBRLQLRKAFS 721
DB 996 KKKKFLQVNRLOLSRTYRPGQRLDSSNDPLPMICGSQLVALNFQTPDKPMQMOALFM 1055
QY 722 ANGCGYVLRPGCMQGVFPNPSDEPLPGQLKKQVLRILISQQLPKPRDSMLGRGETI 781
DB 1056 AGHCGYVLRQPSMRDEARDPDKSLRGLLEPCVICIEVLGARHLPK-----NCRG-IV 1108
QY 782 DPFVEVEILGLVDCSRETRVVDNGNFPYV-EETLVFVMPMPLIALVRLVMDHPDG 840
DB 1109 CFEVELEVAAGAYDSTKQTEFVNGNLPVPAPRPFHEQIJSNPFARLRFVYEDMS 1168
QY 841 -RDFIGORTLAFSSMMPGYRHV-----YLECMEASIFVHAV 877
DB 1169 DQNFIAQATFFYKGLKTCYRAVPLKNNYSEDLIASLILKIDI 1211

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OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=90094370; PubMed=2557343;
RA Emori Y., Homma Y., Sorimachi H., Kawasaki H., Nakanishi O.,
RA Suzuki K., Takenawa T.
RT "A second type of rat phosphoinositide-specific phospholipase C
RT containing a src-related sequence not essential for phosphoinositide-
RT hydrolyzing activity."
RL J. Biol. Chem. 264:21885-21890(1989).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. IT IS A CRUCIAL ENZYME IN TRANSMEMBRANE SIGNALING.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1-D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: Calcium.
CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
CC SYSTEM RECEPTORS.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J05155; AAA1896.1; -.
CC PIR: A34163; A34163.
CC HSSP: P08487; 2PID.
CC
CC InterPro: IPR000008; C2.
CC InterPro: IPR001849; PH.
CC InterPro: IPR001192; PL_PLC.
CC InterPro: IPR000909; PL_PLC_Xdom.
CC InterPro: IPR001711; PL_PLC_Y.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC Pfam: PF00017; SH2; 2.
CC Pfam: PF00018; SH3; 1.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00169; PH; 2.
CC Pfam: PF00387; PL_PLC-X; 1.
CC Pfam: PF00388; PL_PLC-Y; 1.
CC PRINTS: PR00390; PHPLIPASEC.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD000066; SH3; 1.
CC ProDom: PD000093; SH2; 2.
CC ProDom: PD001202; PL_PLC_Y; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00233; PH; 2.
CC SMART: SM00148; PLCXG; 1.
CC SMART: SM00149; PLCYC; 1.
CC SMART: SM00252; SH2; 2.
CC SMART: SM00326; SH3; 1.
CC PROSITE: PS00001; SH2; 2.
CC PROSITE: PS50002; SH3; 1.
CC PROSITE: PS50003; PH_DOMAIN; 1.
CC PROSITE: PS50004; C2_DOMAIN; 2; 1.
CC PROSITE: PS50007; PL_PLC_X_DOMAIN; 1.
CC PROSITE: PS50008; PL_PLC_Y_DOMAIN; 1.

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KW Hydrolyase; lipid degradation; Transducer; SH2 domain; SH3 domain;
 Repeat; Calcium-binding; Phosphorylation.
 FT DOMAIN 20 131 PH.
 FT DOMAIN 312 456 DOMAIN X.
 FT DOMAIN 532 635 SH2 1.
 FT DOMAIN 646 735 SH2 2.
 FT DOMAIN 769 829 SH3.
 FT DOMAIN 930 1044 DOMAIN Y.
 FT DOMAIN 1059 1152 C2 DOMAIN.
 FT ACT_SITE 327 BY SIMILARITY.
 FT ACT_SITE 372 BY SIMILARITY.
 SQ SEQUENCE 1265 AA; 147734 MW; 2C34910D43572723 CRC64;
 Query Match 15.2%; Score 968.5; DR 1; Length 1265;
 Best Local Similarity 25.2%; Pred. No. 7,1e+40;
 Matches 293; Conservative 15; Mismatches 301; Indels 393; Gaps 36;
 QY 74 IRMPSSKREKAKISIDISIOEVSEGRSEVFORYPDGSFDPNCCFSITGHSH--RESIDL 131
 DB 52 VAKSKTKIEGLDIMEIRGRKSKDEKAKAVRHAKDCOCFTIFGCTGFVLTSL 111
 QY 132 VSTSEVARTWVGLKYLAMGIDSESLARKORTROMLKOTPEADKNGDSISIGEV 191
 DB 112 ATDSKEDAVKWLSGKTL--HQEAMNASTPTMIESMLRKQIYSVDQTRNSISLELK 167
 QY 192 QLLHKIN--VNLPRQRYKMFREADTDHOGTLGFEFECAFYKKM-----ST 236
 DB 168 TILPLVNFKVSIGIFLQDKLEIGAKQD-----ELSFQHPHFYKMLEGQKSLIDEF 221
 QY 237 RRDLYLMLTYSNHRDHLDAAL-----QRF-LQEQKMGAVTLESCDIIIEOF-EPCE 289
 DB 222 KKDSVFL--GMDTRDASAVYLODFORLLHEQOELMADLNKREMTKFLIDTMR 278
 QY 290 NKSGLGIDGFTYTRSPADIDNPREHNH--QDMQPSHYVITSSHNTYLVGDOLMS 348
 DB 279 ETAEFFLVDELTYLTFSENSINDEXDAVDMQDNNPLSHYVSSHNITLYLDQLRS 338
 QY 349 QSRVDMVAVLOAGRCVYVDCMDGPDDEPIVHNGYTLTKILKDVETINKYAFIKNE 408
 DB 339 ESSTFATVRLRACRCRCELDWCOPDGRPLIHGWITTTIKIKDDVQVALRDHAFVSS 398
 QY 409 YPVILISNHCSSVIQOKMAQYLDLIDDKLDSVSSSEDTTLPSPOMLKGKILVKKK 468
 DB 399 FVILISIEHCSVEQORHMAKFEVLGDL--LTKPTLASADQLPSPQLREKIIKKK 457
 QY 469 L--PANSDEAE--GEVSDSDADE-----IDDD- 494
 DB 458 LGPRGDVAVNEDKDEHKTOGELYMDSIDQKTRHCAIADAKLSDSIDIEQVEEDP 517
 QY 495 -----CKLLNGDASTNKRRENTAKRL-----DSLKESKIRDCEDPNNE 535
 DB 518 VQDTPPELHFEKMFHKKVSERTSAEKLQYCAETGAKDGTFLVRESE--TFPMY 573
 QY 536 SVSTLSPSGKL----- 546
 DB 574 TLS-FWRSRGVQHCRIIRSTMEGVKYYLTDLNLFNSIYALIQHYREAHLCFAFELRLT 632
 QY 547 -----GRSKAE-EDV-----ESGEDAGA----- 564
 DB 633 DVPVNPNEHESKRWYDRLSRGEADMRLRIPDGAFLRKREGDSVALITFRANGKVKH 692
 QY 565 --SRNGR-LVYGS----- 575
 DB 693 CRINRGRHFVLTSAVFESLVELVSYEKHALYRKMLRYEVTPELLERYNMERDINSI 752
 QY 576 -----FSRRKKKSGKL-----RKASVBERGEG 598
 DB 753 YDVSRYVDPSEINPSMPORTYKALDYAKRKDELTFRCGALLHNVSKEPGGWMKGDYG 812
 QY 599 -----ODSP-GCOSRGA----- 609
 DB 813 TRIQYFFPSNYVEDISAGDAEMEKEQIIEPNLGSICRGILDLNTYNYVAKPGKRNQKAF 872

QY 610 -----TRQ-----KTKMLSRALSD 624
 DB 873 VILPEKKGGDPVPEFATDRVELEFEMFOSIREITWKIDTKENNMKHYERNQIAIELSD 932
 QY 625 LVKTKSVATHDIEEBAASSMOVSSPSEKKAQIILQOKPAQYLRNQOOLSRIYPSRYV 684
 DB 933 LVVYCKPSTSKTDHLENDPFEIRSEFVEIKADSIYKRPVLLRYNKGILRVYPKQGV 992
 QY 685 DSSNTPQEFNAGCOMVALANTQSEGRMLQLNRAKFSANGCGYVLKPGCQGFENPNS 744
 DB 993 DSSNTPQEFNAGCOMVALANTQSEGRMLQLNRAKFSANGCGYVLKPGCQGFENPNS 744
 QY 745 EDPLPGQLKKQ--LVNRIISGQQLPKPRDSMLCDREIIDEVEVEIIGLIPVDCSRQ 800
 DB 1048 YDMPPESSQKILMLTLTVKVLGARHLPK-----LG--RSIACPFVEVEICGAEYDSNKKF 1100
 QY 801 TRVYDNGNPNPW--EELVEMVHMPDELALVPLVMDHPDG-RDFIGORFLARSSMP 856
 DB 1101 TVVYDNGNLSPPWAPTOEVTEIYDPLALFLVTEEDMFSDFNLAHATYPKIGKS 1160
 QY 857 GYRHV-----YLEGMEASIFV 873
 DB 1161 GFRSVPLKNGSIEDIELASILV 1182
 RESULT 11
 PIG2_HUMAN
 ID PIG2_HUMAN STANDARD; PRT; 1252 AA.
 AC P16885;
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase gamma 2
 DE (EC 3.1.4.11) (PLC-gamma-2) (phospholipase C-gamma-2) (PLC-IV).
 GN PLCG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoblast;
 RX MEDLINE=89078616; PubMed=2849563;
 RA Ohta S., Matsui A., Nakawa Y., Kagawa Y.;
 RT "Complete cDNA encoding a putative phospholipase C from transformed
 human lymphocytes."
 RT FEBS Lett. 242:31-35(1988).
 RL
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYME. IT IS A CRUCIAL ENZYME IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PPM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

	Query Match	Best local similarity	15.1%, Score 950.5; DB 1:	length 1282;
	Matches 292; Conservative 164; Mismatches 310; Indels 399; Gaps			
QY	74	IRRRPRKKEKKKIDSIOEVSGSGROSEVFORIPDGSDPNCCSESIYHGS+-RESIDL	131	
DB	52	VAASKRAADIKIEGFIDIMEIKELRPGKNSKPFERAKAVRQKCCCFITLYGQFVLTSL	111	
QY	132	VVSSEVATWYVGLRYLMAGISDEDSLARQTRQWIKQTFEDADKNGSGSLTGEVL	191	
DB	112	AADSKEDANMVLSSGKIL-----HEAMNASTPIITTSWKIYQISVDOTRRNSISLEBK	167	
QY	192	QLLHLKLVNLPQR-VKOMFEADTDHQGLFEFECAFYMM-----STRRL	240	
DB	168	TILPLINEFVSAAKLAKDFEIGA-HKDELSFQFHLFYKKLMEQOKSILDEFKDS	225	
QY	241	YLLMLTYSNKHCHDAASL-----QRL-----QVEQKAGVLTSCQDIIIE	282	
DB	226	SVFILL-----GNDRPDASVAVLHDFRLLTHEQDEHMAQDLNVRERMRKFTDDIMRETAIE	282	
QY	283	QEPSPENKSGLLGIDGFTVYTRSPAGIDFNEHHNVH-DMQTPOLSHYFTSSNHTYL	341	

Db	283	PF-----LFVDFELTYLTFRENSINDEKTDATVADMODANNPLSHYWISSANTYL	331
QY	342	VBGQILMSOSRVMTYAMVLAQACRCVYVDCWDGDPGEPTVHGHTYLTSLKLFKDVETIINK	401
Db	332	TGQQLSSESSPAYIRCLRMGCRGTIELDCMGDPGPKPVIYHGWTRTKIKFDVDVQAIKD	391
QY	402	YAFIKNEYVILLISNHCSSVIOQKMAQYLTLDIGDKLDSVSSSEDATLLPSPOMLKGK	461
Db	392	HAFTVSSPVLISIEHCSVSQDQRHMAKAFKEVGGDL-LTKPLEASADQLPSPQIREK	450
QY	462	ILVKGKLT-----PANT-----SEDAEGEVSDEDSADE-----IDDD--	494
Db	451	IIIKHKKLPGRGDYVNNEDKDKDEHKQOGELYMDSIDQWTRHYCAIADAKLSFDLIE	510
QY	495	-----CKLNGDASTIRKKNVEMNAKLT-----DSLISEK----	525
Db	511	QTMEEVYODIPPELHAFGEKWFHKFKVEKTSAKELILOEYCMETGKDGKFTVRESETPP	570
QY	526	-----	525
Db	571	NDYTLFWRSRGVQCHRIHSTMEGGLTKYLTLDLRRRRYALIOHREHLPCAFLER	630
QY	526	-----IDCEDPNNEFSVTLSPSK	545
Db	631	LTDVPNPNPHESKPWYDLSLRGEADMILRIPRQGAFLIRKRRSDSYAI-TPRARK	689
QY	546	L-----GR-----KSAEEV	556
Db	690	VKHCHINDGHRHFLVGSATFESVELVSTYEKHSILYRKRLRYPVLPBELRYMTERIO	749
QY	557	ESGEDAG-----ASRRN-----GRLVGSFSRRKKGSKLT-----KKAASVEBG	595
Db	750	NSLVDSRMVYDPSEINPSPMPQFTVKALYDYKAKRSDLSFCGALIHVSKPEPGMMKG	809
QY	596	DEG-----ODSP--GGGSRG-----	608
Db	810	DYGRIDQYFSPSNVEDISTADEELEKEQIIEDNPGLSGCRGILDLNTYNYVKABQGRNQ	869
QY	609	-----ATRO-----KRTMKLSRA	621
Db	870	KSFVFLLEPRKQGGDPVEEFTDVEEELFEWFGSIREITWKIDSKENNMKYMKKNQSTAE	929
QY	622	LSDLVYKTKASVATHIDMEEAASSMOVSSSEKKAHIILOOKRAOYLRRQOOLSTITYSS	681
Db	930	LSDLVYCKPTSTKYKDNLEPDRERIRSEVTEKADSIINQKVYDLTKKYNOKLTREYPRG	989
QY	682	YRVDSSNTNPQPFMNAQCCQVALNLYOSEGRMTOLNNAKFSANGCGGYLAKPGCMQGVFN	741
Db	990	QRVDSSNTDFRLMLTLCGSGQVVALNFTQADVKYQMMHAFLESLNGRGYVLOEBSM-----R	1044
QY	742	PNSDDPLPGOLKQ-----LVLRITISQOQLPKPRDSMLGDRGEIIDPEVEVEITIGLPVDCS	797
Db	1045	TEKTYDPPRPSQKILMTLTVKYKLAGRHLPK-----LG--RSIACPVEVEITICAEYGN	1097
QY	798	REGTRVVDNGEFPPTW-----EETLVEVYHMPLEIALVFLVHMDHPIC-RDITGQGTLAFFS	853
Db	1098	KKFTVYVNDGSLPWIAPQEKVTEPEIYDNPALFLRFVYVEEDMSDPNLTAAHATYPIKA	1157
QY	854	MMGCRYHY-----YLEGMEBASITFV	873
Db	1158	VKSGFRSVPLKNGYSEDIETLALV	1182

RESULT 12
PIPL DROME
ID PIPL DROME STANDARD: PRT: 1312 AA.
AC P23455; Q9VNP9;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase classes I and II (EC 3.1.4.11) (phosphoinositide-specific phospholipase C).
PLC21C OR PLC-21 OR CG4574.

OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=91286274; PubMed=206123;
 RA Shortridge R.D., Yoon J., Lending C.R., Bloomquist B.T.,
 RA Perder M.H., Pak W.L.,
 RT "A Drosophila phospholipase C gene that is expressed in the central
 RT nervous system".
 RL J. Biol. Chem. 266:12474-12480(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (CLASS II ISOFORM).
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Nelson C.R., Miklos G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman J.T., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibesworth C.,
 RA Jellai M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.H.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
 RA Rebertus K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CLASS I AND CLASS II (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: NEURONAL CELL BODIES OF THE OPTIC LOBE,
 CC CENTRAL BRAIN, AND THORACIC GANGLIA IN ADULTS, AND THE BRAIN OF
 CC LARVAE.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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CC EMBL: M60452; AAA28819.1;
 CC EMBL: M60453; AAA28820.1;
 CC EMBL: AE003589; AAF51507.1;
 CC PIR: B40879; B40879.
 CC HSSP: P10688; 10AS.
 CC Flybase: Fbgn0004611; Plc21C.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR001192; Pl_Plc.
 CC InterPro: IPR000909; Pl_Plc_xdom.
 CC InterPro: IPR001711; Pl_Plc_Y.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00387; Pl_Plc-Y; 1.
 CC Pfam: PF00388; Pl_Plc-X; 1.
 CC PRINTS: PR00389; PHPLIPASEC.
 CC ProDom: PD001202; Pl_Plc_Y; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00148; PLCXC; 1.
 CC SMART: SM00149; PLCYC; 1.
 CC PROSITE: PS50004; C2_DOMAIN_2; 1.
 CC PROSITE: PS50007; PIP2C_X_DOMAIN; 1.
 CC PROSITE: PS50008; PIP2C_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Transducer; Alternative splicing.
 CC FT DOMAIN 599 715
 CC FT ACT_SITE 722 820
 CC FT ACT_SITE 333 333
 CC FT ACT_SITE 378 378
 CC FT VARSPIC 1057 1063
 CC FT CONFLICT 508 508
 CC FT G -> A (IN REF. 1).
 CC SEQUENCE 1312 AA; 145717 MW; B8DD0EF5A48C2665 CRC64;

Query Match 14.8%; Score 945.5; DB 1; Length 1312;
 Best Local Similarity 25.3%; Pred. No. 9.7e-39;
 Matches 324; Conservative 190; Mismatches 434; Indels 335; Gaps 42;

44 AMQGMQNVK-----LNGSGGLVRYLDEHNSCIRMPRSKRNEKAKISIDS 91
 19 ALDQGEKIRINDDSGRTPTVMVAKKFF-LYWDQN-----NELDIIDYAT 66
 92 IQEVSQSGQS-----EYFQRYPGSGDPNCCSYTHGSHRESLDYS--TSSEA 139
 67 IRDVFQGYARPRDKLRQTVTLGPDQTLLEK-TYVCHGSDFYNNKTFVNCCTRRDIA 125
 140 RTWTGLGYLMAGISDEDSLARORTDQWLKQTFD-----EADKNGDGLSIGEVQLDLH 195
 126 QLTWDGL-----IKLAVSLAQLNGSALMFLQAKHTKLCQDVKS--GRIPVNIKKLPA 177
 196 K-----LNV-NIPROVRKMFREADTDDHOGTLGFEFCFAFYKMSIRRLYL 243
 178 QKEDRKREKALDVTGIPSGKVDSI-----SVSKFQEFDFYNNKYKTLTRSEVER 229
 244 M-LTYSNKHDLDAASLQRFLOYEOK-----MAGVTLESQODIIPQFECPEKNSK 293
 230 FDSIVGSKRCKMSIAQVVEFLNKTQRPRLNELLYPANPAKKEILOEYENKRAK 289
 294 GLIGIDGFTNTRSPAGDIFNPENHHVQDNTOPLSHYFTSSHTYLVGDQLMSQSRD 353
 290 QGLSLDGLFRLYMGDNRIMAPSKLDLDDMDQPMHSHTVFNSSHTVLTGHLGKSSVE 349
 354 MTAWYLQACRCVEVDQDPDEPTVHNGTTLKSLFKYVETIKKVFIRNEYVYL 413
 350 IYRCLLAGRCRVEVDLDFNNGTEPEVIVHGYTVEIPFAKVLALESAPKISEYVIL 409
 414 SIENHSYVQKKMAYLTDIILGRK-----DLSSVSEDPATLPSQMLKGIIVKGR--- 467
 410 SEFNHCNPRQQAQKIANCYCEIFGMDLDPKPSHLEPNDLPPPMILRRILIKNNKH 469

QY 468 -----KLPANISEDAEGERVSDSDSDEIDDDCKLINGASTNRKRENTAKRKLD 518
 Db 470 HHHHHHHHKKRPAGVTPPAANNKLTITANSVD----- 500
 QY 519 SLIKESKRIODEEDNNFNSVSTLSGKLGKRSKAEEDY---ESGEDGASR--RNGRLVY 573
 Db 501 -----AKAAQOVGLSASHEDEGVTRSTANGVDAT 529
 QY 574 GS-----FSRRKKKSKLKKAASVEBG--DEQDSDGGGSRGATRO 612
 Db 530 GTGTGSAAGTAGHAPLQIROSCKDSTGSDSDSDSDSLNTPTNPLSGNEPPPEKA 569
 QY 613 KTKTKLSRALSDLYTKYKSVATHDIEKAAS---WQVSSFETRAHQITLQKPAQYLR 668
 Db 590 KETETAGAEISALVNVQPT--HFSFEENAEKKNRCYEMSGFDEKATTLTKRPIEFVA 647
 QY 669 FNOOLSRITPSRYVSDSVNYNPOFPWNNACCOMVALNYOEGRMLOLNKRAKFSANGCGY 728
 Db 648 YNKHQLSRYVPAGTRDSSNFMOLTNAGCCQLVNLFOITDIAMOLNIGIFEYNARSGY 707
 QY 729 VLKPGCKOG--VFNPNSEDPPLGOLKOLVNLITISGOOLPKPRDSMLGDRGEIIPFVE 786
 Db 708 LKLPERRRDRRLDPEFAESTVDGIAGVSTVLSGQFLDKR-----ANTEVE 757
 QY 787 VEIIGLPVDCSRE--QTRVYDNGFPMV--EETLVF--WYHMEPIALVFLVMDHPIDGRD 842
 Db 758 VDMYGLPAPVYKFKRTKTVYDNGMNPVLDDEPFYKRYVLELASIRTAAYEE--GSK 814
 QY 843 FICQRTLASMMPGYRHYVLEGEERASTFVHVAASDISGKQKALGLGLPL---RGP 898
 Db 815 LIGHRYLPTVIGLPGYRHY-----NLSEVGQPIALASLTLVYVVDY 857
 QY 899 KPGSLDSHAGRPAPRPSVSOHLIKRTASAPTKSQKPRGRGPELVLTGRDNGSKVAD 958
 Db 858 VDDDLNFA-----EALANPKYQSELEKRDIOISVLTDEKALGSAD 901
 QY 959 VYPPGPGAPPAQEGPGSGSPKAPAAVAEKSPVRVPRVYDGGPGPAGMA----- 1012
 Db 902 DLKSGCGKKEKRPVESLAT--SPKRPSTISAANAASVDTYVTRTGCGEISIVAPST 960
 QY 1013 -----ATCMKCYVCS----- 1022
 Db 961 QHSHLSDSVSTISQVSSQDFVDVLAEPLEKILDRHYSEKRLMEKLESLRKHD 1020
 QY 1023 -----CAGVNTGGLQREPPSPBPASROAATROPRARADSLGAPCCGLDHPATGRSRE 1077
 Db 1021 KKKIKIAGOKSSPLEGKRP-----KFAITNKIKYKLSKSLNC--LSPHSEPG--VE 1068
 QY 1078 APKGGARKOGPGSGSGSSSSSPDSPGIPERSFRPE---GACROPGALOGEMSALE 1133
 Db 1069 IPACP--LDLSDSSESAADAAGEDLAGSSSLDGRQESRLRSACR-----Y 1115
 QY 1134 AOKLEIRSK--SPWFSAGKPL 1154
 Db 1116 TSQYREIQEKYHEALYSAAEVYL 1138

QY 1134 AOKLEIRSK--SPWFSAGKPL 1154
 Db 1116 TSQYREIQEKYHEALYSAAEVYL 1138

Query Match
 Best Local Similarity 26.0%; Pred. No. 9.4e-35;
 Matches 293; Conservative 153; Mismatches 325; Indels 274; Gaps 38;

QY 44 AMOEGSMQWYK-----LNGSGKGLVRYFYLDHRS-----CIRMRP 78
 Db 21 SLKGTGKRVKMDSDSTIVTPILRTDPGGF--FYWTQNKETELDLISLVKADARGCKHAK 79

RA MEDLINE-88270495; PubMed-3390863;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.";
 RL Cell 54:161-169(1988).
 RN [2]
 RP ACTIVITY, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX MEDLINE-93203266; PubMed-8454637;
 RA Thon D.-Y., Lee H.-H., Park D., Lee C.-W., Lee K.-H., Yoo O.J.,
 RA Rhee S.G.;
 RT "Cloning, sequencing, purification, and Gq-dependent activation of
 RT phospholipase C-beta 3";
 RL J. Biol. Chem. 268:6654-6661(1993).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DINGICGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- CORRECTOR: Calcium.
 CC -1- SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
 CC parotid gland, liver, uterus, lung, heart, adrenal gland and
 CC ovary. Not detected in spleen, pancreas, intestine, thymus or
 CC kidney.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC
 DR EMBL; M20636; AAA4885.1; -
 DR PIR; A28821; A28821.
 DR HSSP; P10688; 1DXJ.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_Xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00387; C2_1.
 DR Pfam; PF00387; PI_PLC_Y; 1.
 DR Pfam; PF00388; PI_PLC_X; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXG; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467 DOMAIN X.
 FT DOMAIN 540 656 DOMAIN Y.
 FT ACT_SITE 663 761 C2 DOMAIN.
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT MOD_RES 378 378 BY SIMILARITY.
 FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 1216 AA; 92F23691781F788E CR64;

```

OY 79 SRNREKAKISIDISIOEVSEGRSEVFORYPGSDPNCFCFISYHSHRESIDLVSTSEV 138
DB 80 ARPDPLRELD-----VGNIGHLEGRNITYVYGPD-----LVNISH---LNLVAFQEEV 126
OY 139 ARTWVTGLRYLMAGISDESDSLARROTRIDOMLKCOTFDADKNGDSLSIGVLOLMLKLN 198
DB 127 AKEMTNEV-----FSLATNLNLAQNMNSRDAFLKAYTKL-----KLO 162
OY 199 V-----NLPRQVWOMKREADTDHOGTGLFEFECAFYKMMSTR-----DLYLLM 244
DB 163 VTEGRIPLKNTYRLE-SADKRKRYETAL---EACS---LPSRNSINQEDPTDPRVYKVF 215
OY 245 LFTYSNKHDLH-----AASLQRFLOVEQKMGAVTL-----ESCQDII 281
DB 216 LNNLCRPEIDNJFESEFGAKSKRYLTVDDQMDPINKRDPRLNELLPLKQEOVOYLI 275
OY 282 EOEPEPCENKSKGLGIDGTNTYTRSPAGDIPNPEHHVHODMTOPLSHYFTSSHNTYL 341
DB 276 EKEPNNSLAKKQMSVDGFMRLTSGEENGVSPEKLDINEDMSQPLSHYFTSSHNTYL 335
OY 342 VGDOLMSQSRDWMYAWLQACRCVENDGMDG--PDGEPIVHGYTLTKILFKDVIETI 399
DB 336 TAGDLAENSVEWYRQVLLSGCVCVELDCKMGTAEPEVITHGFTMTETISEKVEIEAI 395
OY 400 NKVAFIRNEYPVVILSTENHC-SVYQOKKAAQYLTDLGOKL---DLSSVSEDAATTLPSR 455
DB 396 AECAFKTSPPFILLFSEFNHVSPOKQAKMAYCRLLFGDLMLEPELEKPLESGVLPSP 455
OY 456 QMKGLTLYGKTKLPANISEDAEGRVSDSDADEIDDDCKLNGDASTNKKREVENTAR 515
DB 456 MDLMTKILVKKK-----XSKHSESGSKK 480
OY 516 KIDSLINKESKTRDCEPDNNFSVSTLSPSKLGRKSKAEDEYSEGEDAGASRRNGRLVGS 575
DB 481 KLS-----EQASNTYSDSSVFEPPSPGAGADRESDDDDDDDD-----519
OY 576 FSRKRRKSKLAKKASVVEDEGDDSPGCGSRGATROKTKMLSRALSDLVKTKSVATH 635
DB 530 -----CKSSMDEGAGSEAM-----ATEE-----MSNLVNTIQPKFE 553
OY 636 DIE--MEASGNOVSPSETEKAHQILOQKPAQYLRFNOOOLSRIYPSYVDSNNINPOP 693
DB 554 SEFTSKKKNKSPSEMSFEVETKGLDOLTKSPYEFYNNMQLSRITYPGTRVDSNNVPL 613
OY 694 FNNAGCGVYALTYOSEGRMLQNLRAKFSANGCGCYLKGPGMCO--GVFNPNSEDPLPGQ 751
DB 614 FNNAGCGVYALTYOYVDLAMOINMGMYNKGSGRLKPEPMRRPKDHFDPFTGCIYDGI 673
OY 752 LKKOLVRLTISGOQLPKPRDSMLDGRGELIDPEVEVELIGLVPDCSRE--QTRVVDNGF 809
DB 674 VANITLSVKLTISGO-----FLSDK--VGYIYEVDMFGLPVPTRRKAFKTSQGNV 723
OY 810 NPTM--EETLVF--MVHMPETALVRLVMDHDPGRDFTQORLTLASSMMGRHRYLSGME 867
DB 724 NPWEEEPVIFVKVYLPISACLIRIAEYB--GKFIQHRLIPVQAIRPGHITCLRNER 780
OY 868 E-----ASIFVHYAVSD-----ISGKVK-----QALGLKGLFLRGKPPSL 903
DB 781 NQPLMLPAFVYIEVADYDPTDYADYIELNSPIRYVNLMEGRAKOLALTLIED-----834
OY 904 DSHAAGPPAPPSVQRILIRKTASAPTKSQKGRGRGFPBLVIGTDTSKGVADVYVPG 963
DB 835 -----EEEVKKEADPGETSESEAPSE-----TTRTAENGVNHTATLA 871
OY 964 PGAPAPAP--AQEGSGSGSPRCAPA 987
DB 872 PKPPSOAPHOSAPAGS---VKAPA 892

```

RESULT 14
PIB4_BOVIN
ID PIB4_BOVIN STANDARD; PRT; 1023 AA.

```

AC 007722; 007721; 007723; 007724;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta 4
DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4) (Fragment).
GN PLCB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93317620; PubMed=8327481;
RA Ferreira P.A., Shortridge R.D., Pak W.L.;
RT 'Distinctive subtypes of bovine phospholipase C that have preferential
RT expression in the retina and high homology to the norpa gene product
RT of Drosophila.';
RL Proc. Natl. Acad. Sci. U.S.A. 90:6042-6046(1993).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: calcium.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1A, 1B (SHOWN HERE), 2A
CC AND 2B; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13936; AAA30699.1; -
DR EMBL: L13935; AAC37304.1; -
DR EMBL: L13937; AAA30700.1; -
DR EMBL: L13938; AAA30701.1; -
DR HSSP: P10688; 1OAS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_Xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00387; PI-PLC-Y; 1.
DR Pfam: PF00388; PI-PLC-X; 1.
DR PRINTS: PR00390; PHPLIPASEC.
DR PRODOM: PD001202; PL_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00148; PLCXc; 1.
DR SMART: SM00149; PLCYc; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
DR HydroLase; Lipid degradation; Transducer; Phosphorylation; Calcium;
KW Alternative splicing; 1.
KW NON_TER 1.
FT DOMAIN 149 299 DOMAIN X.
FT DOMAIN 413 529 DOMAIN Y.
FT DOMAIN 536 634 C2 DOMAIN.
FT ACT_SITE 164 164 BY SIMILARITY.
FT ACT_SITE 211 211 BY SIMILARITY.
FT VARSPLOC <1 104 MISSING (IN ISOFORM 2A AND ISOFORM 2B).

```


Mon Mar 31 11:07:17 2003

us-09-927-112-2.rsp

Page 20

Search completed: March 28, 2003, 13:49:37
Job time : 43 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:47:05 ; Search time 54 Seconds
(without alignments)
2148.782 Million cell updates/sec

Title: US-09-927-112-2
Perfect score: 6379

Sequence: 1 MAPPTAGPLPGPALPDPDG.....ALYPHCLRLGLLFWLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524.5	23.9	997	1	phospholipase C (E
2	1517	23.8	1096	1	inositol 1,4,5-tri
3	1459	22.9	764	1	1-phosphatidylinos
4	1297	20.3	895	2	hypothetical prote
5	1287	20.2	745	1	1-phosphatidylinos
6	1285	20.1	756	1	1-phosphatidylinos
7	1258	19.7	756	1	1-phosphatidylinos
8	1244	19.5	709	2	1-phosphatidylinos
9	1009	15.8	1291	2	1-phosphatidylinos
10	997.5	15.6	1290	2	1-phosphatidylinos
11	997	15.6	1176	1	phospholipase C (E
12	986	15.5	1176	1	1-phosphatidylinos
13	985	15.4	1290	2	1-phosphatidylinos
14	968.5	15.2	1265	2	1-phosphatidylinos
15	950.5	14.9	1252	2	phospholipase C (E
16	947.5	14.8	1312	1	phospholipase C (E
17	945	14.8	1216	1	1-phosphatidylinos
18	943	14.8	1305	2	phospholipase C (E
19	939	14.7	751	1	1-phosphatidylinos
20	937.5	14.7	1023	2	phospholipase C (E
21	936	14.7	1216	2	1-phosphatidylinos
22	928.5	14.6	1418	2	phospholipase C (E
23	925	14.5	801	1	1-phosphatidylinos
24	915.5	14.4	1210	1	phospholipase C (E
25	911	14.3	1234	2	phospholipase C de
26	908.5	14.2	1181	2	1-phosphatidylinos
27	908	14.2	1095	1	phospholipase C (E
28	903	14.2	1173	1	1-phosphatidylinos
29	900	14.1	1234	2	phospholipase C-de

30	887.5	13.9	913	2	T46339	hypothetical prote
31	881.5	13.8	1211	2	S68251	phospholipase C, I
32	880	13.8	1299	2	T24299	hypothetical prote
33	872	13.7	1217	2	A45493	phospholipase C-de
34	870.5	13.6	899	2	S51092	probable phosphoin
35	867.5	13.6	1051	2	S27002	phospholipase C (E
36	865.5	13.6	899	2	S55075	1-phosphatidylinos
37	857	13.4	875	1	S66672	phosphatidylinosit
38	852	13.4	1898	2	T42440	phospholipase C ho
39	832.5	13.1	1922	2	T21581	hypothetical prote
40	682.5	10.7	869	1	A47257	1-phosphatidylinos
41	677	10.6	1099	2	T18257	phospholipase C -
42	649	10.2	565	2	T07424	phospholipase C-de
43	623	9.8	600	2	T06420	phospholipase C-de
44	609.5	9.6	581	2	T50841	phospholipase C-de
45	604.5	9.5	551	2	T06777	phospholipase C-de

ALIGNMENTS

RESULT 1	154390	phospholipase C (EC 3.1.4.-) epsilon - human
C:Species: Homo sapiens (man)		
C:Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text.change 10-Sep-1999		
C:Accession: 154390		
R:Kohn, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota, Hum. Mol. Genet. 4, 667-674, 1995		
A:Title: Identification of a novel phospholipase C family gene at chromosome 2q33		
A:Reference number: 154390; MIM:605973; PMID:763346		
A:Accession: 154390		
A:Status: preliminary; translated from GB/EMBL/DBJ		
A:Molecule type: mRNA		
A:Residues: 1-997 <RES>		
A:Cross-references: GB:D42108; NID:g780121; PIDN:BA07688.1; PID:g780122		
C:Genetics:		
A:Gene: GDB:PLCE; PLC-L		
A:Cross-references: GDB:699207; OMIM:600597		
A:Map position: 2q33-2q33		
C:Superfamily: human phospholipase C-specific phospholipase C; 1-phosphatidylinositol domain Y homology		
C:Keywords: phosphoric diester hydrolase		
F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X		
F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y		
Query Match	23.9%; Score 1524.5; DB 1; Length 997;	
Best Local Similarity	36.2%; Pred. No. 1.9e-70;	
Matches 348; Conservative 158; Mismatches 279; Indels 177; Gaps 20;		
OY	41	CMGAMDEGMQVNLKNGSKGLVRYLDEHNSCIRMRSRKN-EKAKTISDSIQEVSGR 99
DB	13	CISPMAGCELKKVRNRSIRYRFLTDQLALHWPESKDLERAKDISAKIRIGK 72
OY	100	QSEVFRYRDSFD--PNCCTSIYHSHRESLDIVSSSEVARTWGLRLMIGSIDE 156
DB	73	NETTFN--NGLADQCECAFSILHGENYESLDLVANSADVANIWSGLRLVRSRKP 130
OY	157	-DSIARQRT-RDQWLKQTFDEADKNGDLSIGEVLDLQNLNVLNPLRORYKQMFREAD 214
DB	131	LPMENQNTPRRMWKIKTFEADVDGNGIMLEDVSLKQNLNPLKEAKIRLKFKEIQ 190
OY	215	TDDHGT--LGEFEPCAFYKMMSTRDLVLMYTSNKHQNDLAASLQFLOEOKMAQV 272
DB	191	KSEKELTFVTEBEFEACECELTREVEVFLVQISKNNEXYDANDMLFLAEQGVTHI 250
OY	273	TLESQDIIIEFPCPEKNSKGLIGDFTNTSPAGDIFPNHHVHODTOPLSHYF 332
DB	251	TEICDITIRRLLESGKQKGLAIDGFTQYLISECQIFRDEQKVAQDMTOPLSHY 310
OY	333	ITSNHTYLVAGQILMSQSRDNYAVNLQAGRCVEVDCWDGPRGERTYHNGYTLKILF 392
DB	311	INSHMTYLLIEDQFRPADIDNGYITRALKMGCRSVELVDGSDNEPILCNRNMHTTWSF 370

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OY 393 KQVIEIINKYAFATKNEYPVILSTIENHCSTYQOKKMAOYLTDLIDGKLIDISSVSEDAATTL 452
Db 371 RSVIEYINKFAPAFASEYPIILICGNHCSTLPOQRYMAOQMKRYGKNTL-YTEAPLPSESYL 429
OY 453 PSPOMLKGKILVYKGLPLPANISEDAEEGYSDSDSADEIDDDCKLLNGDASTNRKRENT 512
Db 430 PSPERLKRMIYKGRKLPD--PDVLEGEYTD 461
OY 513 ANRKLDLSLKESIRCEDEPNPNFVSYTLSPSGKLGRKSAEDVESEGDAGASRRNGRLV 572
Db 462 -----EKAOMSR----- 469
OY 573 VGSFSRRKKKSKLKKAAVEEGDEGQDSPGQSGRGATROKTKMLSRALSDLVYKTSY 632
Db 470 -----MSVDYNG-----QKRIKRELSDLVYICKSY 497
OY 633 ATHDE--MEAASMWQVSEFETKAOHIIQOKPAQVLRNOOOLSKITYSSTRVYDSSNTN 690
Db 498 QYRDEFLSKSNTQWMCSCSFETESRIANEYPEDVYNNKRFSLRITYPSAMIDSSNIN 557
OY 691 PDPFNAGCOMVALYQSEGRMLQINRAKFSANGGCGYVLKFCGCMQGV--FNPNSDEPL 748
Db 558 PDPFNCGCOIYAAMNFQTPGPMMDLHTGWFLLONGGCGYVLRPSIMRDEVSYTSANKGLL 617
OY 749 POLKQVLRITISGOOLPKPRDSMLGDGEIIDPPEVEITIGPVDGREGQTRVYDDNG 808
Db 618 PGVSLAHIKIKITISQNPFPKGCACA--KGDYIDIPVYCLEIHGIPADGCEQKRTKYQONS 675
OY 809 FNPTEEILVFNVMPELALVRFIWDHPIDGRDFIGQRTLFASSIMPGRHYVLEGG--- 865
Db 676 DNPIDDEFEEQVNLPELAMIREFVYLDYDIDGDEFIGQTYTPECIOPQRYRHVPLRSFVG 735
OY 866 --MEBASIFVHAVSDISG-----KYQALGKGLFLR-----GP 898
Db 736 DIMEHVTLEFVHAIYNRSGGKAQKRSLSVRMGKAVREYTMRLRNIGIKITIDIFKIAVNP 795
OY 899 KPGSLD-----SHAAGRPARPSVQRLRLRPAASPTYSQKPG-----RGRFP 941
Db 796 LREALDMENMONAIVSTIKELGDPPT-ASLKQCLLTUSSLRTSDNTPSVSLVYKXDSFP 854
OY 942 EL 943
Db 855 YL 856

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RESULT 2
S62358 1inositol 1,4,5-trisphosphate-binding protein, 130k - rat
N:Alternate names: phospholipase C delta 1 homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S62358; PMID:569328
R:Kamenatsu, T.; Miumori, Y.; Watanabe, Y.; Ozaki, S.; Koga, T.; Iwanaga, S.; Ikehara, Y.
A:Title: A new inositol 1,4,5-trisphosphate binding protein similar to phospholipase C-delta 1
A:Reference number: S62358; PMID:8546702
A:Accession: S62358
A:Molecule type: mRNA
A:Residues: 1-1096 <KANI>
A:Cross-references: EMBL:D45920; NID:g1183843; PIDD:BAAO8351.1; PID:g1183844
A:Accession: S69328
A:Molecule type: protein
A:Residues: 172-191;228-242;1024-1034 <KAN2>
C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinositol-4-phosphate domain y homolog
F:401;543/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homolog
F:585;705/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y homolog

Query Match 23.88; Score 1517; DB 1; Length 1096;
Best Local Similarity 36.18; Pred. No. 5.2e-70;
Matches 349; Conservative 161; Mismatches 278; Indels 180; Caps 22;

```

QY	41	CHCANGBGMQWKLKSGSGVLFRFYUJLDBHNSCLHWPSSRN-EKAKISIDSIQEVSGR	99
Db	112	CJSEWAGELKKVRPNRSNRYNRFFTLTDLOALRWEPSSKDLCEKAKIDSAIEIRLKG	171
QY	100	OSEVFOERYDDGSEF--RPSCEIYHSGRESLIDJVSFSEVARYWGLYLMAAGISDE	156
Db	172	NIETFN--NGLADQICEDECAFSILHGENYESLIDJYANSADYANINWVSGLYVSRKOP	229
QY	157	-USLARQUT-RDQWLKOTFDEADKNGDSLSIGEVJQLLKLNVN-PROVKOMFREAD	214
Db	230	LDFMEGNQTPFRMWLKVFEADADVGNGIMLEDTVELIKQILNPTLESKRILKFEIQ	289
QY	215	TDDHQT--LGRFEECAFQKMSFTRODJYLMLMYLSNKHDLDAASLOFQYQKAGV	272
Db	290	KKEKELITVTEERCEAFCELCSTREYVYFLIOLSKKEKELDNDMLFLEWQGYTH	349
QY	273	TLSECODITIEOPERPENKSGKGLIGIDFTYNTSRPAGIDIRPNHHVNDMOTPLSHY	332
Db	350	TEDMCIDITIRREYLEDSEDRQKGLAIDFTQYLLSPESCDIPDPQKVAADMQPLSHY	409
QY	333	ITSSNNTYLVGQOLMSOSRYDMYAMVLAQGRQCYVNDCSGRDPERVHHGYTLTKILF	392
Db	410	INASHNTYLIEDQFGRPDINGVYBALMGCRSTIELDSDSPNEPILCRNNMMAMLST	469
QY	393	KQVLETINKYAFIKNEYVULSIENHCSVIOQKIMAGYLDLIDGKIDLSS-VSSEDAIT	451
Db	470	RSYLEVINKFAFVASEYPLIICLGNHCSLPQGRVWQOMKVFENKLYTEAPLSSE--SY	527
QY	452	LPSPOMLKGILYVKKKLPANISDGAEGEVSDESDADEIDDDCKLLNGASTNRKAVEN	511
Db	528	LPSPKLKHMIIVYCKRLPS--ESDLEGEVYTDH-----	560
QY	512	TAKRKLDSLIEKSTRDCEPDNNEVSUTLSPSGKLGRKSAEEDVESGEDAGASRRNGRL	571
Db	561	-----EAEKMSRR-----	568
QY	572	VWSEFSRRKKKSKLKAASVEEGDEQDSPGGSGRATQROKTKMLSRALSDLVYKTS	631
Db	569	VSGDYN-----GEQKHIVLCRELSDLVYSICKS	595
QY	632	VATHIDIE--MEASWQVYSFSETKAHQIILQKPAQYLRNOOLSRTPSSYRVYDSNY	689
Db	596	VQYRDFELSMKTQWYWEISCFSEFTLASIRINENEYDEDEVNYNKFFLSHYVPSAMRIDSM	655
QY	690	NPOPPNMGCOMVLANTQSEBGMLOLRKAFSANGGGGYLAKGCMQCY--FNPSSEDP	747
Db	656	NPODFNMGCOIVAMNFOQTRPMDLITGMFLONGGGGYLRLPSIMRDEVSYFSANTKGI	715
QY	748	LPGOLKQOLVLRISGOQLPKRPDMSMGDEGITIDPEVEVEIIGLVPVDSRQETRVYVDN	807
Db	716	VPGVSPLLIHIKILISGONFFRPKACA--KGDYIDPVVCEIHGIRADCSQKRTKVOQN	773
QY	808	GFNTWREETLVFNWHEMELIYLRVLWDHPRIQDPIGQRTLAFSSMFCGRHYVILEG--	865
Db	774	SDNPIFDETFFQVNADELTMVRVLIUDDYIGDEFIGQTTIPEFELQGRYHVRPLRSFV	833
QY	866	---MEASIFVHAVASDISG-----RVKQALGKGLFLR-----	897
Db	834	GDIHEHTLFEVHIATNRSGGAKQKSLSVRMGKKVRETMRLNIGLTIIDIPRIANH	893
QY	898	PKPESLD-----SHAQGRPARSVSQRILIRKIASAPYRSQKPG-----RRCF	940
Db	894	PLRAIIMRENMONALIVSKELGCLPPI-ASLKQCLITLSSRLTISDTPSVSLVMKOCF	952
QY	941	PEL-VLGT 947	
Db	953	PYLEPPLGT 960	

RESULT 3
S1413
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-2 - bov
N; Alternate names: phosphoinositidase C; phospholipase C-delta-2; triphosphoinositide

C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 02-Jun-2000
C:Accession: S14113; S04944
R:Meltrum, E.; Kitz, R.W.; Totty, N.; Parker, P.J.
Eur. J. Biochem. 196, 159-165, 1991
A:Title: A second gene product of the inositol-phospholipid-specific phospholipase C-delta
A:Reference number: S14113; M01D:91160548; PMID:1848183
A:Accession: S14113
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-764 <ME2>
A:Experimental source: brain
R:Meltrum, E.; Katan, M.; Parker, P.
Eur. J. Biochem. 182, 673-677, 1989
A:Title: A novel inositol-phospholipid-specific phospholipase C. Rapid purification and
A:Reference number: S04944; M01D:89325315; PMID:2753038
A:Accession: S04944
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 528-541, 'X', 543-553, 659-669 <ME2>
A:Experimental source: brain
C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-trisphosphate
C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog; pleckstrin repeat homology
C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signal
F:15-122/Domain: pleckstrin repeat homology <PLK>
F:134-166/Domain: calmodulin repeat homology <EF1>
F:110-202/Domain: calmodulin repeat homology <EF2>
F:292-435/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog
F:489-609/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
F:611-725/Domain: protein kinase C C2 region homology <KC2>

Query Match 22.98; Score 1459; DB 1; Length 764;
Best Local Similarity 39.28; Pred. No. 3e-67; Mismatches 263; Indels 134; Gaps 21;
Matches 342; Conservative 133;

29 FLNANILPVERRCGAMQEGMVKLRGSGKGLVRFYLLDEHNSCIKMRPSSKREKAK-- 86
3 YLLGGRIPINDLL-LMKGKTMKRVKSKKLRFRLLDDGWT-VHARQAGRAKPS 60
87 ISIDISGSEVSGROSEVFORPPDSFDPNCCSFYHSGHRESLDIVTSSEVARTWTGL 146
61 FSIISVDIVRGHSEELRNLA-EFPLEOGFTYFGRNSNDLVANSVQEQATWMOGL 119
147 KTLAAGIDEDSLARORTROMLKOTFDEADKNGDSLISGEVLOLHLKLVNLPORV 206
120 QLLVGFVTNMD---QQRLLDQMLSDMFQRKQDQMSGEGVQRLLHLMNVMDQETA 175
207 KMFREADTDHOGTLGEEFCAFYKMWSTRDLYLLMLIYSNKHDLDAASLORFQVE 266
176 FQLFGADT-SQSGTLEEGEEFVFKSLTORPEVDELFEKFSQSGOKLTLLFVDFQEE 234
267 QKMAVGTLESODDIEGEPCEPKSKGLLDGFTNTSRPAGDIFNPEHHNHQDMTO 326
235 QKGERASDLALIDREPSSEGLKRVHLSMDGFLGLYSKDDGDFPRTCHPLXDMTO 294
327 PLSHYFTSSHTYLVGDLMSQSRVDYAWYLAQACRCEVDCWDGPGEPYVHGGTTL 386
295 PLNHVYINSHTYLVGDLQCGSSVEGYIRALKRCRCVEVDLMDGSGEPYVHGGTTL 354
387 TSKILFKDVIETINKAFYKNEYPTLSTENICSYIOOKMAQVYTLTDLGKLLDSSVSS 446
355 TSRIPIKDVVAALGOYAFQTSYPTILSTENICSEWDEIYRHLTELGLQDLTTLALDG 414
447 EDATTPSPOMLKGITLVGKRLPANISDAEGEVSDSDASDELDDCKLLNGDASTNR 506
415 OPTQPLSPEDLKGITLVGKRLMEEEEPALAEAGQA-RLDLEQL----- 464
507 KRVENAKRRLDLSKESKIRDCEDNNFVSSTLSPLSGKLGKSKAAEDVEGEGENAGSR 566
465 -----ESRPOD-----LSP-----RSED----- 477
567 RNRLLVGSFRRKKKSKLKAASVEEDGDDSPGGSGRATROKTKMLSLRSLDLY 626

478 -----KKKKPKAI-----LCRALSALV 494
627 KYKSAVA-----PHDIEMEAASSMOVSSEETKANOILLOOKPAOYLRFNOQLSTRYSSY 682
495 VYKAVFTYSFTH-SREHYHFETSSSEETKAKSLIEAGDEFPQHANMOLSTRYPSGL 552
683 RVDSNVNPOPEWNAAGCQAVANTQSEGRMLQUNRAKTSANSGCYLKPSCM-CQGVF 740
553 RTSSNVNPOPEWNAAGCQAVANTQSEGRMLQUNRAKTSANSGCYLKPSCM-CQGVF 612
741 NPNSDEPLPEQLKKOLY-----LRITSGQLKRPDMSMLGDEGLIDPFVEIIGLPVD 795
613 HP-EREISPFKAQTLTIDEPWLVISGOOLKRVDT--KEQSTVDPVLRVELFGRPD 667
796 CSRQRTVVDNGFNPNWEETLVFWVHMPDIALVRVWDHPDR-DFTGORTLAFSSM 854
668 TTRQETISVENNGFNPNWGTLCFRLVFEALIRRVVADYDMKSRNDPILGQYTLFPGCM 727
855 MFGYRAVYL--EG--MEASIFVHVAVSDIS 881
728 QQGYRHHLLSKQGLSLHPASIFVHICTQEV 759

RESULT 4
T32374
hypothetical protein K10F12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text change 28-Jul-2000
C:Accession: T32374
R:Wohlmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid K10F12.
A:Reference number: 221157
A:Accession: T32374
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-895 <KOH>
A:Cross-references: EMBL:AF025462; PIDD:AA871005.1; GSPDB:GN00021; CESP:K10F12.3
A:Experimental source: strain Bristol N2; clone K10F12
C:Genetics:
A:Gene: CESP:K10F12.3
A:Map position: 3
A:Insertions: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1;
C:Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 20.3%; Score 1297; DB 2; Length 895;
Best Local Similarity 35.0%; Pred. No. 7.3e-59;
Matches 310; Conservative 138; Mismatches 266; Indels 172; Gaps 23;

38 VERRCGAMQEGMVKLRGSGKGLVRFYLLDEHNSCIKMRPSSKREKAKISIDSIOEVS 96
46 VSDCMWYMQTGSDFYKLRNTKQFRFRFSLDADLSYIMWTNNKPKHARALDEIEIR 105
97 EGNQSEVPORYDDGSP---DPNCCSFYHSGHRESLDIVTSSEVARTWTGLRYLMAGI 153
106 LQANTLL-RSSDEVFTDQECLESTIYGNYELDLIASGCDANITWYGMAALNSNK 164
154 SD-EDSLARORTROMLKOTFDEADKNGDSLISGEVLOLHLKLVNLPORVQKQFRE 212
165 YECKPSSQFATLREKIRISVDEFTKNGHLDQTAFAKALHINSRISHRLNKLKE 224
213 ADTDDHOGTLGPE-----PCAFYKMWSTRDLYLLMLIYSNKHDLDAASLORF 262
225 V-----TGAESERSGKIEKSHFVDTLKEIGTRPEYFLWVRKAN-KDTLSQDLRLF 276
263 LQYEQKMAVGTLESODDIEGEPCEPKSKGLLDGFTNTSRPAGDIFNPEHHNHQ 322
277 LREQGMVGYTTCNCTLLIQYVPCSEARBNMLVDTGFTSPLSPDGVDPPNRRVVTM 336
323 DMQPLSHYFTSSHTYLVGDLMSQSRVDYAWYLAQACRCEVDCMD-----GPDGP 378

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Db 337 DMKQFSSXYFTSSSRKSTLYEDOL-GPSSSDGFSALKRNCRFLEIDWPNENDGJTER 395
QY IVHHGYTLTKILFKVDYETINTKAYAFIKNEYPVLLSTIENHCSVYQOKMAOYTLIDGDK 438
Db 396 MVWNGQRTATSKITISSALRIREFAFERSRYPDLTKVSVHCSTDMQVAMLYTHLIGTR 455
QY 439 LDY---SSVSEDAATLPSQMLKGLTVKGLLPANISEDAEAGEVSDSDADEIDDC 495
Db 456 LYLKRPDPTWMDDEKNCPTWDFONRIIVGKLD---NDTDSGEVSEED--DSL----- 506
QY 496 KLNGDASTNKKRVENAKRLDLSLEKIRCEO-----PNNFSVTLSPSGKLGKRS 550
Db 507 -----ASTRR-----KSKRIQCKELSDLVPEFVFNKTLN----- 537
QY 551 KAEDVES---GEDAGARRNGRLVVSFSRRKKSGSKLKAASVEBGDGDSPGGQSR 607
Db 538 ----DLSTAPGSTTMSRRK----- 554
QY 608 GATROKTKMLSLRLSDLVYTKSVATHIDIEMAASSWVSFSETKAHQILQOKPAQYL 667
Db 555 -----LASVTESTCLRLMTYATBERG 575
QY 668 RFNQOOLSRITPSSYRVDSSNYPQPFMAGCOMVALNTQSEGRMLQLNRAKFSANGCG 727
Db 576 QATRNCAVRFEPNPSRVDSNLNPOEFMNGVQVACLNTQPELMDLQEGKFSMDGCG 635
QY 728 YVLRPGCMCGVFNPSSEDPPLQOLKQVLRLISGQQLPKPRDSMLGRGETIDPEFVY 787
Db 636 YVLRPVMMDMFPSPDRPTSPQI---LHLRLISGQLPRPGS--NAKGSADPEFVY 690
QY 788 EILGLPVDSCREQTRVVDNGFNPTEETLVFVNHPELALVFLWHDPIGRDFTIGOR 847
Db 691 EYVGLGDCDAEERTKRVYRDSINPSFDESFOQVSVPELALVFLWHDPIGRDFTIGOR 750
QY 848 TLAFSSMPGGRHYVY---EG--MEASIFVAVASDI--SGKVRQ 886
Db 751 TLPECLDGPYRHYLYLNNEGDPLEHATLFLVAVATNRRGSGKAKK 796

RESULT 5
PC4183
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 - Chinese
M:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide ph
C:Species: Cricetus griseus (Chinese hamster)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: PC4183
R:Leoni, M.A.; Silbert, D.F.
Biochem. Biophys. Res. Commun. 224, 382-390, 1996
A:Title: Genomic organization of the hamster phospholipase C-delta1 gene: Differential
A:Reference number: PC4183; MUID:96295498; PMID:8702399
A:Contents: fibroblast
A:Accession: PC4183
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-745 <LEO>
A:Cross-References: GB:U50564
C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosph
A:Gene: PLCdelta1
A:Introns: 56/1; 132/2; 175/3; 253/1; 320/2; 368/3; 418/3; 471/3; 525/1; 564/1; 623/3; 6
C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat homol
F:8-117/Domain: pleckstrin repeat homology <PLK>
F:129-161/Domain: calmodulin repeat homology <CFI>
F:165-197/Domain: calmodulin repeat homology <CFI>
F:287-429/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:480-601/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:603-713/Domain: protein kinase C C2 region homology <KC2>

Query Match 20.2%; Score 1287; DB 1; Length 745;

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Best Local Similarity 35.8%; Pred. No. 1,9e-58;
Matches 307; Conservative 128; Mismatches 279; Indels 144; Gaps 16;

QY 44 AMOEGQWYKLRGSGKGLVRFYLDHRSCTWRRSRK-----NEKAKSINDSIOVSEGR 99
Db 10 ALLKSGQLKLVKSSSRKRRRTKLODECKTI--WQSRKMRSPESQSLIEDIOEVRMGH 68
QY 100 QSEVFORYPDGSFDPNCCPSIYHSGHRESLDIVSTRSEVAFRTVGLTYLMAGSDSDSL 159
Db 69 RTEGLEKFA-RDIPEDRCPSIYFKDQNTLDLILASADAOHWQGLAKTI---IHSQSM 124
QY 160 ARROTRDQWLKQTFDEADKNGDSSLGSEVYLQHLKTNVLPKRVKQMPREAD---TD 216
Db 125 DQROKIQ-HWISCLRKADKKNQKNMFKELDFLKEINIDYDSTARKIFRECDHQTQD 183
QY 217 DHQGLTFEEPCAFYKMNSTRDLTYLMLTYSNHNDHDAASLQRFLOVEQKMGAVLES 276
Db 184 ----SLEDEIRTFYKMLQRAEIDRVFAEAAGSETLVSKLVTFQHQOOREAPAL 239
QY 277 CODLIEQEPCEPKNSKGLLIGDFTYTRSPADIFNPEHHHODMTOPLSHYFTSS 336
Db 240 ALSLIEREPESETAKAQOMTKDGFIMYTLSDASAFSLAHRRVYQDMDQPLSHYLVSS 299
QY 337 HNTYLVGDOLMSOSRVDMYAVWLQAGCVCVVDMDGDPGEPIYHNGYTLTKILFKDVI 396
Db 300 HNTYLVLEQDLGSPSTETAYITALCKGRCLELDCWDGPNODEPIYHGYTFSKILFYDVL 359
QY 397 ETINKYAFIKNEYPVLLSTIENHCSVYQOKMAOYTLIDGKLDLSVSSSEDAATLPSQ 456
Db 360 RAIIRDYAFKASPIYVILLSTIENHCSLEEQOVVAHRLKAILGML-LDPLDGYTMSLSP 418
QY 457 MLKGLIYKGGK-----LPANISEDAEAGEVSDSDADEIDDCKLNGASTNKKRVEN 512
Db 419 OLKGIILKGGKFGGLPAGGNGPETTVDSDEEAEMDE----- 460
QY 513 AKRLDLSLEKSLRDCEDPNFVSSTLSPSGKLGKRSKAEDVSEGDAGARRNGRLV 572
Db 461 -----A 461
QY 573 VGSFRRKKSGSKLKAASVEBGDGDSPGQSGRCATROKTKMLSLRLSDLVYTKSV 632
Db 462 VRSVOOKSKEDKLNVAPE-----LSDVYICKSV 491
QY 633 ATHDIEMAAS--WQVSFSETKAHQILQOKPAQYLRFNQOOLSRITPSSYRVDSSVY 689
Db 492 HFGGFSNPSTSGCAFYMAGFSENRLRLQEGCNFNFRHNSHLSRITPAGRRDSSVY 551
QY 690 NPQPFMAGCOMVALNTQSEGRMLQLNRAKFSANGCGYVLRGCM--COGVFNPSSEDP 747
Db 552 SPVEMNMGCOIALNFOYTPGPMEDVYLGFDNGACGYLPAFLRDPDTAFNPRALQ 611
QY 748 LPQOLKQVLRLISGQQLPKPRDSMLGRGETIDPEFVEIILGYPDCSRQOTRYVDN 807
Db 612 GPWMAQKRLRLVRIISQQLPKPKVS-----KNSLVDPKVLVEHVGQDVASRQVATINN 667
QY 808 GFNPTEETLVFVNHPELALVFLWHDPIGR-DFIGORTLAFSSMPGRHYVY--- 863
Db 668 GFNPMDWTEFEFVAVAPDLALVFLVEYEDYDASSKNDFTIGOSTIIPNNSLKGGRHYHLLSK 727
QY 864 --EGMEASIFVAVASD 879
Db 728 NGDQHSATLFLYKISLD 745

RESULT 6
A55943
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 (vai
M:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
C:Species: Homo sapiens (man)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: A55943
R:Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King,
J. Biol. Chem. 270, 5495-5505, 1995

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A:Title: Cloning and identification of amino acid residues of human phospholipase Cdelta
 A:Reference number: A55943; M01D:95197554; PMID:7890667
 A:Accession: A55943
 A:Molecule type: mRNA
 A:Residues: 1-756 <CH2>
 A:Cross-references: GB:009117; NID:9483919; PIDN:AAA73567.1; PID:9483920
 A:Experimental source: aortic smooth muscle
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphospho
 C:Genetics:
 A:Gene: GDB:PLCD1
 A:Cross-references: GDB:6075994
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
 phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat homol
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signa
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:176-208/Domain: calmodulin repeat homology <EF2>
 F:298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
 F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 20.1%; Score 1285; DB 1; Length 756;
 Best Local Similarity 35.6%; Pred. No. 2.4e-58;
 Matches 308; Conservative 134; Mismatches 265; Indels 158; Gaps 19;

QY 44 AMOEGMOMVTLRGSGKGLVRFYLLDEHRSCTRMPSRK---NEKAKISIDSIOEVSEGR 99
 DB 21 ALLKGSOLIKVSSSSWRERFYKLOEDCKIT-WQESRKVMKRPESLFEDIOEVRMCH 79
 QY 100 QSEVFORYP---PDGSPDNCFCSIYHSHRESLDVSTSEVARTWTGLRTYLAAGISD 155
 DB 80 RTEGIEKFAVDPE---DRCFEIVFKDQKNTLDLIAESPADAQHMVGLNHT---IHH 131
 QY 156 EDLSARQRTRDOLKTPPEADKNGSGSISIEGVQLLHKLVNVPDQVKOMPREAD- 214
 DB 132 SGSMDOQRKLO-HWHSCLRKADKNKNKMSFEKLOFLKELIYOVDSTARKITFECH 190
 QY 215 --TDHOGTGLFEFCFAFYKMASTRDLYLMLTYSNHKNHDLDAISLORELOVEORMAGV 272
 DB 191 SOTD-----SLEDEIEAFYKMLQTVRVEIDRTPAAGPGFTSLVDLVFLAQOREEAA 246
 QY 273 TLESCODIIEFEPCEPKNSKGLGIDGFNTYTRSPAGDIFNEHHVHODMQLPSHYF 332
 DB 247 GPALALSLIEHYESETTKAQRMTKDFMTYLLSADGSFSLAHHRYVDMQOSHYL 306
 QY 333 ITSSNHTLVVDOLMSOSRVDMYAVLQAGRCVVDVCMGDPDEPIVHHGYTLTKTLF 392
 DB 307 VSSNHTLVLEDOLAGPSSTATYTRALCKGRCLEDCMGPNRPIIYHGYFTSKTLF 366
 QY 393 KDVETINKYAFIKNEYPVILSIENHCSVLIQOKMAQYTFDILGDKL---DLSSVSEDA 449
 DB 367 GCVLAIDYAFKASPYVILSTLENHCTLEGOVRMARHLIAILGPMILNRPDLGVN--- 423
 QY 450 TILSPQMLKGLILYKGLKPLANTSEDAEAGE-----VSDEDSADEIDDDCKLNGASTN 505
 DB 424 -SLSPEDKLGKILKGLGGLPPGGEGGPATVVSDEDAEMEDAEV----- 473
 QY 506 RKRVENTAKRKIDSLIKESKIRDCEDPNPNSVSTLSPSGKLGKRSKAEDEVESGEDAGAS 565
 DB 474 RSRVQHKP-----KEDKLR----- 487
 QY 566 RNRGLVGSFSRRKKKSKLKAASVEEGDEGQDSPPGQSRGATROKTMKLSRALSDL 625
 DB 488 -----LAQELSDM 495
 QY 626 VKYTSVATHDIEMEA---SSMOVSFSETRKAHIILOOKPAOYLRFNQOOLSRITSSY 682
 DB 496 VIYCKSVHFGGSPGTPGQAFYEMASSENKALRLDLDESGNGYRAHVGSLSTRYAGW 555
 QY 683 RVDSNYPNPFTWAGCCQVVALYQSEGRMLQLNRAKFSANGCGCYVLKPCM--COGVF 740
 DB 556 RIDSNSYSPVEMWNGGQVALNFQTPGPEKMDVYQDRFQDNAGACGYVLKPAFLRDPNGTF 615

QY 741 NPNSDEPLFGOLKODLVRLIISGQQLPKPRDSMLGDCRCEITDPVEVEIICLPYDCSREQ 800
 DB 616 NPKALAQGPWMAKRRLNIRIVISGQQLPKVKN-----NKNSIYDPKVTVEIHGSDVARSQ 671
 QY 801 TRVVDNGNRPVTEELVYVNMVMPETALVRLVMDHDIQR-DFICQVTLFSSMMMGYR 859
 DB 672 TAVITNKGPNWMDVEFAEVVVDLALRFLVEDYDASSKNDFIGOSTIFLNSIKQGR 731
 QY 860 HVLV-----EGMEASIFVHVAVSD 879
 DB 732 HVHLSKNGDQHSATLFFVKISIQD 756

RESULT 7

B28821
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 02-Jun-2000
 C:Accession: B28821; 155942
 R:Sub, P.G.; Ryu, S.H.; Moon, K.H.; Sub, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A:Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; M01D:88270495; PMID:3390863
 A:Accession: B28821
 A:Molecule type: mRNA
 A:Residues: 1-756 <SUH>
 A:Cross-references: GB:M20637; GB:J01336; NID:9206219; PIDN:AAA4186.1; PID:9206220
 A:Experimental source: brain
 R:Yagisawa, H.; Tanase, H.; Nojima, H.
 J. Hyper tens. 9, 997-1004, 1991
 A:Title: Phospholipase C-delta gene of the spontaneously hypertensive rat harbors pol
 A:Reference number: I55942; M01D:92098966; PMID:1684614
 A:Accession: I55942
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411, 'M', 413-422, 'S', 424-462, 'D', 464-626, 'A', 628, 'K', 630-667, 'A', 669-756
 A:Cross-references: GB:S74591; NID:9241276
 A:Note: this translation is not annotated in Genbank entry S74591, release 113.0
 A:Note: spontaneous hypertensive mutant
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphos
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p
 phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat ho
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; st
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:176-208/Domain: calmodulin repeat homology <EF2>
 F:298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
 F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y
 F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 19.7%; Score 1258; DB 1; Length 756;
 Best Local Similarity 35.8%; Pred. No. 5.8e-57;
 Matches 308; Conservative 131; Mismatches 273; Indels 148; Gaps 19;

QY 44 AMOEGMOMVTLRGSGKGLVRFYLLDEHRSCTRMPSRK---NEKAKISIDSIOEVSEGR 99
 DB 21 ALLKGSOLIKVSSSSWRERFYKLOEDCKIT-WQESRKVMKRPESLFEDIOEVRMCH 79
 QY 100 QSEVFORYPDGSPDNCFCSIYHSHRESLDVSTSEVARTWTGLRTYLAAGISDSDL 159
 DB 80 RTEGIEKFA-RDIPDRCFEIVFKDQKNTLDLIAESPADAQHMVGLNHT---IHHSGM 135
 QY 160 ARQRTRDOLKOTFDEADKNGDGLSLGELYQLLHKLVNVPDQVKOMPREAD---TD 216
 DB 136 DORQKLO-HWHSCLRKADKNKNKMSFEKLOFLKELIYOVDSTARKITFECH 194
 QY 217 DHOGTGLFEFCFAFYKMASTRDLYLMLTYSNHKNHDLDAISLORELOVEORMAGV 274
 DB 195 ----SLEDEIEAFYKMLQTVRVEIDRTPAAGPGFTSLVDLVFLAQOREEAPAL 250
 QY 275 ESCODIIEFEPCEPKNSKGLGIDGFNTYTRSPAGDIFNEHHVHODMQLPSHYFIT 334

Db 251 --ALSIEREPESEETAKAROMTKDGLMTLISADGNAFLAHRRYVODMDQPLSHYLS 308
 QY 335 SSHAHTYLVGDOLMSOSRDVMTAWVLQAGRCVENDCMGDPGEPIVHHGYTLTSTKLFKD 394
 Db 309 SSHAHTYLVGDOLMSOSRDVMTAWVLQAGRCVENDCMGDPGEPIVHHGYTLTSTKLFKD 368
 QY 395 VJETINKFAFKNEPVYLTSTENHCSTYQOKMAQYLTDLIGDKLIDSSVEDATPLPS 454
 Db 369 VIRAIRDYAFKASFPYLTSLLENHCSTLEQORVMAHRLALIGPLT-LDQPLDGVYTSILPS 427
 QY 455 POKLKGKILVKGK-----LPANISEDAGEVSEDESDADELDDCKLLNGASNNRRVE 510
 Db 428 PEQJLKGKILVKGKILGGLLPAGENGSEATVSDVEAEAEDEAV-----RSQVQ 478
 QY 511 NTARKRLDILKEKIRDCEDPNFVSVTLSPSGKLGKRSKAEDVDSGEDAGASRRNGR 570
 Db 479 H-----KPKRD----- 484
 QY 571 LVVGSFRRKKKSKLKKAASVEEGDGGDPSGGQSGATRQKTKMLKLSALSDLYKTK 630
 Db 485 -----KIKLVBELSDMTIYCK 500
 QY 631 SVATHDIEMEAASS---WOVSSFSEETAKHQLQOKPAQYLFNOQOLSRITPSSRYDSS 687
 Db 501 SVHGGFSSPSTSGQAFYEMASFSERALLDQESGNGFVRHNVSCLSRTYIPAGWRTDSS 560
 QY 688 NYNPOPFMMNCCOMVALANTOSSEGRMQLNRAKFSANCGCYVLKPCGM--CQGFVFNPNSE 745
 Db 561 NYSVEVMNNGCGOYVALNFOTPGPEMDVYLGCFODNCGCYVLPAPFLRDPNTTFSRRL 620
 QY 746 DPLPGQKQOLVRIISGQOLPKPRDMLGDRGEITDPFEVEITLIPVDCSREQTRVD 805
 Db 621 TQGPWMPERLRYRIISGQOLPKVKN---NKNSIYDPKVIYHIGVGRGTSRQRAVIT 676
 QY 806 DNGFNPTWETLVFWVHMPIALVRLVWDHDPGR-DEIGORTLAFSSMMGGRHRYVL- 863
 Db 677 NNGFNPMDEFEFEVYVLPDLALVRMVEDYSSSKNDIGOSTIPWNSLKQGYRNVHL 736
 QY 864 ----EGMEASIFVAVASD 879
 Db 737 SKNGDQHPSATLFEVKISID 756

RESULT 8
 C28821
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 - bovine
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide ph
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 02-Jun-2000
 C:Accession: C28821
 R:Stahl, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A:Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MUID:88270495; PMID:3390863
 A:Accession: C28821
 A:Molecule type: mRNA
 A:Residues: 1-709 <SUH>
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosph
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
 C:phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat homol
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signa
 F:16-81/Domain: pleckstrin repeat homology (fragment) <PLK>
 F:93-123/Domain: calmodulin repeat homology <EF2>
 F:129-161/Domain: calmodulin repeat homology <EF2>
 F:251-393/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F:444-565/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
 F:567-677/Domain: protein kinase C C2 region homology <KC2>

Query Match 19.5%; Score 1244; DB 2; Length 709;
 Best Local Similarity 35.9%; Pred. No. 2.8e-56;
 Matches 298; Conservative 124; Mismatches 255; Indels 154; Gaps 19;

OY 73 CIRRRPSKKNKAKISIDSIQVSEGRSEVFOR-----PDGSPDNCFCSYHSHRES 128

Db 9 CTITW---QEEESQLFSTIEDIOEVRMGRHTEGKEFARVPE-----NRCSIVFKQDRNT 60
 QY 129 LDIIVTSSEVARTVGLRYLMAGISDEDSIARQRTROWLKQTFDEKDKNGDSLSIG 188
 Db 61 LDIIVTSSEVARTVGLRYLMAGISDEDSIARQRTROWLKQTFDEKDKNGDSLSIG 116
 QY 189 EYVOLLHLKLVNLPKRVYKQMRDAD---TDHOGTLGFEFCFVKKMSTRDLYLML 245
 Db 117 ELONFLKEINLQVDDSYARKIFKECHDSQTD---SLEDEEYETYYKILTORKEIDRFE 172
 QY 246 TYSNHDHDLAASLQRFLOVEOK--MAGVTLSCQDIIQEFPCENSKSLGIDGFTN 303
 Db 173 EATGSKETLSVQQLVYTFLOHQREBAGAL--ALSLEIREPSTAAQROMTDGLM 230
 QY 304 YTRSPAGDIFNPBHHHODMOTPLSHVFTTSSHTYLVGDOLMSQSRDMYAWVLQAGC 363
 Db 231 YLISADGSAFIDLADRVYQDMQDQPLSHYLVSSHTYLVGDOLMSPSTEAIVTALCKGC 290
 QY 364 RCVEVDCMDGDPGEPIVHHGYTLTSTKLFKDYETINKFAFKNEYPVYLTSTENHCSTYQ 423
 Db 291 RLLELDMDGPRQEPYLYHGYFTSKILFCDVVRAIRDYAFKASFPYLTSLLENHCSTLEQ 350
 QY 424 OKMAQYLTDLIGDKLIDSSVEDATPLSPOMLKGKILVKGKRLPANISEDAGEE-- 481
 Db 351 QRYVMAHRLITLGPML-LDRPLDGVYTSILPSPEOLRGKILVKGKILGGLPGEENGPEA 409
 QY 482 --VSEBDSADELDDCKLLNGASNNRRVENYAKRKILDSIKRDCEDPNFVSVT 539
 Db 410 TVVSDDEDAEAEDEAV-----RSQVQHS-----KDKLR----- 440
 QY 540 LSPSGKLGKRSKAEDVDSGEDAGASRRNGRLVYGPSRRKKKSKLKKAASVEEGDGG 599
 Db 441 ----- 440
 QY 600 DSPGQSGATRQKTKMLKLSALSDLYKTKSVATHDIEMEAASS---WOVSSFSEETAKH 656
 Db 441 -----LAKELSDMTIYCKSVHFRGPPSGTSGQAFYEMSSFSERALL 482
 QY 657 QILOOKPAQYLFNOQOLSRITPSSRYDSSNYPQPFMMNCCOMVALANTOSSEGRMQLN 716
 Db 483 RLQESGNGFVRHNVNHSRTYIPAGWRTDSSNYSPEVMNNGCGOYVALNFOTPGSEMDV 542
 QY 717 RAKFSANCGCYVLKPCGM--CQGFVFNPNSEDPPLQOLKQOLVRIISGQOLPKPRDML 774
 Db 543 QGRFLNDACGYVLPAPFLRDPNTTFSRRLAHGPMWTPKRLAVRYISGQOLPKVKN--- 599
 QY 775 GDRREITDPFEVEITLIPVDCSREQTRVDNNGFNPTWETLVFWVHMPIALVRLVW 834
 Db 600 --NKNSIYDPKVIYHIGVGRGTSRQRAVYTNNGFNPMWTELEFEVAVDELALVRVVE 658
 QY 835 DHDPIGR-DEIGORTLAFSSMMGGRHRYVL-----EGMEASIFVAVASD 879
 Db 659 DYDASSKNDPIGOSTIPLKSLKQGYRNVHL 756

RESULT 9
 S00666
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) isozyme II -
 N:Alternate names: phosphoinositidase C-specific phospholipase C-II; phospholipase C, 148K
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 04-Feb-2000
 C:Accession: S00666
 R:Stahl, M.L.; Ferenz, C.R.; Kelleher, K.L.; Kritz, R.W.; Knopf, J.L.
 Nature 332, 269-272, 1988
 A:Title: Sequence similarity of phospholipase C with the non-catalytic region of src.
 A:Reference number: S00666; MUID:88156363; PMID:2831461
 A:Accession: S00666
 A:Molecule type: mRNA
 A:Residues: 1-1291 <STA>
 A:Cross-references: EMBL:Y00301; NID:9638; PIDN:CA68406.1; PID:9639
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosph
 diesterase domain Y homology; SH2 homology; SH3 homology

C:Keywords: phosphoric diester hydrolase
 F:322-464/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain x hom
 F:550-657/Domain: SH2 homology <SH21>
 F:668-756/Domain: SH2 homology <SH22>
 F:798-846/Domain: SH3 homology <SH3>
 F:952-1073/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain y hom

Query Match 15.8%; Score 1009; DB 2: Length 1291;
 Best local similarity 26.1%; Pred. No. 6.5e-44;
 Matches 308; Conservative 151; Mismatches 317; Indels 404; Gaps 35;

74 IRRPSSRKNEKAKISIDISIOEVSEGRSEVFORV-PDGSF--DPNCCFSIYHGS--HRES 128
 Db ITWSRGADKEGADIREIKELRPGKTSRDPYQEDPAFRPDQSHCFVILYGMERLKT 119
 Oy 129 LDVSTSEVARTWGLRYLMAGISDEDSL-ARRORTDQWLKOTFEDADKNGDGLSI 187
 Db 120 LSLQATSEDEVNMWIRGLTWLM-----EDTLQAPPLQIERMLRKQFYSVDRNRREDRISA 174
 Oy 188 GEVYLQLLHKLNLVNLPRQVKOMFREADTDDHOGT--LGFEEPCAFYK--NMSTRDLYLL 243
 Db 175 KDLKNNLSQVNTFRVPMNR--FLREKLTLEQRTSDITTYGQFQALYSLMTYSAOKTMDLP 231
 Oy 244 MLYTS-----NHKDHLDASLQRF-----LQVEQKAGVLTSCODITIQ 283
 Db 232 FLRASALRAGERELCRVSLPERFOQLFLEYQGLMAVDRLOVQEFMLSLRDLPLREIEBP 291
 Oy 284 FEPCPEKNSKGLIGIDGFTNTYTRSPAGDIFNPEHHVHOD--MTQPLSHYFTSSHNTYLV 342
 Db 292 Y-----FLDEFTYFLFSKENSISWNSQLDEVCPTMNNPISHWISSSHNTYLT 340
 Oy 343 GDOLMSQSRVDYAWYLQAGRCVEVDWCMDGPDGEPIVNHGYTLTSKILFKVDIETINKY 402
 Db 341 GDQFSSSSSEIATARCRLMCRCEIEEDCWDGPGPMVYIYGHITLTKIKESDVLHTIKH 400
 Oy 403 AFITKNEVPILSTIENHCVTIQKKMAQYLTDLIGDKLIDSSVSESDATILPSPQMLKGI 462
 Db 401 AFVASEPVLITIEDHCSIADQORMAQYFKKVLGDTL-LTRPVDAADGLPSNQLKRI 459
 Oy 463 LVYGGKLPKPA-----NISEDAEAG----- 480
 Db 460 LIRKKILAEASAEVETVSWYSNDISNISKINILYLEDPVNHFWPHYFVLTSKIY 519
 Oy 481 -EVSDESDADEIDDCILKNG--DASTNRKV-----ENTAKRKIDS----- 519
 Db 520 SEERSQGNDEDEEPKREASGSETLHSNEKWFHGKLGAGRGRIARELLTEYCIEGTAP 579
 Oy 520 ---LIKES-----KIRDC----- 529
 Db 580 DGSFLVRESETEVDYTLSEFWRNCKVOCHRIHSKQDAGTRKPFILTNLVDPDSLITHY 639
 Oy 530 ----- 532
 Db 640 QQVPLRCNEFMRLSERVPQTNHESKEWYHASTLRAQAEHMLMRVPDGAFLVKKRNEP 699
 Oy 533 NNFVS----- 538
 Db 700 NSYALSFAREGKIKHCRCVQOEGQTYMNGSEFDSLVDLISYERKHPYLRKMKLRYPINEE 759
 Oy 539 -----TISPS-GKL--GR-----SKAAEE 554
 Db 760 ALEKIGTAEPDYGALYBGRNPGFYVYANPMPTFKCAVKALEFYAQRDELTFTKSAITQ 819
 Oy 555 DVESE-----DAGASR----- 566
 Db 820 NVEKEGGMWRGDDYGGKQOLMPSPSYVEWVSPALPEPERHLDENSPDGLKRGVLDVP 879
 Oy 567 -----RNGRLVGSFSRKKKSKLKAASVE-----GDQDODSPGQOSR 607
 Db 880 ACQIAYREGKNNRLEFVSISMAVHMSLDVAADSOEELQDWKIREVAQOTARLITE 939
 Oy 608 GATROKTKMLSRALSDLVYKTKSVATHD--TEMEAASWQSSSFSETKAHQILQO-KPA 664

Db 940 GKMMERR-KKIALELSELVYVCPVPDEKICTERACVYDMSSFPETKAEKYVNKAKG 998
 Oy 665 QYLRFNQOOLSRITPSSRYVSDSSNYNPQPFWMAGCQWALNYSOEGRMQLNRAKESANG 724
 Db 999 KFLDYNNQLQSLRITPKQGRDSSNYDPLPMWIGCSQVVALNFGQPPKPMQNALFLAG 1058
 Oy 725 GCGVYLKPCMCQGVENPNSEDLPLGQLKKOLYLRISGQLKPKPRSMGLDGEITIDPF 784
 Db 1059 HCGVYLQPSVYRDEAFPEFDEKSLRGLEPCACIEVIGARHLK-----NGRG-IYCPF 1111
 Oy 785 VEVEITGLPVDCSRQFRVYDNGENFPTW--EETLVFWHPEILVRFVMDHDPIC-RD 842
 Db 1112 VEIEVAGAEVYSIQKTEFVYDNLNVPYAKPAPHQISNPEFAPFLFVYEEDEMFSDON 1171
 Oy 843 FIGORTLAESSMMPGIRHY-----YLGEERASIFVNAV 877
 Db 1172 FLAQATFPVKGKLTGYRAVPLKNNYSEGLFELASLVLKIDV 1211

RESULT 10

A36466
 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 04-Feb-2000
 C:Accession: A36466
 R:Burgess, W.H.; Dionne, C.A.; Kaplow, J.; Mudd, R.; Friesel, R.; Zilberstein, A.; Sc
 M01. Cell. Biol. 10, 4770-4777, 1990
 A:Title: Characterization and cDNA cloning of phospholipase C-gamma, a major substrat
 A:Reference number: A36466; MUID:90355993; PMID:2167438
 A:Accession: A36466
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1290

 A:Cross-references: GB:M34667; NID:q190037; PID:AAA36452.1; PID:q190038
 C:Genetics:
 A:Gene: GDB:PLG1; PLC1
 A:Cross-references: GDB:120299; OMIM:172420
 A:Map position: 20q12-20q13.1
 C:Superfamily: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase II; 1-phosph
 A:Keywords: phosphoric diester hydrolase
 A:Keywords: phosphoric diester hydrolase
 F:322-464/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain x
 F:550-657/Domain: SH2 homology <SH21>
 F:668-756/Domain: SH2 homology <SH22>
 F:798-846/Domain: SH3 homology <SH3>
 F:952-1073/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain y

Query Match 15.6%; Score 997.5; DB 2: Length 1290;
 Best local similarity 25.1%; Pred. No. 2.5e-43;
 Matches 306; Conservative 157; Mismatches 331; Indels 423; Gaps 35;

74 IRRPSSRKNEKAKISIDISIOEVSEGRSEVFORV-PDGSF--DPNCCFSIYHGS--HRES 128
 Db 60 ITWSRGADKEGADIREIKELRPGKTSRDPYQEDPAFRPDQSHCFVILYGMERLKT 119
 Oy 129 LDVSTSEVARTWGLRYLMAGISDEDSL-ARRORTDQWLKOTFEDADKNGDGLSI 187
 Db 120 LSLQATSEDEVNMWIRGLTWLM-----EDTLQAPPLQIERMLRKQFYSVDRNRREDRISA 174
 Oy 188 GEVYLQLLHKLNLVNLPRQVKOMFREADTDDHOGTLCGFEEPCAFYK--NMSTRDLYLLNL 245
 Db 175 KDLKNNLSQVNTFRVPMNRFLRE-RLTDLEROSDITTYGQFQALYSLMTYSAOKTMDLP 233
 Oy 246 TYS-----NHKDHLDASLQRF-----LQVEQKAGVLTSCODITIQE 285
 Db 234 EASTLRAGERELCRVSLPERFOQLFLEYQGLMAVDRLOVQEFMLSLRDLPLREIEBP 292
 Oy 286 PCPEKNSKGLIGIDGFTNTYTRSPAGDIFNPEHHVHOD--MTQPLSHYFTSSHNTYLVGD 344
 Db 293 Y-----FLDEFTYFLFSKENSISWNSQLDAVCPDTMNNPISHWISSSHNTYLTGD 342
 Oy 345 QMSQSRVDYAWYLQAGRCVEVDWCMDGPDGEPIVNHGYTLTSKILFKVDIETINKYAF 404

Db 343 QFSSESLIENAVARCLRMGRCIELDCWDGDPMEVLYHGHITLTIKFSDVLTIKFHA 402
 QY 405 IKNEYPVILSIENHCYVLOQKMAQYLTLDIGDKLDSVSSSEDAITLPSOMKGLIY 464
 Db 403 VASEPYVILSIENHCYVLOQKMAQYLTLDIGDKLDSVSSSEDAITLPSOMKGLIY 464
 QY 465 KGRKL-----PAN-----ISE 475
 Db 462 KHKKLKAGSAVEEYPMYSEMDISNSIKNGILYLEDPVNHBMYPHYFVLSKITYSE 521
 QY 476 DA-----EEGEYSDSDADEIDDOCKTLNGASTNRKKEVETAKRKIDS----- 519
 Db 522 ETSSDQNEDEEPEKVESSSTELSHNEKFGKLAGRGD-RHIAERLLTEYCITGAPD 580
 QY 520 ---LIKES-----KIRDC----- 529
 Db 581 GSEFLVRESEFVGDTYLSFMRNGKQVCHRIHSDAGTKFPLTDLVDSLYLTTHQ 640
 QY 530 -----EDPN 533
 Db 641 QVPLRCNEFMRLSEVPOTNAHESKEWYHASTRAQAHEMLMRYPRDGAFLVRKNEBN 700
 QY 534 NFSVS----- 538
 Db 701 STAFSPRAEGKIKHCRVQEGQVYMLGNSEPSYDLISYEKHPLYRKMLRYPLINEA 760
 QY 539 -----TLSPS-GKL-GR-----KSKAED 555
 Db 761 LEKIGFAEDYQALYEGNRPGEYVEANPMPTFKCAVKALFDYKAOREDELTPFKSATIQN 820
 QY 556 VESGE-----DAGASR----- 566
 Db 821 VEKQEGMMRGDYGCKKQIMFSPNYVEEMVNVALEPEREHLIDENSPGLDILRGVLDVPA 880
 QY 567 -----RNGRLVYGSFRRKKKSKLKAAVSE-----GDEQDPSGQSGRG 608
 Db 881 COLAIRPEKGNRRLEFVTSISMAVHMSLDVAADQOELODKVKKIRVQAQADAKRLLEG 940
 QY 609 ATROCKTMYLSPALSDLYKTSVATHD--IEMEAASSMOVSSSEFETAHOILOO-KPAQ 665
 Db 941 KIMERR-KKIALELSELVYVCPVFPDEKRTGTERACYRDMSSPFEYKAEEYVNNAKGK 999
 QY 666 YLENOOOLSRITPSSSYVDSNYPNPOFWMNAGCOMVALNTQSEGRMQLNRAKPSANG 725
 Db 1000 FLOYRRLDLSRIYPKGRLDSNDYPLMPCGSQLVALNQTQDPKPMOMQALFMRGR 1059
 QY 726 GGYVLKPGCMQGVYNPNSDPLBQGLKQVLRLISGOQLPKPRDSMLGDRGETIDPEV 785
 Db 1060 CGYVLQPTMDEADDPDKSSLRGLFPCALSTIEVLGARHLPK-----NGRG-IVCFEV 1112
 QY 786 EVELIIGLPVDCSRQOTRVVDNGENPTW-EETLVFVMPVMPALVRLVPLWMDHPIC-RDF 843
 Db 1113 ELEVAGAEYDSTKQTEFEVYVNGINLPWPAKPFHFOISNPEFALRLREYVEEDMFSDQNF 1172
 QY 844 IGOITLAFSSMMPGYRRV-----YLEGMEASIVHVAV----- 877
 Db 1173 LAQAFPEYVKGKTYRAVPLKNNYSEDLIELASLILKIDIPAKENGDLSPRSGTSLNERG 1232
 QY 878 SDISGKYKQALGLKLF 894
 Db 1233 SDASGOLFHRARGSF 1249
 RESULT 11
 A48047
 phospholipase C (EC 3.1.4.-) beta-4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence: revision 10-Sep-1999 #text_change 02-Jun-2000
 C:Accession: A48047; JN0691
 R:Lee, C.W.; Park, D.J.; Lee, K.H.; Kim, C.G.; Rhee, S.G.
 J. Biol. Chem. 268, 21318-21327, 1993
 A:Title: Purification, molecular cloning, and sequencing of phospholipase C-beta 4.
 A:Reference number: A48047; MUID:94012687; PMID:8407970

A:Accession: A48047
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1176 <LSE>
 A:Cross-references: GB:115556; MUID:9404071
 A:Experimental source: Brain
 A>Note: sequence extracted from NCBI backbone (NCBIP:138517)
 R:Kim, M.J.; Bahk, Y.Y.; Min, D.S.; Lee, S.J.; Ryu, S.H.; Suh, P.G.
 Biochem. Biophys. Res. Commun. 194, 706-712, 1993
 A:Title: Cloning of cDNA encoding rat phospholipase C-beta4, a new member of the phos
 A:Reference number: JN0691; MUID:93343926; PMID:7688223
 A:Accession: JN0691
 A:Molecule type: mRNA
 A:Residues: 1-254, 'M', 256-307, 'A', 309-416, 'E', 418-469, 'K', 471-504, 506-545, 'DE', 548-73
 'M', 1045-1176 <KIM>
 A:Cross-references: GB:118962
 A:Experimental source: Brain
 A>Note: the authors translated the codon AAC for residue 140 as Lys, CAG for residue
 messenger molecules, inositol 1,4,5-triphosphate and diacylglycerol in response to t
 odicesterase domain y homology
 C:Keywords: phosphoric diester hydrolase
 F:315-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x
 F:565-685/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y
 Query Match 15.68; Score 997; DB 1; Length 1176;
 Best Local Similarity 29.7%; Pred. No. 2,4e-43;
 Matches 292; Conservative 142; Mismatches 326; Indels 224; Gaps 32;
 QY 99 ROSEVFORYPDGS--FPNCCFSYH----- 122
 Db 18 QEGAVFPRFESVFEPPNCLFKVDFGFLYKMSCKEGVLECSLINSIRLAIPKDP 77
 QY 123 -----GSHRESLD-----LVTSSEVARTWYGLRLMAGIS 154
 Db 78 KIILALESVKSSENDLEGRILCYCSGTDLVNIGFTYVMAENPITQWYBGLRSIHNHR 137
 QY 155 DEQSLARQRTROWLKTQFDEADKNGDGLSGE-----VLQILKRLNVL 201
 Db 138 -ANNVSPMTCIKKMMKLA--LNTSGKIPVRSITRTFASGTEKVFQALKEF--GL 191
 QY 202 PRORVKMFREADTDHOGTLGFEFCFAFYKMYSTRDYLMLLYSNK--CHLDAASIQ 260
 Db 192 PSCGNDEIRPAFT-----YEKFEYLQKICPTIDIEDLFPKINGKTYLTVQDLY 243
 QY 261 RFLQVEQKAGVY-----LESCDITEPEPCPNKSKGLIGDFTYTRSPAGDI 312
 Db 244 SFINEHQDRRLLELFPYDAKRAMQIEMTEPEDELLKKGLISSDGCRLMDEANP 303
 QY 313 FNEHHNVHODMTPOLSHTFTSSNHTYLVGOLMSQSVYDMYAVYLAQAGCYEVDSCD 372
 Db 304 VFLDRLELVQEMDHPLAHFTISSNHTYLTGROFGGKSSVEVRYVLLAGCGVELDCWD 363
 QY 373 --GPDEPVIYHNGYTLTKLEKVDLETINKYAFKNEYPVILSIENHCYVLOQKMAQY 430
 Db 364 GKGEDEPITITGKAMCTDILFKVDYQAIKFAFYAETSEPVILSPENNCKSQYQOMSKY 423
 QY 431 LFDILGD--KIDLSVSSEDAITLPSQMLKGLILYVKGKLPANISDAEAGEYSDSDS 487
 Db 424 CEDLFGDILLKALSHPLPEGRLLPSPNDLKRKILINKRLKPEVEKQDEALKSMNEA 483
 QY 488 ADE-----IDDCKLNLNDASTNRKRYENTAKRKIDSILKESKIRDCEDNPNNSVSTLS 541
 Db 484 GESAAPASITLED-----NEELESADQEEA-----H 512
 QY 542 PGSKIGRKKAEEDYSEGDAGASRRNRRLVYGSFRRKKKSKLKAAVSEGDGEGDS 601
 Db 513 PYKKGNEISAD-----FSHKEAVANSYKGLVYVE--DEQAMM 550
 QY 602 PGQSGCATROKTKTKLRALSDLYKTKSVATHIDEM--EAASSMOVSSSEFETAHOIL 659

Db 551 ASYKTVGA-----TTNIHPLSTMINVAQPVKFGFVHAEBRNHYNMSSFNVCGLYL 605
 Oy 660 OOKPAOYLFEENOOLSRIPSSYRVDSNTNPOPFWMAGCQWALNTQSEGMLOLNRAK 719
 Db 606 KTHAIEFVYNNKROMSRIRPKGGRVDSNTNPOPFWMAGCQWALNTQSEGMLOLNRAK 665
 Oy 720 FSANGCGGVKPGCMQ--GVFNPNSEDLPLGKQKQVLRITISGQOLPKPRDSMLGDR 777
 Db 666 FEYNSGGLLPDEFERRDRDFPESETPVGVIAATCSVVISQ-----FLSDK 717
 Oy 778 GEIIDEFVEVEIIGLPVDCSRED--TRVVDNGFNPWT--EETLVF--MWMPEIALVRELY 833
 Db 718 K--IGYEVDMYGLPTDITREKFRBVMNNGNLNVNESEFVRKVLIPDLAVLRLAV 775
 Oy 834 WDHDPIDRDFIGORTLAESSMMPGRHYTL--EGMEAS--IFVHVA--VSDISGRV 884
 Db 776 YDGN---NKLIGRILPLDGLAGYRHISLRNENKPLPLPTFCIVLKYTVPPDGLDI 832
 Oy 885 KOLGLKGLFLR-----GPKRGLSDSHAAGRPPARPSV--SOR 920
 Db 833 VDLSDPKKFLSTTEKRAQDLRAMGIETSDIADVPDTSKNDKKANAKANVTPQSSS 892
 Oy 921 ILRRTASAPTKSOKPGRKGPPELV 944
 Db 893 ELRPTTAAALGSGGEAKKGI-ELI 915

RESULT 12

A53970
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit
 C:Species: Drosophila melanogaster
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2000
 C:Accession: A53970
 R:EMBL, Y.; SUGAYA, R.; AKIMARU, H.; HIGASHIJIMA, S.; SHISHIDO, E.; SAIGO, K.; HOMMA, Y.
 J. Biol. Chem. 269, 19474-19479, 1994
 A>Title: Drosophila phospholipase C gamma expressed predominantly in blastoderm cells at
 A:Reference number: A53970; MIM:94308233; PMID:8034716
 A:Accession: A53970
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1236 <EMO>
 A:Cross-references: GB:029806
 C:Genetics:
 A:Gene: plc-gammad
 A:Cross-references: Flybase:FBgn0003416
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphatidyl
 hodiesterase domain Y homology; SH2 homology; SH3 homology
 C:Keywords: phosphoric diester hydrolase
 F/326-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F/589-688/Domain: SH2 homology <SH2B>
 F/701-789/Domain: SH2 homology <SH2>
 F/831-879/Domain: SH3 homology <SH3>
 F/979-1095/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y ho

Query Match 15.5%; Score 986; DB 1; Length 1236;

Best Local Similarity 25.0%; Pred. NO. 9.3e-43;

Matches 315; Conservative 177; Mismatches 328; Indels 440; Gaps 42;

Oy 30 LSANILPVERCKMAGCMQWVNLKSGSKLVRFYIDERSICR-----W-----RP 78
 Db 7 MSAPLIGMEEDITGLMGTITVTKLIGKQRRPR-----RLMLRLRETRQLMKTAVATQT 61
 Oy 79 SRNKEKATISIDISQEVSEGRSEVFORYPDC--SFDPNCCFSYVHSH--RESIDLVST 134
 Db 62 PRIDEGAIOLREIREIVNGKSKFEFLFADDCQFESSKCFVILHGNHFKLSFSVAL 121
 Oy 135 SSEVARTVNTGLRYLMAGISDEDSLAKRQKTR--DQWLKQTF-----DEADKNGDG 183
 Db 122 SEIEDNNVNRGLRYMY-----KDLGARYPLQIDRMRLREYQLEINVTFSAKATEGSPA 176
 Oy 184 SLISGEVQLLKLNLVNLPRQVRKQMFREADTDHQTGLGFEFCAFYKMM-----ST 236
 Db 177 QVTIKDFKLFLAGVSCKMTGKFMHFTEDVARRKH--LKPDDFSRLQKLLPNGFASV 234

Oy 237 RRDYLMLTFYSNKHDLDAASLOFLQVEOK-----MAGVTLES--CODLIIDQFEPCE 289
 Db 235 LSGGVANFPPSEDOQVVRRELKQFLETREBDVSASEISMAIASFTIRFQDVE---R 291
 Oy 290 NKSGLGIDGFYMYTNSPADIFNPENHHVQMTOPLSHYFTTSHNTYLVGDQLMSQ 349
 Db 292 DVEEPLTFEPFVDFLESKQNDLWNSKYDFQDMNPLSSYSWYASSHNTYLVGDQFSSE 351
 Oy 350 SRVDYAVANLAGRCVVCDCWDGDGEPIVHNGYTLTKLFPDVIETINKYAFINEX 409
 Db 352 SSCENYARALMGRCCTELDCMNGPDNLPTFPHGHTITSKIFKPDVYIKTKIDHAFISSEY 411
 Oy 410 PYLISIEHNSVYLOQKKAQYLTDLGDKLDSVSSVEDATLTPSPQMLKGLILKCKKL 469
 Db 412 PYLISIEQNSLEQGRNNAQALIEVFGDM-LTQPCDRNEQHLSPSPOLRRKILKHKKL 470
 Oy 470 P-----ANISDAEAG----- 480
 Db 471 POFDDIANGISSTGSLGRHSSLGAGAGAHGENDGENRKYFKGLLYFKDPYDKSNLY 530
 Oy 481 -----EYSDSDADEIDD-----CKLNG-----DASTN----- 505
 Db 531 QFVLTROELIYSSEINESRNGSEDDFCGLSSCSLNNMQOKKODISANDELHGENWF 590
 Oy 506 -----RRKVENTAKR-----KL----- 517
 Db 591 HGKLEGRKREADLLKTKYHFGDGTFLVRESATFVGDYSLSEFWRNRNHRKILKHBNG 650
 Oy 518 -----DSL-----IKE----- 523
 Db 651 SKIKYLVENFVDSLXLIVYRKMLLSSSEIILKEPVYQPKRHEQMFHPPTTEQ 710
 Oy 524 -----SKIRCE-----DPNNF----- 535
 Db 711 AREGGLRLIGSLPVSVOSINAFVIFSTINRKIKHCRIMQEGCLYGDIFMNFESLYSL 770
 Oy 536 -SVSTLSP-----SGKLGRSKAE--DYEGS-EDAGAS----- 565
 Db 771 INYTRNPLRYNKLSPVSOELRLQALAEAGDHSGGHDNGASNTWGSMLBENTYCK 830
 Oy 566 -----RRNCRLYVGSFSPRRKK--GSKLKAASY----- 592
 Db 831 ALYSYANKPDELSPFKKALITNVQRDNSSMMWIGDYGKIKKHLNANYKYVDSTTEYN 890
 Oy 593 ---EGDDEQ-----DSPG----- 603
 Db 891 SLNEEGTGDGTDSEILFGAVASLFEESNDPGIIFKLIQTPMQNPVIGFDNQETAYEMI 950
 Oy 604 -----GOSGATROKK--TKLSRLASDLVYTKTSVATHDIEEAASSW--QVSS 649
 Db 951 KATQEAALIASOLASERKKERTARVAKESDILITFRSVPRE-----HSMIFQEMSS 1004
 Oy 650 FSETKAH--QLLOOKPAOYLFEENOOLSRIPSSYRVDSNTNPOPFWMAGCQWALNTQ 708
 Db 1005 FPETKAKQFOQNTQLFSLYHNNQISRYVPKQGRDSSNFNMPWNGSQWALNTQ 1064
 Oy 709 EGRMLQINRAKFSANGCGVYLPKCMQCGVNPNSDEL--PQQLKQVLRITISQOLP 767
 Db 1065 GDKAMQLOAKFRRNNGCGGILKPSFKMSDSFNPN--NPLCLDLSSEVKSIRILAAHRL 1122
 Oy 768 KPRDSMLGDGELLIDPEVEEIIIGLPVDCSREDQTRVVDNGFNPWT--EETLVF--MWMPEIA 827
 Db 1123 R-----GKSNNDPIVELIGASDTDTGVKRTKVIENGFPVNNSESEFVNRVPOFA 1174
 Oy 828 LVRLVMDHDPGR--DFIGORTLAESSMMPGRHYTL--EGMEASIFVHVAVSDIS 881
 Db 1175 ILREYQDEDMFARTHTIAQACVPLFCIRQGYRSVILRNKFSSELEISLILINKIANVT 1234

RESULT 13

A51317
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) II - rat

Query Match	15.4%	Score 985;	DB 2;	Length 1290;
Best Local Similarity	25.6%	Pred. No. 1.1e-42;		
Matches 303; Conservative	157;	Mismatches 313;	Indels 410;	Gaps 26;

[illegible]

QY	132	VSTSEVAFRTMYGJRTYLAGISDEDSIARQRTDQWIKQFFEDADKNGDSISIGVL	191
Db	112	ATDSKEDAVKMLSGKL-----HOEAMNASTPTMIESWIKKOIYSVDOTRRNSISRELK	167
QY	192	OLMLKLN-----VULPRORYKQMFREARDIDHOGITGFEFECAFYKMM-----ST	236
Db	168	TIPLVMEKVSXGKIFLKDKLVEIGAQK-----ELSEFOFLFKKLMFEDQKSIDDEF	221
QY	237	RROJLLMLLYTSNKHDLDASL-----QRFLQYBQKAGVYTESCODIIEOF-EPCEPE	289
Db	222	KKDSSEVIL---GNTORPRDASAVYLODFORFLHEQOELMADOLKVKVERMTKFIIDTYMR	278
QY	290	NKSGLLGIGOFETYUTSPADJFENDEHHNVH-ODMTOPLSHYETSNNHYVGDOLMS	348
Db	279	ETAPREFVDEFLTYLFSRKNSTIMDKRTAIVDMQDMMNPLSTMYTSSSHNTYLVGDQJRS	338
QY	349	QSRVDMTAMYLQAGCRCEVEYDCWDGPDGEPIVHGHGYTLTKILFKDVIETINKYAFIKNE	408
Db	339	ESSEAVYICRLRAGRCRIELDCWDGPDGPKPIYHGHGFTTKIFPDVYQAIHDHAFVTS	398
QY	409	XPVLLSTENHCXYLOQKMAOYLITDILGKDLSSVSSDATLTPSPOMLKGILLYKCK	468
Db	399	FPVLLSTEEHCSEYQOEHMAKVEKVEYLGDL-LTKPTEASADOLTPSPOLREKILIKRK	457
QY	469	L-----PANISEDAE-----GEVSDSDADE-----IDDD-494	
Db	458	LGRPGVDVAVEDKQKDEHKIQOGLYMWDSIDQKMTKHYCAIDAKLTSFSDIEQVEYEDP	517
QY	495	-----CKLANGASTNRKREVENTAKRL-----DSLKESKIRDCEDPNNF535	
Db	518	VQDPPTPELHEGKEWPKFKVESRFSASEKILDEYCAETGAKDGTFTVRESE---TFPNDY573	
QY	536	SVSTLSFSGKL-----ESGDAGA-----546	
Db	574	TLS-FMRSGRVQHCRIKSTMEGWMMKYIYLDNLTFNSIYALIQHREAHLCAEELBLT632	
QY	547	-----GRKSKAE-EDV-----ESGDAGA-----564	
Db	633	DPVBNPNDHESKRPWYXDLRSGCAEDMLMRIPRDGAFLLRKREGDYSVAITFRANGKYKH692	
QY	565	---SRNRGR-LVYGS-----575	
Db	693	CRINDGRHYVLGTSATFESVLYELVSYIEKHALIKYKMLRYVYTBELLERYMEDJNSL752	
QY	576	-----FSRRKKGSKL-----KKAASVEGDGEG598	
Db	753	YDVSRMYVDPESEINPSMWPQRTVKALDYKAKRSEDLTFRCGALINNVSKPEGMMKGDYG812	
QY	599	-----ODSP-GGGSRA-----609	
Db	813	TRIOQYPPSNVVEDISAGDAEEMEKOTIEDNPLGSCIGLIDLNTYNNVYKAPQGNOKAF872	
QY	610	-----TRQ-----KKTWKLSTRALSD624	
Db	873	VFILEPKKQGDPRPEAFATDVEELFEMPQDSIREITWKIDTKENMKMYWRNOSTIAIELSD932	
QY	625	LVKTTKSAVATHIDMEAASSWOYSSFSSEKRAHOIIOQKRAQYILRPNQOOLSTIYSSYRY684	
Db	933	LVVYCKEPTSKTKDLENDPREIREISREVEYTRKADSIYKQKPFVDLLRTRNOKGLTRVYKQGV992	
QY	685	DSNYNPNOPFNAGCQWVALNYOESGRMLOLNARFSANAGGCGYVLKPCMQOGVFNNNS744	
Db	993	DSNYNPNOPFNAGCQWVALNYOESGRMLOLNARFSANAGGCGYVLKPCMQOGVFNNNS744	
QY	745	EDPLPGLOKQO---LVLRITISGOOLPKPRDSMLGDRGEIIDPFVEVEITIGLVPVDCSREQ800	
Db	1048	YDPMPEPESOKRIIMTLTVKVLGAFARHLPK-----LG--RSIACPFVEVEICAGETYSNFKF11000	
QY	801	TRVYDQNGCFNPJW---BEFLVFWVNMHPETALVPLVWMDPDIG-RDFIGQRTKLATSSMMP856	
Db	1101	TTVYNDNGSLSPVMPQEKATYEIYDPMNLAFLEFLVEEDMFSDPFLAHAVYPIKIGIKS11600	

Oy 857 GYRHY-----YLEGKEASIFV 873
|:| | | | | | | | | |
Db 1161 GFRSVPLKNGYSIEDIELASLV 1182

RESULT 15

S02004

phospholipase C (EC 3.1.4.3), phosphoinositol-specific - human

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 04-Feb-2000
C:Accession: S02004
R:Ohta, S.; Matsui, A.; Nazawa, Y.; Kagawa, Y.
FEBS Lett. 242, 31-35, 1988

A:Title: Complete cDNA encoding a putative phospholipase C from transformed human lymphocytes
A:Reference number: S02004; MUID:89078616; PMID:2849553

A:Accession: S02004
A:Molecule type: mRNA
A:Residues: 1-1252 <OHT>

A:Cross-references: EMBL:X14034; NID:g35513; PIDN:CAA2194.1; PID:g35514
C:Superfamily: 1 phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y homology; SH2 homology; SH3 homology

C:Keywords: phosphoric diester hydrolase
F:314-456/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x
F:532-635/Domain: SH2 homology <SHA>
F:646-735/Domain: SH2 homology <SH>
F:776-824/Domain: SH3 homology <SH>
F:923-1047/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match	14.98:	Score	950.5:	Db 2:	Length	1252:
Best Local Similarity	25.18:	Pred. No.	6.2e-41:			
Matches	292:	Conservative	164:	Mismatches	310:	Indels
					399:	Gaps
QY	74	IRWRPSRRNEKAKTISIDSIQFVSESGROSEVQRYRYPDGSFDPNCCFSYIYHGS--RESID	1311			
Db	52	VAMSTADKIGFGLDIMEIKRIEGRKNSKDEERAKAVAKOKEDCCFFTLITYGTSQFVLSPTLSL	1111			
QY	132	VSTSEVARTVWTGIGRYLMAGISDEDSLARQRRIDOMKQTFPEAKKNGDSLSIGEV	1301			
Db	112	AADSSEEDVYNNLSGKLTL---HOEAMNASTPTIIEMLRKQIYSDVOTRNNISLIELK	167			
QY	192	QLHLKLVNLPOR--VKOMFREADOTDDHOGTLGFEERCAFYKYM-----STRRL	2401			
Db	168	TILPILNFKYSSAKFLKQKFEIGA--HKDELSPFQHLFVKKLMFEQKSLIDEFKDS	2251			
QY	241	YLMLTYSNMKHDHLDASL-----ORFL-----QVEOKAGVTLSCODITIE	2821			
Db	226	SVFLL---GNDRDPAASVYLHDFORFLDHEOQHMAODINKVAERMTKFLDTMRETAE	2821			
QY	283	QFEPCEPKNSKGLGIDGFTVYTRSPAGDINPEPHNVH--ODMOPILSHFTSSNHTYL	3411			
Db	283	PF-----LFVDFELTYLFSRENSIINDEXKYDAVDMODMNNPLSHYVISSNHTYL	3311			
QY	342	VGDOLMSOSRVDMTAWYLQACRCCEVYDCMGDPGERIVHGYTLTKLFFKDIETINK	4011			
Db	332	TGDOLRSESESEAYIRCLRMCRGRIELDCMGDPGRKPIYIGMTRTKIKFDPVYQAIKD	3911			
QY	402	YAFINERPVLLSTENHGSVLOQKKMAQYLLDIDKMLDLSVSSEDATLPLSPQMLKKG	4611			
Db	392	HAFLVTSFVPVLLSTIEHRCSEVQQRMAAKAFKFEVGGDL-LTKPTASADQLPSPSQIREK	4501			
QY	462	ILVKGKKT-----PANI-----SEDAEGEVSDEDSADE-----IDDD--	4941			
Db	451	IIKKKKLKGPRGDDVYNNEDKKDKHKGQGLLYMMDSIDQMKTRHYCAIAAKLSFSDIE	5101			
QY	495	-----CKLNGDASTNRKRVENTAKKL-----DSLIREK--	5251			
Db	511	QTMEEVPEQDIPPELHFGKFWKFKYKKEKRTSAEKLQECYCMETGKDGDTFLVRESETFP	5701			
QY	526	-----	5251			
Db	571	NDYTLSPFRSGRVQHCRIIRSTMEGTLKYITLDNLRRFRMTALIQHRETHLPCEAEELR	6301			
QY	526	-----IRDCEDPNNEVSSTLSBSGR	5451			

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Db 631 LTDPVNPNEPHESKPWYDLSIRGAEEDMLMRIPDGAFLIRKREGSDSYAI-TERARGK 689
QY 546 L-----GR-----KSKAEEDV 556
Db 690 VKHCRINEDGHHFVLGTSAYPESLVELVSYEKSLYRKMRIRYPVPELLERYNTFERDI 749
QY 557 ESGEDAG-----ASRRN-----GRLVGSFSRRKKKSKL-----KKAASVEEG 595
Db 750 NSLDVSMYDPSEINSMQRTYKALYDKAKRSDLSFCRGALIHNSKEPGMWKG 809
QY 596 DEG-----QDSP-GGQSRG-----608
Db 810 DYGTRIQQYFSPSNYVEDISTADFELEKQILEDNPLGSLCRGILDNTYNYVKAPOGKNO 869
QY 609 -----ATRO-----KTKMLSRA 621
Db 870 KSEVFILLEPKEOGDPVVEFATDRVBELEFEMFQSIREITWKIDSKENNMKYWEKNQSIATIE 929
QY 622 LSDLVKYYTKSVATHDIEMEAASSWQVSSFSSTKAHQILQCKPAQOYLRFNQQOLSRITYPSS 681
Db 930 LSDLVVYCKPFSKTKDNLENDFREIRSFVETKADSIIRQKPVDLKYNQKGLTRVYPKG 989
QY 682 YRVDSSNTNPOPEMNAGCOMVALNTOSEGRMLQINRAKFSANGGCGYVLKPGCMCGVFN 741
Db 990 QRVDSNNDPEFRLMLCGSQWALNFOZADKYQMNMHALFSINGRTGYVLOPESM-----R 1044
QY 742 PMSDPLDGLKQKQ-----LVLRITSGQOLPKPRDSMIGDRGEIIDPFVEVELIGLPVDCS 797
Db 1045 TEKTDPMPEPESQKILMTLTIVKVLGARHLPK-----LG--RSIACPVEVEICGAEYGN 1097
QY 798 REQTRVYDDNGFNPTW--EETLVEMVHMPETALVRFLVWDHPDG--NDFIGORTLAFSS 853
Db 1098 KFKTTVVDNGLSPIWAPTQEKVTEFYDPMIAFLRFVYVEEDMFSDBNFLAHATYPIKA 1157
QY 854 MMEGYRHY-----YLEGMEBASIFY 873
Db 1158 VKSGFRSVPLKNGYSEDEIELASLLV 1182

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Search completed: March 28, 2003, 13:52:36
 Job time : 66 secs

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 13:39:09 ; Search time 80 Seconds
(without alignments)
2010.419 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPRAGPLPGRALPREDPG.....ALYWNHCLRTLLPLWACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	6092.5	95.5	1239	23 ABB08205	Human lipid metabo
2	4941	77.5	1619	23 AAU07498	Human lipid metabo
3	3225	50.6	621	23 ABB07493	Human lipid metabo
4	3163	49.6	1014	23 ABB08001	Human lipid metabo
5	2343	36.7	787	22 ABB03659	Novel human diapo
6	2343	36.7	787	22 AAE14673	Human phosphatidyl
7	1524.5	23.9	997	23 AA017367	Human phospholipas
8	1517	23.8	1096	22 AA01596	Novel human phosph
9	1441	22.6	762	22 AAE10440	Novel human phosph
10	1441	22.6	762	23 AAE14268	Human phospholipas

11	1439	22.6	828	23 ABB08008	Human lipid metabo
12	1432	22.4	762	23 AAU076816	Human phospholipas
13	1385.5	21.7	759	23 AAE14270	Human phospholipas
14	1372.5	21.5	785	23 AAE14269	Human phospholipas
15	1325.5	20.8	731	23 ABB07492	Human lipid metabo
16	1290	20.2	789	22 AAG63220	Amino acid sequenc
17	1279.5	20.1	736	22 AAB47516	Human phospholipas
18	1278.5	20.0	736	23 AAE21821	Human phospholipas
19	1277.5	20.0	794	23 ABB66693	Human novel polype
20	1277.5	20.0	794	23 ABB66721	Human novel polype
21	1258	19.7	756	21 AAY81394	Rat phospholipase
22	1256.5	19.7	466	22 AAB85125	Human protein sequ
23	1106	17.3	677	22 AAB94673	Human protein sequ
24	1085.5	17.0	608	23 AAU076817	Human phospholipas
25	1006.5	15.8	1093	23 ABB08201	Human lipid metabo
26	1002	15.7	567	22 AAE11925	Human G121 (or C5
27	990	15.5	1236	22 ABB60480	Drosophila melanog
28	985	15.4	1290	17 AAB90583	Phospholipase C-ga
29	945.5	14.8	1312	22 ABB60755	Drosophila melanog
30	939	14.7	1216	22 AAM79193	Human protein SEQ
31	939	14.7	1216	23 ABB08204	Human lipid metabo
32	931	14.6	178	23 ABB65980	Human DITRP polype
33	896.5	14.1	1058	22 AAM80177	Human protein SEQ
34	852	13.4	1898	23 ABB07352	Amino acid sequenc
35	841	13.2	1579	23 ABB66735	Human novel polype
36	840.5	13.2	1809	22 AAE13101	Human phospholipas
37	723.5	11.3	1054	23 AAU11619	P. patens signal t
38	719	11.3	214	22 AAU07352	Novel central nerv
39	713	11.2	214	22 AAM43569	Human polypeptide
40	685.5	10.7	628	23 AAU11620	P. patens signal t
41	682.5	10.7	869	15 AAU53732	S. cerevisiae Plc1
42	622	9.8	324	22 AAU07205	Novel central nerv
43	599.5	9.4	306	22 AAB94419	Human protein sequ
44	593.5	9.3	561	17 AAR91932	Phosphatidylinosit
45	522.5	8.2	340	22 AAE11930	Human Cg121 (or C5

ALIGNMENTS

RESULT 1
ABB08205
ID ABB08205 standard; Protein: 1239 AA.
XX ABB08205;
XX 04-MAR-2002 (first entry)
DE Human lipid metabolism enzyme-5 (LME-5).
XX
XX Human: LME-5; lipid metabolism enzyme-5; cytosolic; neuroprotective;
KW immunosuppressive; anti-inflammatory; cardiovascular; gene therapy;
KW enzyme therapy; cancer; neurological disorder; autoimmune disorder;
XX inflammatory disorder; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200185956-A2.
PD
XX 15-NOV-2001.
PF 11-MAY-2001; 2001WO-US15210.
XX
XX 11-MAY-2000; 2000US-203511P.
PR 25-MAY-2000; 2000US-207903P.
PR 07-JUN-2000; 2000US-210150P.
PR 23-JUN-2000; 2000US-213392P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-Young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;

23-NOV-2000; 2000US-227429P.
 PR 08-SEP-2000; 2000US-231370P.
 PR 15-SEP-2000; 2000US-23312P.
 PR 29-SEP-2000; 2000US-236885P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PI Griffin JA, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;
 PI Walla NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M;
 PI Lai P;
 DR WPI: 2002-280936/32.
 DR N-PSDB: ABK12390.
 XX
 XX New lipid metabolism enzymes, useful for diagnosing, treating or
 PT preventing immune system disorders (e.g. Crohn's disease), neurological
 PT disorders (e.g. Parkinson's disease), or cell proliferative disorders
 PT (e.g. cancers) -
 XX
 XX Claim 50; Page 113-117; 122pp; English.
 PS
 CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the
 CC polynucleotide sequences encoding them. The LMM polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LMM, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LMM-6.
 CC
 XX
 SO Sequence 1619 AA;
 Query Match 77.5%; Score 4941; DB 23; Length 1619;
 Best Local Similarity 84.2%; Pred. No. 0;
 Matches 973; Conservative 2; Mismatches 14; Indels 166; Gaps 5;
 QY 9 LRGPAALPPEDPGPPSRMLFLSANTLPV-VERCMGAMOGMOMVLRGSGKLVFFYL 67
 DB 473 LRGVAAPP-----LTVASLPCPVERKGMQMGOMVLRGSGKLVFFYL 519
 QY 68 DEHRSCIRWRRSRKNEKAKISIDISQIEVSEGRQSEVFORYPDGSFDPNCCFSITYHSGHRE 127
 DB 520 DEHRSCIRWRRSRKNEKAKISIDISQIEVSEGRQSEVFORYPDGSFDPNCCFSITYHSGHRE 579
 QY 128 SLDLVSTSSVARTVYTGRLTYLMAGISDEDSLARKQRTDQ----- 168
 DB 580 SLDLVSTSSVARTVYTGRLTYLMAGISDEDSLARKQRTDQYPMARDIGCCRPDRPLGCS 639
 QY 169 -----MLKOTFDEADKNGDGLSISGEVYLQLLHKLNVMLPRQRYK 207
 DB 640 PWGGLSFGSHGTGEVAGQRYEMLKOTFDEADKNGDGLSISGEVYLQLLHKLNVMLPRQRYK 699
 QY 208 QMER-----EADTDHOGTLGFEFCARYKMM 234
 DB 700 QMERVAGHAWLEQGLKACSODRALVEYPMGTQGLALQEAQTDHOGTLGFEFCARYKMM 759
 QY 235 STRDYLMLLTYSNHNDHDAASLOFLOVEOKMAGVTLESCODIIEOPEPEPKSKS 294
 DB 760 STRDYLMLLTYSNHNDHDAASLOFLOVEOKMAGVTLESCODIIEOPEPEPKSKS 819
 QY 295 ILGIDGFTNTYRSPAGDIFNPENHNHVDMTOPLSHYFITSNHTYLVGDOLMSOSRVD 354
 DB 820 ILGIDGFTNTYRSPAGDIFNPENHNHVDMTOPLSHYFITSNHTYLVGDOLMSOSRVD 879
 QY 355 YAWVLQAGRCVEYDCKDGDDEPTVHNGYTLTKLIFKQVIEFTINKYATKNEYPTLS 414
 DB 880 YAWVLQAGRCVEYDCKDGDDEPTVHNGYTLTKLIFKQVIEFTINKYATKNEYPTLS 939
 QY 415 IENHCSTYQOKKMAQYLTDLIGDKLDLSSVSSSEDAATLTPSPOMLKGILVKGKLPANIS 474

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 DB 940 IENHCSTYQOKKMAQYLTDLIGDKLDLSSVSSSEDAATLTPSPOMLKGILVKGKLPANIS 999
 QY 475 EDAREGEVSDSDGADIEDDDCKLLNGDASNNRRKRVENFTARKRLDLSIKESKINDCEDPNN 534
 DB 1000 EDAREGEVSDSDGADIEDDDCKLLNGDASNNRRKRVENFTARKRLDLSIKESKINDCEDPNN 1059
 QY 535 FSVSTLSPSGKLGK----- 549
 DB 1060 FSVSTLSPSGKLGKRVAKKVTPLMPTGPPDSQPVGPPPNRGSVQAPGPGMGRAAV 1119
 QY 550 -----SKAEDEYEGEDAGARRNGRLVGS 575
 DB 1120 GAVCCGVAERKRVYVMRAIYASLQCCSIOGCGRSKAEDEYEGEDAGARRNGRLVGS 1179
 QY 576 FSRKKKSKLTKAASVEEDGDDSPGCGSRGATROKTKMKSRLALSDLVKTKSVATH 635
 DB 1180 FSRKKKSKLTKAASVEEDGDDSPGCGSRGATROKTKMKSRLALSDLVKTKSVATH 1239
 QY 636 DIEMEAASMWQVSFSETKAHQILQOKPAQYLRFENQOQLSRIPSSYRVDSNNPQPF 695
 DB 1240 DIEMEAASMWQVSFSETKAHQILQOKPAQYLRFENQOQLSRIPSSYRVDSNNPQPF 1299
 QY 696 NAGCOMVALNTQSEGRMQLNRAKFSANGCGGYLAKGCMQGVFNNSDPLPGOLKQ 755
 DB 1300 NAGCOMVALNTQSEGRMQLNRAKFSANGCGGYLAKGCMQGVFNNSDPLPGOLKQ 1359
 QY 756 LVLRITISGQQLPKPRDSMLDGRGELIDPFVEVEILGLPVDCSRQRTVYVDNGENFTWEE 815
 DB 1360 LVLRITISGQQLPKPRDSMLDGRGELIDPFVEVEILGLPVDCSRQRTVYVDNGENFTWEE 1419
 QY 816 TLVFWHMPETALVFLVWDHDPDGRDPTGRTGLTAFSSMMNGYHNYLLEGEEASIVVH 875
 DB 1420 TLVFWHMPETALVFLVWDHDPDGRDPTGRTGLTAFSSMMNGYHNYLLEGEEASIVVH 1479
 QY 876 AVSDISGVKQALGLKGLFGRPKRGSLSHAAGRPAPRPSVORILRTASAPTKSQK 935
 DB 1480 AVSDISGVKQALGLKGLFGRPKRGSLSHAAGRPAPRPSVORILRTASAPTKSQK 1539
 QY 936 GRGPEPELVLTGRTDGSKGVADVVPPGPAPEAPAOEGSGSPKGAAPAAVAEKSPV 995
 DB 1540 GRGPEPELVLTGRTDGSKGVADVVPPGPAPEAPAOEGSGSPKGAAPAAVAEKSPV 1599
 QY 996 RYRPREVLDPGPAG 1010
 DB 1600 RYRPREVLDPGPAG 1614
 RESULT 3
 ABB07493
 ID ABB07493 standard; Protein: 621 AA.
 XX
 AC ABB07493;
 DT 23-APR-2002 (first entry)
 XX
 DE Human lipid metabolism molecule (LMM) polypeptide (ID: 2965233CD1).
 XX
 KW Lipid metabolism molecule; LMM; cytosolic; neurotropic; neuroprotective;
 KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;
 KW cardiovascular; antiHIV; antiemetic; antiallergic; hypertensive; human;
 KW cancer; gene therapy; protein therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200204490-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-US21432.
 XX
 PR 07-JUL-2000; 2000US-216801P.
 PR 07-JUL-2000; 2000US-216803P.

PR 14-JUL-2000; 2000US-218233P.
 PR 21-JUL-2000; 2000US-220046P.
 PR 26-JUL-2000; 2000US-220739P.
 PR 04-AUG-2000; 2000US-222824P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 PI Tang YT, Asimzai Y, Das D, Thornton M, Lu DAM, Tribouley CM;
 PI Yue H, Gandhi AR, Walla NK, Khan FA, Lu Y, Yao MG, Hafalia ATA,
 PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugh MR;
 XX
 DR WPI: 2002-164631/21.
 DR N-PSDB; ABA94696.
 XX
 PT Lipid metabolism molecules useful in diagnosing, treating or preventing
 PT cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
 PT skin and cardiovascular disorders
 XX
 PS Claim 1; Page 112-113; 128pp; English.
 XX
 CC The invention provides human lipid metabolism molecule (LMM) polypeptides
 CC and polynucleotides. The LMM polypeptides can be expressed by standard
 CC recombinant methodology. The LMM polypeptides are useful for diagnosing
 CC or treating a condition or disease associated with the expression of LMM,
 CC or screening for compounds that specifically bind to or modulate the
 CC activity or expression of LMM. They are also used to generate antibodies
 CC and assess the toxicity of test compounds. The LMM polypeptides,
 CC modulators and antibodies are specifically useful for diagnosing,
 CC treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
 CC melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
 CC cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/
 CC inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
 CC or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
 CC esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
 CC disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
 CC disorders (e.g. hypertension, arterial dissections, vascular tumours, or
 CC thrombolysis). The present sequence represents a human LMM polypeptide
 CC sequence.
 CC
 SO Sequence 621 AA:
 Query Match 50.6%; Score 3225; DB 23; Length 621;
 Best Local Similarity 99.0%; Pred. No. 1.2e-241;
 Matches 614; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MAPPTAGPLPGALPPDPDPDPESRWLFLSANILPVERCGANQEGMVKILGSGSG 60
 DB 2 MAPPTAGPLPGALPPDPDPDPESRWLFLSANILPVERCGANQEGMVKILGSGSG 61
 QY 61 LVRFYLLDEHRSICIMRPSRKNEKAKISTDSIOEVSSEGRSVFQRYDGSFDPNCCFSI 120
 DB 62 LVRFYLLDEHRSICIMRPSRKNEKAKISTDSIOEVSSEGRSVFQRYDGSFDPNCCFSI 121
 QY 121 YHGSRESLIDVSTSEVARTWVGLRLVLMAGISDEDSLARRORTDQMLKOTFEADKN 180
 DB 122 YHGSRESLIDVSTSEVARTWVGLRLVLMAGISDEDSLARRORTDQMLKOTFEADKN 181
 QY 181 GDGSLSTIEVQLHLKLVNLPQRQVKMFEADTDHOGTLGFEBCAFYTKMSTRDL 240
 DB 182 GDGSLSTIEVQLHLKLVNLPQRQVKMFEADTDHOGTLGFEBCAFYTKMSTRDL 241
 QY 241 YLLMLTYSNNHDDHDAASLQRFLOVEOKMAGVTLESCODITEOPPEPENSKLLGIDG 300
 DB 242 YLLMLTYSNNHDDHDAASLQRFLOVEOKMAGVTLESCODITEOPPEPENSKLLGIDG 301
 QY 301 FTNNTSRAGCIFNDEHHVHODMTQPLSHYFTTSSNTVLYVGDOLMSOSRVDMYAVWLQ 360
 DB 302 FTNNTSRAGCIFNDEHHVHODMTQPLSHYFTTSSNTVLYVGDOLMSOSRVDMYAVWLQ 361
 QY 361 AGRCRVEVDKDPDGPRIYHGGTILSKILFKVITETINKYATIKNEYPIYLSTENHCS 420
 DB 362 AGRCRVEVDKDPDGPRIYHGGTILSKILFKVITETINKYATIKNEYPIYLSTENHCS 421

QY 421 VTQOKKMAQYLTDLIDGKIDLSVSSSEDAATLPSQMLKGLVKGKLPANISEDAEG 480
 DB 422 VTQOKKMAQYLTDLIDGKIDLSVSSSEDAATLPSQMLKGLVKGKLPANISEDAEG 481
 QY 481 EYSDSEDAEIDDDCKLLNGDASTNRKRENTARKRLDLSIKESTIRCEPPNPFVSTL 540
 DB 482 EYSDSEDAEIDDDCKLLNGDASTNRKRENTARKRLDLSIKESTIRCEPPNPFVSTL 541
 QY 541 SPFGKLGKRSKAEEVSEGEDAGASRRNGRLVYGSFSRRKKSGKILKAASVEEGDEGOD 600
 DB 542 SPFGKLGKRSKAEEVSEGEDAGASRRNGRLVYGSFSRRKKSGKILKAASVEEGDEGOD 601
 QY 601 SPFGSGRGATRKCKMKLSR 620
 DB 602 SPFGSGRGATRKCKSSVPSTR 621
 XX
 PS RESULT 4
 AB08001
 ID ABB08001 standard; Protein: 1014 AA.
 AC ABB08001;
 XX
 DT 27-AUG-2002 (first entry)
 DE
 XX
 KW Human Lipid metabolism enzyme (LME)-1 (Id: 7472210CD1).
 KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective;
 KW neurotrophic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;
 KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;
 KW gene therapy; protein therapy; enzyme.
 OS Homo sapiens.
 XX
 PN WC200229036-A2.
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31302.
 XX
 PR 06-OCT-2000; 2000US-238388P.
 PR 13-OCT-2000; 2000US-240616P.
 PR 02-NOV-2000; 2000US-245719P.
 PR 08-NOV-2000; 2000US-247503P.
 PR 17-NOV-2000; 2000US-249503P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 PI Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;
 PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;
 PI Lal PG, Tribouley CM;
 XX
 DR WPI: 2002-315862/35.
 DR N-PSDB; ABI60537.
 XX
 PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and
 PT Creutzfeld-Jakob disease -
 PT
 XX
 PS Claim 1; Page 110-113; 127pp; English.
 XX
 CC The invention relates to human lipid metabolism enzymes (LMEs) and
 CC encoding polynucleotides. The LMEs can be expressed by standard
 CC recombinant technology. The LME polypeptides, polynucleotides and
 CC modulators may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate LME expression such as cancer
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
 CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
 CC pectoris and mitral valve prolapse). The present sequence represents
 CC the human LME-1 polypeptide.
 CC

SQ Sequence 1014 AA:
 Query Match 49.6%; Score 3163; DB 22; Length 1014;
 Best Local Similarity 63.5%; Pred. No. 1.7e-236;
 Matches 607; Conservative 141; Mismatches 172; Indels 36; Gaps 9;
 29 FLNANLTPYERQMGOMVLRGSGKGLVRYLYDERSCIRMPKRNKAKIS 88
 18 FLVNDNSVFYERCMVMSQSTQWIKRKTKRGTGLVLFYDERHTRILKMPKSKSEAKLL 77
 89 IDSIOEVSERQSEVFORYPDGSFDPNCCFSIYHGSRESLQVSTSEVARTWTGLRY 148
 78 IDSIYVTEBROSEIFHRQAEQNFDPSCFTIYHGNHMSLDLITSNPEARATWITGLAY 137
 149 LMAGISDESLARQRTROMLKQTPDEADKNGDSLIGEVQLQHLKLNVLPRQVNO 208
 138 LMAGISDESLARQRTROMLKQTPDEADKNGDSLIGEVQLQHLKLNVLPRQVNO 197
 209 MFEADDDHOGTLGFEFCAPFKMASTRDLYLMLTYSNKHDLDAASLOFLOVEOK 268
 198 MFEADDDHOGTLGFEFCAPFKMASTRDLYLMLTYSNKHDLDAASLOFLOVEOK 257
 269 MAGVTLSCODIIEQEPCEPNKSKGLIGDFTNTTSPAGDIFNPENHHVQDMTOPU 328
 258 MNVTTDYCDIIEKFEVSEENKKNVGLIEGFTNMRSPACDIFNPLHEVYQDDOPL 317
 329 SHFITSNHTYLVGQQLMSQSRVDYAWVLOAGCQVEVDCMDGPDGEPVHHGTYLS 388
 318 CNVYIASNHTYLVGQQLMSQSRVDYAWVLOAGCQVEVDCMDGPDGEPVHHGTYLS 377
 389 KILFKDVIETINKYAFIKNEYPVILSIENHCSYIOQKMAQVLTDLIGDKLDSVSSSD 448
 378 KILFKDVIETINKYAFIKNEYPVILSIENHCSYIOQKMAQVLTDLIGDKLDSVSSSD 437
 449 ATTLPSQMLKGLVKGKLPANISDAEVEGVSDESDADEIDDOCKL-LNODASINRK 507
 438 CKOLPSPQSLKGLVKGKLPANISDAEVEGVSDESDADEIDDOCKL-LNODASINRK 497
 508 RVEHTARKIDSLIKESKIRNDCEDPNFVSSTLSPSGKLKRS--KAEENV-ESGEDAGA 564
 498 QVEFIRKTESLKESSIRNDCEDPNFVSSTLSPSGKLKRS--KAEENV-ESGEDAGA 553
 565 SRNRGLVVGSSFRKKGSKLTKKAASVEGDEGDS--PGQSGRATNOKTKMLSRA 621
 554 -KSHGRSLMTNFGKHKTKTKRSKSYSTDDEEDTQOSTGEGCOLYLRGRRKTKMLCRE 612
 622 LSDLVKTKSVATHDIEEAASSQVSSFTSKAHOLIQQPAGYLPFNOQLSRIPSS 681
 613 LSDLVKTKSVATHDIEEAASSQVSSFTSKAHOLIQQPAGYLPFNOQLSRIPSS 671
 682 YRVDSSNYPQPFNNAGCQVAVLYQSEGRMLQLNRAKFSANGGCGVYLKPGCMCGVFN 741
 672 YRVDSSNYPQPFNNAGCQVAVLYQSEGRMLQLNRAKFSANGGCGVYLKPGCMCGVFN 731
 742 PNSEDPLRGQKQVLVRIISGQQLPKPRDSMLDGRGEITDPYVEVEITGLPVCCSRQT 801
 732 PFGSDPLRANPKQVILKVISGQQLPKPRDSMLDGRGEITDPYVEVEITGLPVCCSRQT 791
 802 RYVDNDNGNPMTEETLVPMVMPETALRYLWMDHPIGRDPIGORTLAFSSMMPGYRHY 861
 792 RYVDNDNGNPMTEETLVPMVMPETALRYLWMDHPIGRDPIGORTLAFSSMMPGYRHY 851
 862 YLEGEBAEASIFVAVASDISG-----KVKQALGKGLPLRGPRG 901
 852 YLEGEBAEASIFVAVASDISG-----KVKQALGKGLPLRGPRG 911
 902 SLDSNAGRPAPBSVQRIILKRTASATPKSQPCRGEPPELYLGTROGSGVAD 957
 912 SSENNS--HYVKKRSIGRIILKRTASAPAKGRRKSKMGFQEMV-BIKDSVSEATPD 964

RESULT 5
 ABG13669

ID ABG13669 standard; Protein; 787 AA.
 AC ABG13669;
 XX 18-FEB-2002 (first entry)
 DT Novel human diagnostic protein #13660.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 PI N-PSDB; AAS77856.
 DR WPI, 2001-639362/73.
 DR N-PSDB; AAS77856.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensic, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT Claim 20; SEQ ID No 44028; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and
 PS polypeptide (II) sequences. (I) is useful as hybridization probes,
 PS polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 PS and gene mapping, and in recombinant production of (II). The
 PS polynucleotides are also used in diagnostics as expressed sequence tags
 PS for identifying expressed genes. (I) is useful in gene therapy techniques
 PS to restore normal activity of (II) or to treat disease states involving
 PS (II). (II) is useful for generating antibodies against it, detecting or
 PS quantitating a polypeptide in tissue, as molecular weight markers and as
 PS a food supplement. (II) and its binding partners are useful in medical
 PS imaging of sites expressing (II). (I) and (II) are useful for treating
 PS disorders involving aberrant protein expression or biological activity.
 PS The polypeptide and polynucleotide sequences have applications in
 PS diagnostics, forensic, gene mapping, identification of mutations
 PS responsible for genetic disorders or other traits to assess biodiversity
 PS and to produce other types of data and products dependent on DNA and
 PS amino acid sequences. ABG00010-ABG30377 represent novel human
 PS diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 787 AA:
 Query Match 36.7%; Score 2343; DB 22; Length 787;
 Best Local Similarity 61.4%; Pred. No. 6.4e-173;
 Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;
 239 DLVLLMLTYSNKHDKDLDAASLOFLOVEQKMAGYTLESODIIEQEPCEPNKSKGLIGI 298
 1 DLVLLMLTYSNKHDKDLDAASLOFLOVEQKMAGYTLESODIIEQEPCEPNKSKGLIGI 60
 299 DGFNNTYRSPAGDIFNPENHHVQDMTOPUSHFYTSNHTYLVGQQLMSQSRVDYAWY 358
 61 EGFNNTYRSPAGDIFNPENHHVQDMTOPUSHFYTSNHTYLVGQQLMSQSRVDYAWY 120
 359 LQAGRCVYDQWMDGPDGEPVHHGTYLSKILFKDVIETINKYAFIKNEYPVILSIENH 418

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Db 121 LQEGRCVEYDCWDGDPGEFVHGHGTYLTLSKILFRDVEETINKNAFVKNPEVILSTENH 180
QY 419 CSVYIOOKKMAQYLTDLIGDKLIDSSVSSEDAITTPSPQMKGLKLVGKKLPANISDEAE 478
Db 181 CSTQOQKRIAYLIGTIGTIDLDSSVDTGECQKLPSPQSLKGLVYKKLPYHLGDDAE 240
QY 479 EGEVSDSDADEIDDDCKL-LNGDASTNRKRVENTAKRKIDSLIKESKIRDCEDPNPNSV 537
Db 241 EGEVSDSDADEIDDECKFKLHYNSNGTTEHQVESFIRKLESLIKESQITDKEDPPDSFTV 300
QY 538 STLSPSGKLGKRS--KAEDV-ESGEDAGASRRNGRLVVGFSRRKKGSKLKAASVEE 594
Db 301 RALKAKTHGELNHLKQSPVKSBSG----KSHGSLMTNFGKHKKTKTSRSKSKYSTDD 355
QY 595 GDEGDS---PGQSRGATROKTKMKLSRALSDLVKTKSVATHDIEEAASSWQVSFS 651
Db 356 EEDTQOSTGKEGQLYRLGRRTMKLCRELSDLVYVYTNNSVAADI-VDDGTGNAVLSFS 414
QY 652 ETKAHQILQOKPAQYLFENQOOLSRIPSSRYVDSNNYNPQFPWNAQCOMVALNTQSEGR 711
Db 415 ETKAHQVVOOKSEQFMITYNOKQLTRIPSAVRIDSSNFNPLPYWNAQCOLVALNTQSEGR 474
QY 712 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDPPLQOLKQVLRLITISGQLEPKRPD 771
Db 475 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDPPLQOLKQVLRLITISGQLEPKRPD 534
QY 772 SMIGRGEIIDPFVEVEIIGLPVDCSREQT RVVDNGFNPTEETLVFWHPEITLVF 831
Db 535 SMIGRGEIIDPFVEVEIIGLPVDCSREQT RVVDNGFNPTEETLVFWHPEITLVF 594
QY 832 LVVDHPRIQGRDFTGRTLPSSMPPGRVRLVLEGEAEATFVAVASDISG----- 882
Db 595 LVVDHPRIQGRDFTGRTLPSSMPPGRVRLVLEGEAEATFVAVASDISG----- 882
QY 883 -----KVKQALGLKGLFLRGPCKPSLDSHAAGRPAPRPSVORILRTASAPRK 931
Db 655 SYTILFLGATNKRQLOGKGLFNKNPRHSSENN--HYAKRSLGRIILRTASAPRK 712
QY 932 SOKPGRGPEPELVGTGRDGSKGVD 957
Db 713 GRKSKMGFOEMV-EIKDSVSEATRD 737

```

RESULT 6
ID AAE14673
XX AAE14673 standard; Protein; 787 AA.
XX AAE14673;

26-JUL-2002 (first entry)
Human phosphatidylinositol-specific phospholipase C-1-like enzyme.

Human: phosphatidylinositol-specific phospholipase C-1-like enzyme;
PI-PLC-like enzyme; chromosome 3; asthma; cancer; central nervous system;
CNS disorder; Parkinson's disease; dementia; COPD; protein therapy;
chronic obstructive pulmonary disease; gene therapy; vaccine.

Homo sapiens.

MO200226996-A2.

04-APR-2002.

24-SEP-2001; 2001WO-EP11012.

27-SEP-2000; 2000US-235552P.

(FARB) BAYER AG.

Zhu Z;

WPI: 2002-372128/40.
N-PSDB: AAD31081.
Isolated polynucleotides encoding human phosphatidylinositol-specific phospholipase C-1-like enzymes, useful for preventing, diagnosing and treating e.g. asthma, cancer, a CNS disorder or chronic obstructive pulmonary disease -
Claim 25; Fig 2; 125bp; English.

The invention relates to polynucleotide encoding human phosphatidylinositol-specific phospholipase C-1-like enzyme (PI-PLC-like enzyme). Human PI-PLC-like enzyme gene is located on chromosome 3. The PI-PLC-like enzyme polypeptide and polynucleotide may be used in the prevention, diagnosis and treatment of diseases associated with enzyme dysfunction, e.g. asthma, cancer, central nervous system (CNS) disorder (e.g. Parkinson's disease, dementia) and chronic obstructive pulmonary disease (COPD). The polynucleotide and polypeptide may be used to treat disorders associated with decreased PI-PLC-like enzyme expression by rectifying mutations or deletions in a patient's genome that affect the activity of PI-PLC-like enzymes, by expressing inactive proteins or to supplement the patient's own production of PI-PLC-like enzymes. The polynucleotide and its complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples. The PI-PLC-like enzymes may also be used as antigens in the production of antibodies and in assays to identify modulators of PI-PLC-like enzyme expression and antagonists may be used to down-regulate expression and activity of the enzyme and as diagnostic agents for detecting the presence of PI-PLC-like enzyme in samples. The present sequence is human phosphatidylinositol-specific phospholipase C-1-like enzyme.

Sequence 787 AA:

Query Match 36.7%; Score 2343; DB 23; Length 787;
Best local Similarity 61.4%; Pred. No. 6, 4e-173;
Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;

```

QY 239 DLYLMLTYSNHNKHDLAASLQRLVQEQMAGVLTLESODITGEFPEENKSKGLGT 298
Db 1 DLYLMLTYSNHNKHDLAASLQRLVQEQMAGVLTLESODITGEFPEENKSKGLGT 60
QY 299 DGFNTYRSPAGDIFENFHHVHDMTOPLSHYFTISNHTYVYGQOLSSQSVNDYNAV 358
Db 61 EGFNFMRSAPACIDFENLHVEYVQDMQPLCNTYITASSNHTYVLTGQOLSSQSVNDYNAV 120
QY 359 LQAGRCVEYDCWDGDPGEFVHGHGTYLTLSKILFRDVEETINKNAFVKNPEVILSTENH 418
Db 121 LQEGRCVEYDCWDGDPGEFVHGHGTYLTLSKILFRDVEETINKNAFVKNPEVILSTENH 180
QY 419 CSVYIOOKKMAQYLTDLIGDKLIDSSVSSEDAITTPSPQMKGLKLVGKKLPANISDEAE 478
Db 181 CSTQOQKRIAYLIGTIGTIDLDSSVDTGECQKLPSPQSLKGLVYKKLPYHLGDDAE 240
QY 479 EGEVSDSDADEIDDDCKL-LNGDASTNRKRVENTAKRKIDSLIKESKIRDCEDPNPNSV 537
Db 241 EGEVSDSDADEIDDECKFKLHYNSNGTTEHQVESFIRKLESLIKESQITDKEDPPDSFTV 300
QY 538 STLSPSGKLGKRS--KAEDV-ESGEDAGASRRNGRLVVGFSRRKKGSKLKAASVEE 594
Db 301 RALKAKTHGELNHLKQSPVKSBSG----KSHGSLMTNFGKHKKTKTSRSKSKYSTDD 355
QY 595 GDEGDS---PGQSRGATROKTKMKLSRALSDLVKTKSVATHDIEEAASSWQVSFS 651
Db 356 EEDTQOSTGKEGQLYRLGRRTMKLCRELSDLVYVYTNNSVAADI-VDDGTGNAVLSFS 414
QY 652 ETKAHQILQOKPAQYLFENQOOLSRIPSSRYVDSNNYNPQFPWNAQCOMVALNTQSEGR 711
Db 415 ETKAHQVVOOKSEQFMITYNOKQLTRIPSAVRIDSSNFNPLPYWNAQCOLVALNTQSEGR 474
QY 712 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDPPLQOLKQVLRLITISGQLEPKRPD 771

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Db 475 MMDLNRAKRAKANGCIVYALKPOOMCKGTNPISGDLPLANPKKQILAKVISQOLPKPPD 534
 Qy 772 SMLDGEIIDEPEVEEIIIGLVDYCSREQTRVVDNGFNPTVEETLVEMPELALVRF 831
 Db 535 SMDGDEIIDEPEVEEIIIGLVDYCSREQTRVVDNGFNPTVEETLVEMPELALVRF 594
 Qy 832 LVMDHDPIDGRDPLIGORTLAFSSMMPGRVLYLECMEEASIFPHVAVSDISG----- 882
 Db 595 LVMDHDPIDGRDPLIGORTLAFSSMMPGRVLYLECMEEASIFPHVAVSDISG----- 654
 Qy 883 -----KVQALGKGLFLRGPCKGSLDSHAAGRPAPRPSYSORILKRTASAPTK 931
 Db 655 SYTLIFLIGATKTRQGLKGLFKNKPRHSSSENN--HYVKKRSIGDILKRTASAPAK 712
 Qy 932 SQRGRGPEPELVLTGRDYGSKGVAD 957
 Db 713 GRKSKMGFEQENV-EIKDSVSEATRD 737

RESULT 7
 AA017367
 ID AA017367 standard; protein; 997 AA.

AA017367;

19-JUL-2002 (first entry)

Human phospholipase C epsilon.

Km aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
 Km insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
 Km transmembrane receptor PKR7; collagen type XVIII alpha 1;
 Km platelet derived growth factor receptor alpha; laminin M chain;
 Km subtilisin like protein PACE4; nidogen.

OS Homo sapiens.

PN EP1191107-A2.

PD 27-MAR-2002.

XX 21-AUG-2001; 2001EP-0250300.

XX 25-SEP-2000; 2000DE-1048633.

XX (SCHD) SCHERING AG.

XX Hess-stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;

PI Regidor P, Scotti S;

XX WPI: 2002-317413/36.

DR In vitro diagnosis and monitoring of endometriosis, comprises

PT detecting reduced expression of specific gene products, e.g. from the

PT fibronectin gene -

PS Claim 1; Page 20-21; 21pp; German.

CC The present invention relates to a method for the in vitro diagnosis of
 CC endometriosis by determining the amount of gene product from at least one
 CC specific gene in a patient sample and comparing this with the amount of
 CC gene product in a control sample. A reduced level is indicative of
 CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
 CC transmembrane receptor PKR7, collagen type XVIII alpha 1,
 CC platelet derived growth factor receptor alpha, laminin M chain,
 CC subtilisin like protein PACE4 or nidogen. The method is useful for
 CC initial diagnosis of endometriosis, and also for monitoring progress and
 CC treatment of the disease. The present sequence is human phospholipase C
 CC epsilon.

xx
 SQ Sequence 997 AA;

Query Match 23.9%; Score 1524.5; DB 23; Length 997;
 Best Local Similarity 36.2%; Pred. No. 4.1e-109;
 Matches 348; Conservative 156; Mismatches 279; Indels 177; Gaps 20;

Qy 41 CMGAEQGMQWVKLRGSGKGLVRFYLDDEHRSCTMRPSRKN-EKAKISIDSIGVEGR 99
 Db 13 CISFMQACELKATVAPNRIRINREFTLDTDLALRMPSKSKDLKAKDISAIREIRGK 72
 Qy 100 OSEVFORYPDGSFD---PNCFSIYHSGHRSGLDVSISSEVATWYGLRYLAGISDE 156
 Db 73 NTEFTTN--NGIADICEDCAFSLIHGENYESLDLVANSAVANIMWSGLYVSRKOP 130
 Qy 157 -DSLARRORT-ROWLKOTFDEADKNGSGSLSEIGVOLLKRLVNVNIPROVKOMFREAD 214
 Db 131 LDFMGNONTFRFMYLKVFEADVDGNGIMLEDYSVLILQNLPTLKEAIRLKFKEIQ 190
 Qy 215 TDDHOGT--LGFEEPCAFYKMMSTRDLYLMLTYSNHKLDAASLQRLQVQKNAV 272
 Db 191 KSEKELTRFVTEEEFCEAFCELCETREYVFLVQISKNEKELYDANDLMLFEAEQGYTHI 250
 Qy 273 TLESCODITTEOPPCPENKSKGLGIDGFTNTTRSPAGDINPEHHVHODMTOPLSHYF 332
 Db 251 TEDICLDIIRRYELSEEGKQGFALIDFTQYLLSSECDIDPEQKKAODMTOPLSHY 310
 Qy 333 ITSSHNTYLVGQOLMSOSRVDYAWVLQAGRCVVDCEWDGPDGEPIYHGYTLTSKILF 392
 Db 311 INASHNTYLIIEQFRGADINGTIRALKMGCRSVELVSDGSDNPIICNNNMTHHSF 370
 Qy 393 KVIETINTKATKNEYPIVILSIENHGSYIQKKAQVYITLIDGKLDLSSVSSDATTL 452
 Db 371 RSVIEYINFAFVASEYPIILCLGNHCSLPQKVAQMKKFKFNKL-YTEADLPSESYL 429
 Qy 453 PPSQMLKGLIKVKKGLPLANISEDAEEGVSDESDADEIDDCXKLDNGDASTNRKREVT 512
 Db 430 PSEPEKLRMIVYKGRKLPSD--PDVLEGEVTDSD----- 461
 Qy 513 AKRKLDLILKESKIRDCEDPNFNSVTLSPSGKLKRSKAEDVESGEDAGASRRNGRLV 572
 Db 462 -----EQAQMSRR----- 469
 Qy 573 VGSFSRRKKKSKLKAASVYEGDEGDSFGQSGRATQKTKMLKSLSLVYKTSYV 632
 Db 470 -----MSVDYNGE-----OQIIRCRELSDVLSICSV 497
 Qy 633 ATHDIE--MEAASSQVSSPSETKAHQILOOKPAQYLRFNQOOLSRTPSSYRVDSNNTN 690
 Db 498 QYRDFELSKSQNYEMCSFSETEASRIANEYEDDVNTNKKFLSIYSAMRIDSSNLTN 557
 Qy 691 POPFWNAGCOMVALNTQSEGRMLQLNRAKFSANGCGGYLKGCCQGV--FNPNSEDL 748
 Db 558 PODFWNCGQIVAMNFQTPGPMADLHTGWFLONGCGGYLRSIMDEVSYSFSAANTKGL 617
 Qy 749 PGOLKQVLRIISGOOLPKPRDSMLGDGEIIDEPEVEEIIIGLVDYCSREQTRVVDNG 808
 Db 618 PGVSPILALHKIKISQGFPRPKGACA--KQVDIDPVYCIIEHIGIPADCSDEQRTKYQONS 675
 Qy 809 FNPTVEETLVFVIMPELALVRFVMDHDPIDGRDPLIGORTLAFSSMMPGRVHYLYEG--- 865
 Db 676 DNPIFDTEPFQVNLPELMIIRFVLDLDDVIGDFEIGQYTIPEGLQPGVRHPLMSFVG 735
 Qy 866 --MEASIFVHVAVSDISG-----KYKQALGKGLR-----GP 898
 Db 736 DIMEHVTLFVHIAITNNSGGKAKQKRSLSYRMGKKVREYTMNLIDKTIIDIFKIAVHP 795
 Qy 899 KPGSLD-----SHAAGRPAPRPSYSORILKRTASAPTKSQKPC-----RRCPP 941
 Db 796 LREADIRENMQNAIYSIKELGCLPPL-ASLKQCLTLSSRLTTSNTPTSVSLYMDSPF 854
 Qy 942 EL 943

Db 855 YL 856

RESULT 8
AAW01596

ID AAW01596 standard; Protein; 1096 AA.

AAW01596;

17-MAR-1997 (first entry)

Inositol-1,4,5-triphosphate binding protein.

IP-3; inositol-1,4,5-triphosphate; phospholipase C-delta 1;
drug testing; screening; diagnostic; cancer; inflammatory disease;
tumour; circulatory organ disease.

Rattus sp.

JP08266283-A.

15-OCT-1996.

31-MAR-1995; 95JP-0075876.

31-MAR-1995; 95JP-0075876.

(HIRA/) HIRATA M.

(MITK) MITSUI TOATSU CHEM INC.

WPI; 1996-512670/51.

N-PSDB; AAT58225.

Structural gene encoding protein capable of binding with
inositol-1,4,5-tri-phosphate - useful for creation of drugs and
diagnostics for, e.g. circulatory organ diseases, inflammatory
diseases, etc.

Claim 2; Page 6-11; 13pp; Japanese.

This sequence is a 130 KD protein capable of binding inositol-1,4,5-
triphosphate (IP-3). The protein has approx. 38.2 percent homology with
phospholipase C-delta 1 (PLC-delta 1). The DNA (AAT58225) encoding it,
is important for the creation of drugs and diagnostic agents for various
diseases, e.g. circulatory organ, inflammatory and nerve diseases,
malignant tumours and cancers.

Sequence 1096 AA;

Query Match 23.8%; Score 1517; DB 17; Length 1096;
Best Local Similarity 36.1%; Pred. No. 1.8e-108;
Matches 349; Conservative 161; Mismatches 278; Indels 180; Gaps 22;

41 CGAAGGQWYKLRGSGKGLVRFYLDHRSICIMWRSRKN-EAKAISIDISQVSEGR 99

112 CTSFQAGCELKAKVPSNRITVFFLTDLOALKEPSKDKLEKAKDISAIEIRLKG 171

100 QSEVFRYPDSFD--PNCFSIYHGSRLDVTSSSEAVRTWYGLYLMAAGISDE 156

172 NTEFRN--NGIADQICDCAFSLIHGNYESLDIVANSAYANIMVSGLYLVSRSKOP 229

157 -DSLARRRT-RDWLKTQTEADAKNGDSISGEVLOLHLKLVNVLPRQVKKOMFREAD 214

230 LDFMGNQNTFRFVWLKTFEADVDGNGIMLEDTSVELIKQLMPTLKEKIRIKFEIQ 289

215 TDDHGT--LGFEECAFYKAMSTRDLILMTYSNKKHDLAASLQRTQVQKMAV 272

290 KSKELITRVTEEECEAFCELCRPEYVFLVQISKKEKELANDMLFLEVQGVTHV 349

273 TLESQDIIIEFPCPEKSKGLIGIDFTYTRSPADGIPNPHHNVHODMOPSLSHYF 332

350 TEDMDIIRRYELSEORQKGFALIDGFTYLLSPEDIDFPEQKRVADDMQPLSHY 409

QY 333 ITSSHTYLVGQQLMSQSHVDMYAMTLQAGCRVCEVDCWDGPDGEPYVHGGYTLTKILF 392

DB 410 INASHNTYLVIEDQFRPADINDGVYALKWGCRSIELDYSDGPDNPIICNNRNAMLLSF 469

QY 393 KDVIETINKYAFKNEYPIVLIENHGSYIOCKKAQYLTDLGKLDLSS-VSEDAAT 451

DB 470 KSVLEYINKFAVASSEYPLICLGNHCSLPQORVAVQOMKRVGNKLYTEAPLSE--SY 527

QY 452 LPSQMLKGLIVKGGKLLPANISEDAEGVESEDSADEIDDCILNGDASTNRKRVEN 511

DB 528 LPSPELKMILIVKGGKLLPS--ESDLIGEFTYDDE----- 560

QY 512 TAKRKIDSLIKESKLRDCEDPNNFSVTLSPSGKLGKRSKAEDEVEDSAGASRRMRL 571

DB 561 -----EEMEMRR----- 568

QY 572 VYGFSPRRKKKSKLKAASVEGDEGDSFGGSGRATROKTKWLSRALSDLVKTKS 631

DB 569 VSGDYN-----GEOKHIMLCRELSDIVSICKS 595

QY 632 VATHDIE--MEAASSMOVSSEFETKAQIIOQKPAQYLFNQOOLSRTPSSVYDSSNY 689

DB 596 VQYRDFELSMKTQNYWEICSFSESLASIANEYEDFVYNNKFLSRVYSAMRIDSSNL 655

QY 690 NPQPTWNAQCQWALNTQSEGRMLQLNFAKPSANGCGYVLKPCMCQGV--FNPNSDEP 747

DB 656 NPQDFWNCQOIVAMNEFTPGPMMDLHTGWELQNGCGYVLRPSIMDEVSYSANRGI 715

QY 748 LPGLKQVLVRIISGOOLPKPRDMLGDRGELIDPVEVEHILPVDCSREQTRVYDDN 807

DB 716 VGVSPPLILHIKITISGQNFPPKAGCA--KGDVIDPYVCEIHHIPADCEORRTVQON 773

QY 808 GNPFTVEETLVENVHMDIALVRLVMDHPIDGDFIGORTLAFSSMPGYRHVYLEG-- 865

DB 774 SDNPLFDETFEFGVNLPELWVRVILLDDOYIGDFIGQTIIPRECLOPGRHVPRLSFV 833

QY 866 ---MEASIFVHAVVSDISG-----KVKQALGLKGLFLR-----G 897

DB 834 GDIMEHVTLLFVHAITNRSGGKAQKRSLSYRMGKKVREYTMRLNIGLKTIDDIKLIYAH 893

QY 898 PKPGLSD-----SHAAGRPAPPSVSGORILRTASAPTSQKRG-----RGRF 940

DB 894 PLRAIIMREMNAIYVVELGCLPPI-ASLKQCLITLSSRLTSDSPSVSLVWKDF 952

QY 941 PEL-VLGT 947

DB 953 PYLEPLGT 960

RESULT 9

ID AAE10440 standard; Protein; 762 AA.

AAE10440;

10-DEC-2001 (first entry)

Novel human phospholipase protein #7.

Human; novel human protein; NHP; phospholipase protein; phospholipid;
phospholipase C delta-4; cell activation; signal transduction; cancer;
drug screening; biological disorder; mental disorder; medical disorder;
gene therapy.

Homo sapiens.

MO200168871-A2.

20-SEP-2001.

13-MAR-2001; 2001WO-US07994.

13-MAR-2000; 2000US-0188885.

PR 15-MAR-2000; 2000US-0189693.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Hu Y, Nepomnitchy B, Donoho G, Hilbun E, Turner CA, Abulin A;
 XX Friedrich G, Zambrowicz B, Sands AT;
 XX MPI: 2001-582456/65.
 DR N-PSDB: AAD17564.
 XX
 PT New polynucleotides encoding human phospholipase protein involved in
 PT cell activation and signal transduction, useful for drug screening,
 PT diagnosis and in gene therapy of biological disorders
 XX
 XX Claim 11: Page 41-43; 45pp; English.
 CC The present sequence is novel human protein (NHP), phospholipase
 CC protein. Phospholipases hydrolyse phospholipids and play a key
 CC role in the cell activation and signal transduction. NHPs share
 CC structural similarity with animal phospholipases, including phospho-
 CC lipase C delta-4. NHP oligonucleotides are useful in conjunction with
 CC polymerase chain reaction (PCR) to screen libraries, isolate clones,
 CC and prepare cloning and sequencing templates, and alternatively as
 CC hybridisation probes for screening libraries and assessing gene
 CC expression patterns. They are used in the identification, selection
 CC and validation of novel molecular targets for drug discovery, where
 CC identification and characterisation of human genomic clones is helpful
 CC for identifying polymorphisms, determining the genomic structure of a
 CC given locus/allele and designing diagnostic tests. The microarray
 CC comprising NHP cDNA is useful for screening collections of genetic
 CC material from patients having a particular medical condition, which
 CC is used to identify mutations associated with a particular disease and
 CC also as diagnostic or prognostic assay. NHP nucleotide sequences are
 CC useful for drug screening. Nucleotide construct encoding NHP products
 CC are used in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo. The
 CC NHP sequences are useful for generating antibodies, as reagents in
 CC diagnostic assays, for identifying other cellular gene products related
 CC to NHP and as reagents in assays for screening for compounds that are
 CC useful in the treatment of mental, biological or medical disorders and
 CC diseases. They can be used to therapeutically augment the efficacy of
 CC chemotherapeutic agents used in the treatment of breast or prostate
 CC cancer.
 CC
 XX
 XX Sequence 762 AA:
 SQ
 Query Match 22.6%; Score 1441; DB 22; Length 762;
 Best Local Similarity 38.3%; Pred. No. 8.5e-103;
 Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;
 QY 45 MOEGMOWKLRGSGKGLVRYLDEHRSICRW--RPSRKNKAKISIDSIQEVSEGRSE 102
 DB 18 MOEGMPKRYKRSKMKLRFRLQNDQMV-WHARQARSGAKSPFSIVETIRNGHSD 76
 QY 103 VQRTYPDGSGEDPNCSESTYHSHRESIDLVSTSEVARTVTCGRYIMAGISDESLARR 162
 DB 77 LIRSLAEELPLEOGFTLVFHG-RRSNIDLMANVSZEAQIMWRLGLVDLVTSMD---H 131
 QY 163 QRTDQWLKQTFDEADKNGSGLSIGEVQLDLKRLNVLPRQRYKQMFREADTDHGGTL 222
 DB 132 QERIDQWLSDFQKDGKNOGKMSFOEYORLHLMANVEMOEYAFSLFOAADT-SQSGTL 190
 QY 223 GFEFCFAFYKMMSTRDLTYLMTYSNKHDLDAASLQRLQVQKMAVGTLESQDITE 282
 DB 191 EGEEFVQFYKALTRAEVQELFESFSADGOKLTLEFLDLQEQKSRDCTSEALALID 250
 QY 283 QEECPREKKSGLGIGFTYTRSPAGDJFNPENHNHVDOMTOLSHYFTSSHNTYLV 342
 DB 251 RYEPSSDGKLNHVLNMOGFLSYLCKSGDGLFNPACLPYODMTPLNHYFLCSSHNTYLV 310
 QY 343 GDQLMSQSRVDMYAVLQAGRCVYDCMDGPDDEPIYHNGYTLTKILFEDVLETINKY 402
 DB 311 GDQLCGGSSVSGYIRALKRCRCVCEVDYWDGPPSEPPYVYHGHITLSRLFDVAVTAQY 370

QY 403 AFIRNEYPVILSIENHCSVIOQKMAQYLTIDGLDKLDLSSVSEDAATPLPSPOMLGKI 462
 DB 371 AFQTSIDPVILSLFTHCSWBDQOTMARHLELLEIGQLSTLIDQVLPQPSPEELRRKI 430
 QY 463 LVKQKLLPANISDEAEEGVSEDESDADEIDDDCKLLNGDASTNRKRVENAKKRLSLIK 522
 DB 431 LVKQKLL--TLEEDL--EYEEBEAEBELEB-----SELAL 461
 QY 523 ESKTRDCEPDNPNFVSVLTPSGKLGKRSKAEDEVEGSEDGASNRGRLVYGSFRRKK 582
 DB 462 ESOFTEPEFO-----EQNLQND-----KKK 484
 QY 583 GSKLKAASVEGDEGODSPGQSGRATROKTKMLSRALSDLVKTKYSAV---THDIE 638
 DB 485 SKPI-----LCPALSLVLYIKSVSFRSFTH--S 511
 QY 639 MEAASSWQVSSFSFETKAQIILQOKPAOYLRLRNOOOLSRIVSSYRVDSNNVNPQPFNAG 698
 DB 512 KEHYHFEISFSFETKARLRKEAGNEFVQHNWQLSVYPSGLTDSNTNPQELNAG 571
 QY 699 COMVALNTQSEGRMLQNRKAFSANGCGYVLRKPCM--CGVFNPNSEDPPLPQOLKOL 756
 DB 572 COMVAMNQTAGLEMDICDGHFRQNGCGYVLRKDFLRDIQSSFRP--EKPISPFKQTL 629
 QY 757 VLRIISGQQLPKPRDSMLGRCEIIPVEVEIIGLPVDCSREQTRVYDNGFNPTEET 816
 DB 630 LHOVISGOOLPKVDT---KEGSIVDPLVKQIFGVRLDTARQETINVENNGFNPYQOT 686
 QY 817 LVFWHMEIALVRLVMDHPDIGH-DFIGORTLAFFSMPGGRVRYLV---EG--MEBAS 870
 DB 687 LCFRLVPEPLARVVMVDYDKSKNDITGQYTLPLWTCMOGYRHHLSKDGISLRPAS 746
 QY 871 IFVHVAVSDISGKVRQALGLK 892
 DB 747 IFVVICIQE-----GLEG 759
 RESULT 10
 ID AAE14268
 ID AAE14268 standard; Protein; 762 AA.
 AC AAE14268;
 XX
 XX 07-MAR-2002 (first entry)
 DT
 XX
 XX Human phospholipase C delta 5 (PLCD5) protein #1.
 DE
 XX Human; phospholipid C delta 5; PLCD5 protein; deep vein thrombosis;
 KW angina pectoris; percutaneous transluminal coronary angiography; PTCA;
 KW thrombo embolic insult; disseminated intravascular coagulation;
 KW arteriosclerosis; epilepsy; depression; neurodegenerative disease;
 KW stroke; rheumatoid arthritis; immune disorder; chromosome localisation;
 KW vaccine; gene therapy.
 XX
 OS Homo sapiens.
 PN WO200183771-A2.
 XX
 XX 08-NOV-2001.
 PD
 XX 27-APR-2001; 2001WO-BP04784.
 PF
 XX 29-APR-2000; 2000EP-0109318.
 PR
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Brandt S, Duecker K, Gietz J;
 PI MPI: 2002-034515/04.
 DR N-PSDB: AAD23721.
 DR
 XX New phospholipase C delta 5 polypeptides, useful for treating deep vein

[illegible]

Best Local Similarity 37.68;

Query Match	22.68;	Score 1439;	DB 23;	Length 828;
Best Local Similarity	37.68;	Pred. No. 1.4e-102;		
Matches 343;	Conservative 149;	Mismatches 280;	Indels 140;	Gaps 22;

[illegible][illegible]

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QY 103 VFQRPDSPDNCCFSIYHSGHRESLDVSTSEVARTVVTGLRYLMAGISDEDSLARR 162
DQ 77 LIRSLAEPLLEGGFTIVFHG-RRSNIDLMANSVEEAQIMMRGILLVDLVTSM-----H 131
QY 163 QRTDOWMLKOTFDEADKNGDGSISGEVQLDHLKLVNLPQARKQKQKREADDHOGTL 222
DQ 132 QERDOWMLKOTFDEADKNGDGSISGEVQLDHLKLVNLPQARKQKQKREADDHOGTL 222
QY 223 GFEFCAFYKMASTRDLYLMLTYSNHKNHDLDAASLQRFQVQKMAQVTLSCODITE 282
DQ 191 EGEEFVQFYKALTKRAEVOELFESFADGGKTLLEFLDLQEQKRCDSSELALELD 250
QY 283 QFEPCPNKSKGLGIDGFTVYTRSPAGDIPNPHHNVODMTPOLSHTYTSHTNYLV 342
DQ 251 RYKSDSGKRLHVLSDMDFSLYSCSKDIDFNPACIPRYODMTPOLNHFYCSSHNTYLV 310
QY 343 GDOLMSQSRVDMYAVNLQAGRCVCEVDCMDGPDGEPIVHNGYLLSKILFKDVIETINKY 402
DQ 311 GDOLCGQSSVEGYTRALKRGRCCEVDMGPDGEPVYVHNGYLLSKILFKDVIETINKY 370
QY 403 AFIKNEYPVILSTENHCNCSYIQKKMAQYLTDLGKLDLSSVSEDAATLPSFQMLKGI 462
DQ 371 AFTSDYPVILSTENHCNCSYIQKKMAQYLTDLGKLDLSSVSEDAATLPSFQMLKGI 430
QY 463 LVGKKLIPANISDEAEGEVSDSDADEIDDCKLINGASTRKRKVENTAKKIDSLIK 522
DQ 431 LVGKKLIPANISDEAEGEVSDSDADEIDDCKLINGASTRKRKVENTAKKIDSLIK 522
QY 523 ESKIRDCEDPNPNSVSTLSPGKLGKRSKRAEDVESGEDAGASRRNGRLVGSFSRKKK 582
DQ 462 ESQFETEPERQ-----EQMLQNKD-----KKKK 484
QY 583 GSKLTKAASVEEBDEGDSPGSGSRATROKTKMTKLSRLSDLVKTKSVA---THDIE 638
DQ 485 SKRI-----LCPALSSIVTYLTKSVSFRSTH--S 511
QY 639 MEAASSOVSESETKAHQILQOKPAOYLRFNOOQLSRYPSRYDSNVDPDPFPMAG 698
DQ 512 KEHYHFEIISFSETKAKRLIKEAGNEFYQHTMOLSKRYPGCLRTDSSNYPQELMAG 571
QY 699 COMVALNTQSEGRMLOLNKAKSANGCGYVLPKPCM--CGGVFNPNSEDLPLGOLKQL 756
DQ 572 COMVALNTQSEGRMLOLNKAKSANGCGYVLPKPCM--CGGVFNPNSEDLPLGOLKQL 756
QY 757 VLRIISGQOLPKPRDMLDGEIIPPEVEEIIIGLPVDCSREQRVVDNKNFTWEET 816
DQ 630 LIGVYSQOLPKPRDMLDGEIIPPEVEEIIIGLPVDCSREQRVVDNKNFTWEET 816
QY 817 LVFNVHMPRIALVRLVWDHDPGR-DEIGQRTLAFFSSMMPGRVYVL---EG--MEAS 870
DQ 687 LCFKVLVPELAMLRFVVMYDWMKSRNDFIGVYTLPMTCMOQGYRIIHLKSDGISLRAS 746
QY 871 IFVHVAVSDISGKVAQALGK 892
DQ 747 IFVVICIDF-----GLRG 759

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XX Homo sapiens.
OS WO200183771-A2.
PD 08-NOV-2001.
XX
PE 27-APR-2001: 2001WO-EP04784.
PR 29-APR-2000: 2000EP-0109318.
XX
PA (MERE) MERCK PATENT GMBH.
PI Brandt S, Duecker K, Gleitz J;
XX WPI: 2002-034515/04.
XX N-PSDB: AAD23723.
XX
PT New phospholipase C delta 5 polypeptides, useful for treating deep vein
PT thrombosis, instable angina pectoris, percutane transluminal coronary
PS angiography, disseminated intravascular coagulation and epilepsy
PS Claim 1; Page 48-50; 51pp: English.
XX
XX The patent discloses phospholipid C delta 5 (PLCD5) proteins and their
XX corresponding polynucleotides. PLCD5 sequences are useful for treating
XX coronary angiology (PTCA), thrombo embolic insult, percutane transluminal
XX intravascular coagulation, arteriosclerosis, epilepsy, depression,
XX neurodegenerative diseases, stroke, rheumatoid arthritis and immune
XX disorders. PLCD5 sequences are also useful as vaccines for inducing
XX immunological response in a mammal. PLCD5 DNAs are also useful for
XX studies and in gene therapy. The present sequence is PLCD5 protein
XX from human.
XX
XX Sequence 759 AA;
SQ
Query Match 21.7%; Score 1385.5; DB 23; Length 759;
Best Local Similarity 37.8%; Pred. No. 1.7e-98;
Matches 326; Conservative 147; Mismatches 251; Indels 139; Gaps 23;
QY 45 MOEGMOWKLVGSGGLVRFYUUDENRSCIRW--RPSKRNKAKISDSIQEVSSEGRSS 102
DQ 18 MOEGMOWKLVGSGGLVRFYUUDENRSCIRW--RPSKRNKAKISDSIQEVSSEGRSS 102
QY 103 VFQRPDSPDNCCFSIYHSGHRESLDVSTSEVARTVVTGLRYLMAGISDEDSLARR 162
DQ 77 LIRSLAEPLLEGGFTIVFHG-RRSNIDLMANSVEEAQIMMRGILLVDLVTSM-----SMDH 132
QY 163 QRTDOWMLKOTFDEADKNGDGSISGEVQLDHLKLVNLPQARKQKQKREADDHOGTL 222
DQ 132 QERDOWMLKOTFDEADKNGDGSISGEVQLDHLKLVNLPQARKQKQKREADDHOGTL 222
QY 223 GFEFCAFYKMASTRDLYLMLTYSNHKNHDLDAASLQRFQVQKMAQVTLSCODITE 282
DQ 191 EGEEFVQFYKALTKRAEVOELFESFADGGKTLLEFLDLQEQKRCDSSELALELD 250
QY 283 QFEPCPNKSKGLGIDGFTVYTRSPAGDIPNPHHNVODMTPOLSHTYTSHTNYLV 342
DQ 251 RYKSDSGKRLHVLSDMDFSLYSCSKDIDFNPACIPRYODMTPOLNHFYCSSHNTYLV 310
QY 343 GDOLMSQSRVDMYAVNLQAGRCVCEVDCMDGPDGEPIVHNGYLLSKILFKDVIETINKY 402
DQ 311 GDOLCGQSSVEGYTRALKRGRCCEVDMGPDGEPVYVHNGYLLSKILFKDVIETINKY 370
QY 403 AFIKNEYPVILSTENHCNCSYIQKKMAQYLTDLGKLDLSSVSEDAATLPSFQMLKGI 462
DQ 371 AFTSDYPVILSTENHCNCSYIQKKMAQYLTDLGKLDLSSVSEDAATLPSFQMLKGI 430
QY 463 LVGKKLIPANISDEAEGEVSDSDADEIDDCKLINGASTRKRKVENTAKKIDSLIK 522
DQ 431 LVGKKLIPANISDEAEGEVSDSDADEIDDCKLINGASTRKRKVENTAKKIDSLIK 522

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 22:01:49 ; Search time 167 Seconds
(without alignments)
8511.657 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338181 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	0.5	1365	1 US-08-114-072-1	Sequence 1, Appli
C 2	21	0.5	1365	2 PCT-US94-09361-1	Sequence 1, Appli
C 3	20	0.4	1062	2 US-08-466-103A-13	Sequence 13, Appli
C 4	20	0.4	2377	4 US-09-479-195-1	Sequence 1, Appli
C 5	20	0.4	2372	3 US-09-280-420-1	Sequence 1, Appli
C 6	20	0.4	4425	2 US-08-749-169A-1	Sequence 1, Appli
C 7	20	0.4	4425	2 US-09-130-032A-1	Sequence 1, Appli
C 8	20	0.4	4488	4 US-08-406-030A-3	Sequence 3, Appli
C 9	20	0.4	62804	4 US-09-800-960-3	Sequence 3, Appli
C 10	19	0.4	703	4 US-09-276-531-31	Sequence 31, Appli
C 11	19	0.4	1420	1 US-08-358-171-1	Sequence 1, Appli
C 12	19	0.4	1420	1 US-09-090-947-1	Sequence 1, Appli
C 13	19	0.4	3870	1 US-08-138-641-1	Sequence 1, Appli
C 14	19	0.4	3870	1 US-08-138-133-1	Sequence 1, Appli
C 15	19	0.4	3893	1 US-08-138-641-3	Sequence 3, Appli
C 16	19	0.4	3893	1 US-08-138-133-3	Sequence 3, Appli
C 17	19	0.4	3955	4 US-09-214-278-4	Sequence 4, Appli
C 18	19	0.4	4464	2 US-08-400-159-7	Sequence 7, Appli
C 19	19	0.4	4483	3 US-08-611-729A-7	Sequence 7, Appli
C 20	19	0.4	5163	3 US-08-700-651-1	Sequence 1, Appli
C 21	19	0.4	5163	3 US-08-928-361B-4	Sequence 4, Appli
C 22	19	0.4	5318	3 US-08-700-651-2	Sequence 2, Appli
C 23	19	0.4	5318	3 US-08-928-361B-3	Sequence 3, Appli
C 24	19	0.4	5511	3 US-08-928-361B-2	Sequence 2, Appli
C 25	19	0.4	7334	3 US-08-928-361B-1	Sequence 1, Appli
C 26	19	0.4	7507	2 US-08-975-765-1	Sequence 1, Appli
C 27	19	0.4	7714	4 US-09-479-122-26	Sequence 26, Appli

28	19	0.4	10317	3 US-09-058-746-1	Sequence 1, Appli
29	19	0.4	10317	4 US-09-438-142-1	Sequence 1, Appli
30	19	0.4	80161	3 US-09-036-987A-1	Sequence 1, Appli
31	19	0.4	80161	4 US-09-370-700-1	Sequence 80, Appli
32	18	0.4	41	1 US-08-447-411-80	Sequence 23, Appli
33	18	0.4	43	1 US-08-049-473-23	Sequence 23, Appli
34	18	0.4	43	1 PCT-US94-04190-23	Sequence 23, Appli
35	18	0.4	43	5 PCT-US94-04190-23	Sequence 11, Appli
36	18	0.4	44	4 US-09-161-241-42	Sequence 11, Appli
37	18	0.4	45	4 US-09-549-770B-11	Sequence 12, Appli
38	18	0.4	46	4 US-09-549-770B-12	Sequence 13, Appli
39	18	0.4	47	4 US-09-549-770B-13	Sequence 14, Appli
40	18	0.4	48	4 US-09-549-770B-14	Sequence 15, Appli
41	18	0.4	48	4 US-09-549-770B-15	Sequence 15, Appli
42	18	0.4	50	1 US-08-049-473-34	Sequence 34, Appli
43	18	0.4	50	1 US-08-312-648-34	Sequence 34, Appli
44	18	0.4	50	5 PCT-US94-04190-34	Sequence 34, Appli
45	18	0.4	53	1 US-08-049-473-7	Sequence 7, Appli

ALIGNMENTS

```

RESULT 1
US-08-114-072-1/c
; Sequence 1, Application US/08114072
; Patent No. 5624823
; GENERAL INFORMATION:
; APPLICANT: Sachs, David.
; APPLICANT: Leguenn, Christian.
; APPLICANT: Megaw, Sykes.
; APPLICANT: Biancho, Gilles
; TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,072
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-017
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-114-072-1

```

Query Match 0.5%; Score 21; DB 1; Length 1365;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3334 CTCGGAAGCCCGCCAGCCAGG 3354
Db 1066 CTCGGAAGCCCGCCAGCCAGG 1046

RESULT 2
PCT-US94-09361-1/c
Sequence 1, Application PC/TUS9409361
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09361
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-017PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-09361-1.

Query Match 0.5%; Score 21; DB 5; Length 1365;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3334 CTCGGAGAGCCGAGCCGAG 3354
Db 1066 CTCGGAGAGCCGAGCCGAG 1046

RESULT 3
US-08-466-103A-13/c
Sequence 13, Application US/08466103A
Patent No. 5856124
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Edisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1059
OTHER INFORMATION:
US-08-466-103A-13

Query Match 0.4%; Score 20; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 CGCCTGAGAGCTGCTGAGTG 4405
Db 52 CGCCTGAGAGCTGCTGAGTG 33

RESULT 4
US-09-479-195-1/c
Sequence 1, Application US/09479195
Patent No. 6326526
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Gilkoff, Valentin K.
TITLE OF INVENTION: MELATONIN RECEPTOR-DEFICIENT MICE AND USES THEREOF
FILE REFERENCE: 10217/727002
CURRENT APPLICATION NUMBER: US/09/479,195
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/122,527
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,565
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2377
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1270)...(2328)
OTHER INFORMATION: Intron coding sequence between positions 1464 and
OTHER INFORMATION: 1465
US-09-479-195-1

Query Match 0.4%; Score 20; DB 4; Length 2377;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 CGCCTGAGAGCTGCTGAGTG 4405
Db 1321 CGCCTGAGAGCTGCTGAGTG 1302

RESULT 5
US-09-280-420-1/c
Sequence 1, Application US/09280420
Patent No. 6037131
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
TITLE OF INVENTION: MELATONIN 1A RECEPTOR GENE

TITLE OF INVENTION: REGULATORY REGIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,701
FILING DATE:
APPLICATION NUMBER: 60/022,185
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1270...2328
OTHER INFORMATION: Intron coding sequence between positions 1464
US-09-280-420-1
Query Match 0.4%; Score 20; DB 3; Length 2772;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 GCCTGAGAGCTGCTGAGTG 4405
|||||
Db 1321 GCCTGAGAGCTGCTGAGTG 1302

RESULT 6
US-08-749-169A-1
Sequence 1, Application US/08749169A
Patent No. 5846770
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-749-169A-1
Query Match 0.4%; Score 20; DB 2; Length 4425;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCCGCGCCCTCG 3183
|||||
Db 73 GCCCGCGCCGCGCCCTCG 92

RESULT 7
US-09-130-032A-1
Sequence 1, Application US/09130032A
Patent No. 5986056
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-130-032A-1
Query Match 0.4%; Score 20; DB 2; Length 4425;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCCG 3183

Db 73 GCCCGCGCGCGCGCGCTCCG 92

RESULT 8

US-08-406-030A-3/c
; Sequence 3, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heutlein, Michael W.
; APPLICANT: Hauge, Brian W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3
Query Match 0.4%; Score 20; DB 4; Length 4488;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCCG 3183

Db 2422 GCCCGCGCGCGCGCTCCG 2403

RESULT 9

US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: Ye, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match 0.4%; Score 20; DB 4; Length 62804;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4513 GCCCGCACACCGCGCGCC 4532

Db 19561 GCCCGCACACCGCGCGCC 19542

RESULT 10

US-09-276-531-31
; Sequence 31, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT01
CLONE: 713784
US-09-276-531-31

Query Match
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4126 TGGAGAGACCGCTGCTC 4144
DB 312 TGGAGAGACCGCTGCTC 330

RESULT 11
US-08-358-171-1/c
Sequence 1, Application US/08358171
Patent No. 5763578
GENERAL INFORMATION:
APPLICANT: FONG, Henry K.W.
TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,171
FILING DATE: 16-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 17..889

US-08-358-171-1

Query Match
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3342 GCCCCAGCCGAGGAGGCG 3360
DB 469 GCCCCAGCCGAGGAGGCG 451

RESULT 12
US-09-090-947-1/c
Sequence 1, Application US/09090947
Patent No. 6008338
GENERAL INFORMATION:
APPLICANT: FONG, Henry K.W.
TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,171
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 17..889
US-09-090-947-1

Query Match
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3342 GCCCCAGCCGAGGAGGCG 3360
DB 469 GCCCCAGCCGAGGAGGCG 451

RESULT 13
US-08-138-641-1
Sequence 1, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:

APPLICANT: Koblán, Kenneth S.
APPLICANT: Pompliano, David I.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-641-1
Query Match 0.4%; Score 19; DB 1; Length 3870;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 TGGACTGCTGGGATGGGCC 1555
DB 1097 TGGACTGCTGGGATGGGCC 1115
RESULT 14
US-08-138-133-1
Sequence 1, Application US/08138133
Patent No. 5519163
GENERAL INFORMATION:
APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MERCHANT, KEVIN J.
TITLE OF INVENTION: INHIBITORS OF PHOSPHONOSITIDE-SPECIFIC
TITLE OF INVENTION: PHOSPHOLIPASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MUTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-641-3
Query Match 0.4%; Score 19; DB 1; Length 3870;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 TGGACTGCTGGGATGGGCC 1555
DB 1097 TGGACTGCTGGGATGGGCC 1115
RESULT 15
US-08-138-641-3
Sequence 3, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:
APPLICANT: Koblán, Kenneth S.
APPLICANT: Pompliano, David I.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3893 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-641-3
Query Match 0.4%; Score 19; DB 1; Length 3893;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 TGGACTGCTGGGATGGGCC 1555

Mon Mar 31 09:40:38 2003

us-09-927-112-1.oligo.rni

Page 7

Db 1097 TCGACTGCTGGAGTGGCC 1115

Search completed: March 29, 2003, 13:11:14
Job time : 575 secs

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QY 4561 TCTGCCCCACCCAGCTTGGCTCCGATGTAGAACTGAGAGCGGCGAGTACAGAGTAA 4620
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QY 4621 CGGGGCCCGAGCCCG 4635
DB 4621 CGGGGCCCGAGCCCG 4635

RESULT 2

US-09-927-112-3
/ Sequence 3, Application US/09927112
/ Patent No. US2002010674A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Meyers, Rachel
/ APPLICANT: Silos-Santiago, Immaculada
/ TITLE OF INVENTION: 3254, a novel human phospholipase C and
/ FILE REFERENCE: 38155-20048.00
/ CURRENT APPLICATION NUMBER: US/09/927,112
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: US 60/246,808
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 3624
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-927-112-3

Query Match 78.2%; Score 3624; DB 10; Length 3624;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1741	AAGAAAGGGCAGCAAGCTGAAGAAAGGGCGGCGCAGCTGTGAGGAGGAGATGAGGGCTCAGGAC	1800
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Qy	2295	GCCTCTCTGACTCTGTGGTAAGTACACAAAGTCCGGTGGCCACCCGACATGATGATGAG	2354
Db	1861	GCCTCTCTGACTCTGTGGTAAGTACACAAAGTCCGGTGGCCACCCGACATGATGATGAG	1920
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Qy	2415	CAGAAAGCGGCGCAGTACCTTACGCTTTCACACAGACAGCTCTCCCGATATACCCCTCC	2474
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Qy	2895	GTGCACATGCGGAGATGTGCGCTGTCTCGCTTCTGTCTGTGGACCAACGATCCCATGCGG	2954
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Qy	2955	CGTGACTTCAATTTGGCAGAGGACGCTGTGACTTACAGACATGATGCAAGGCTTACAGAC	3014
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Db	3001	CTGTGCTCTGAGACGGCCCCGGGCTGTCTGGGATGGCCGCCACATGTGATGAAGTGTGGTG	30600
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Db	3361	CAACCGGGGGGCGCTGACAGGAGAGATAGTGCCTTTGTTGCTCAAAAGCTGGAGAGATC	34200
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RESULT 3
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; Sequence 1912, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OR INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18

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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent version 3.0
SEQ ID NO 1912
LENGTH: 426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1912

Query Match 0.4%; Score 20; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 234 CATCTTCGTCATGTCGCTG 215

RESULT 4
US-09-292-758-106
Sequence 106, Application US/09292758
Publication No. US20020197602A1
GENERAL INFORMATION:
APPLICANT: Burner, Glenna C.
APPLICANT: Brown, Joseph P.
TITLE OF INVENTION: Nucleic Acid Sequences and Proteins
TITLE OF INVENTION: Associated With Aging
FILE REFERENCE: 017473-001110US
CURRENT APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: US 60/081,887
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 106
LENGTH: 498
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(498)
OTHER INFORMATION: n = a,t,c or g
US-09-292-758-106

Query Match 0.4%; Score 20; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3044 CATCTTCGTCATGTCGCTG 3063
Db 200 CATCTTCGTCATGTCGCTG 219

RESULT 5
US-09-815-242-7987

Sequence 7987, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7987
LENGTH: 1530
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1530)
US-09-815-242-7987

Query Match 0.4%; Score 20; DB 10; Length 1530;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 835 CCAGCAGCGAGTGGCGCGC 854
Db 785 CCAGCAGCGAGTGGCGCGC 804

RESULT 6
US-09-835-996A-7
Sequence 7, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Dumanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A

;; CURRENT APPLICATION NUMBER: US/09/835,996A
;; PRIOR FILING DATE: 2001-04-16
;; PRIOR APPLICATION NUMBER: US 60/197,137
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/714,936
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: US 09/667,298
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 09/631,451
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 09/598,042
;; PRIOR FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 7
;; LENGTH: 1840
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (140)..(1840)
US-09-835-996A-7

Query Match 0.4%; Score 20; DB 10; Length 1840;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 1130 TGCCGCTGCTGAGGTGA 1149

RESULT 7
US-09-804-969-14
;; Sequence 14, Application US/09804969
;; Patent No. US20020081595A1
;; GENERAL INFORMATION:
;; APPLICANT: Hu Yi
;; APPLICANT: Nepomichy, Boris
;; APPLICANT: Donoho, Gregory
;; APPLICANT: Halbun, Erin
;; APPLICANT: Turner, C. Alexander Jr.
;; APPLICANT: Abuin, Alejandro
;; APPLICANT: Friedrich, Glenn
;; APPLICANT: Zambrowicz, Brian
;; APPLICANT: Sands, Arthur T.
;; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides Et
;; FILE REFERENCE: LEX-0148-USA
;; CURRENT APPLICATION NUMBER: US/09/804,969
;; CURRENT FILING DATE: 2001-03-13
;; PRIOR APPLICATION NUMBER: US 60/188,885
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: US 60/189,693
;; PRIOR FILING DATE: 2000-03-15
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14
;; LENGTH: 2289
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-09-804-969-14

Query Match 0.4%; Score 20; DB 10; Length 2289;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 991 TGCCGCTGCTGAGGTGA 1010

RESULT 8
US-09-908-664-3

;; Sequence 3, Application US/09908664
;; Patent No. US20020115178A1
;; GENERAL INFORMATION:
;; APPLICANT: Millennium Pharmaceuticals, Inc.
;; APPLICANT: Meyers, Rachel
;; APPLICANT: Rudolph-Owen, Laura
;; APPLICANT: Tsai, Fong Yin
;; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
;; FILE REFERENCE: 38155-20022.00
;; CURRENT APPLICATION NUMBER: US/09/908,664
;; CURRENT FILING DATE: 2001-07-17
;; PRIOR APPLICATION NUMBER: US 60/218,675
;; PRIOR FILING DATE: 2000-07-17
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 2289
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-908-664-3

Query Match 0.4%; Score 20; DB 10; Length 2289;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 991 TGCCGCTGCTGAGGTGA 1010

RESULT 9
US-09-917-800A-1339
;; Sequence 1339, Application US/09917800A
;; Patent No. US20020119462A1
;; GENERAL INFORMATION:
;; APPLICANT: Wendrick, Donna
;; APPLICANT: Porter, Mark
;; APPLICANT: Johnson, Kory
;; APPLICANT: Castle, Arthur
;; APPLICANT: Elashoff, Michael
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Molecular Toxicology Modeling
;; FILE REFERENCE: 44921-5038-US
;; CURRENT APPLICATION NUMBER: US/09/917,800A
;; CURRENT FILING DATE: 2001-07-31
;; PRIOR APPLICATION NUMBER: US 60/222,040
;; PRIOR FILING DATE: 2000-07-31
;; PRIOR APPLICATION NUMBER: US 60/222,880
;; PRIOR FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: US 60/290,029
;; PRIOR FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US 60/290,645
;; PRIOR FILING DATE: 2001-05-15
;; PRIOR APPLICATION NUMBER: US 60/292,336
;; PRIOR FILING DATE: 2001-05-22
;; PRIOR APPLICATION NUMBER: US 60/295,798
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: US 60/297,457
;; PRIOR FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/298,884
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: US 60/303,459
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 1740
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1339
;; LENGTH: 2573
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-09-917-800A-1339

;; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D42148

Query Match 0.4%; Score 20; DB 10; Length 2573;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2686 AGCTCAAGAGAGCTGTG 2705
1653 AGCTCAAGAGAGCTGTG 1672

RESULT 10
US-09-908-664-1
; Sequence 1, Application US/09908664
; Patent No. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (257)...(2545)
US-09-908-664-1

Query Match 0.4%; Score 20; DB 10; Length 2629;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 TGCCGCTGCTGTGAGGTGA 1540
Db 1247 TGCCGCTGCTGTGAGGTGA 1266

RESULT 11
US-09-804-969-20
; Sequence 20, Application US/09804969
; Patent No. US20020081595A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Donoho, Gregory
; APPLICANT: Hilburn, Erin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abuin, Alejandro
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides En
; FILE REFERENCE: LEX-0148-USA
; CURRENT APPLICATION NUMBER: US/09/804,969
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,885
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 60/189,693
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2709
; TYPE: DNA

; ORGANISM: homo sapiens
US-09-804-969-20

Query Match 0.4%; Score 20; DB 10; Length 2709;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 TGCCGCTGCTGTGAGGTGA 1540
Db 1248 TGCCGCTGCTGTGAGGTGA 1267

RESULT 12
US-09-944-413-6
; Sequence 6, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296


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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US200201560041ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US200201560041ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 6
; LENGTH: 3441
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-413-6
Query March 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3164 GCGCCCGCGCGCGCCCTCG 3183
Db 36 GCGCCCGCGCGCGCCCTCG 55
RESULT 13
US-09-944-403-6
; Sequence 6, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austlin
; APPLICANT: Hillan, Kenneth
```

```

; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,403
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 15, 1997
; PRIOR APPLICATION NUMBER: 60/069,684
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 6
LENGTH: 3441
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-403-6

Query Match 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCG 3183
DB 36 GCCCGCGCGCGCGCGCTCG 55

RESULT 14
US-09-944-896-6
Sequence 6, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Batson, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gutney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 896
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 656
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A1eember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A1eember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 6
LENGTH: 3441
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-896-6

Query Match 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCG 3183
DB 36 GCCCGCGCGCGCGCGCTCG 55

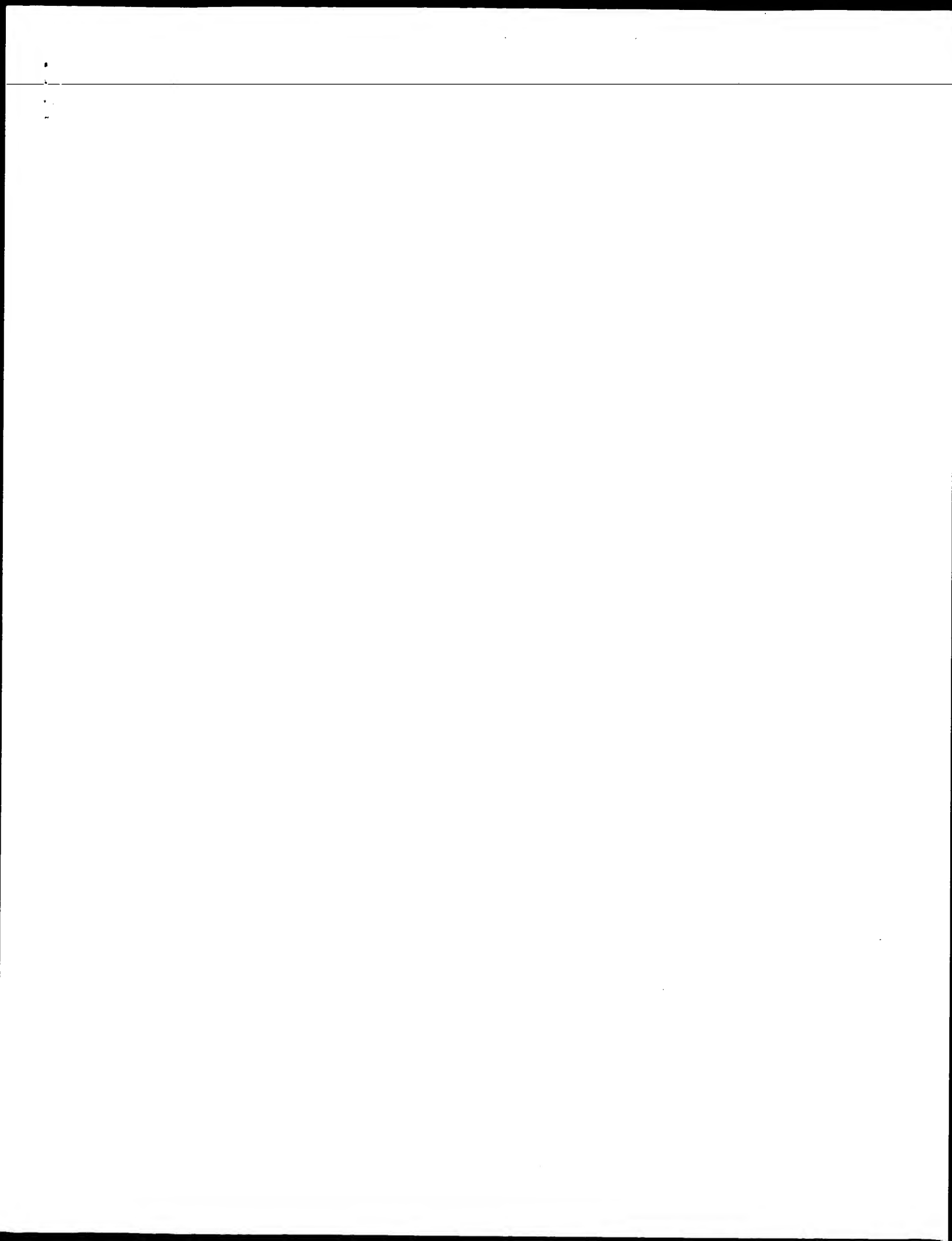
RESULT 15

US-09-944-944-6
 ; Sequence 6, Application US/09944944
 ; Patent No. US20020173463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gettsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austen
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kijavini, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/866, 028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067, 411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 278
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 425
 ; PRIOR FILING DATE: December 12, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 696
 ; PRIOR FILING DATE: December 15, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 694
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 702
 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069, 873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068, 017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070, 440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074, 086
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074, 092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075, 945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112, 850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113, 296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146, 222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216, 021
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 09/218, 517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254, 311
 ; PRIOR FILING DATE: March 3, 1999

;; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. US20020173463A1member 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. US20020173463A1member 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: March 2, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: December 1, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: February 28, 2001
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 6
 ; LENGTH: 3441
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-944-944-6

Query Match 0.4%; Score 20; DB 9; Length 3441;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3164 GCCCGGCGCGCGCGCGCGCGCG 3183
 DB 36 GCCCGGCGCGCGCGCGCGCGCG 55

Search completed: March 29, 2003, 17:03:25
 Job time : 513 secs



GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:52:40 ; Search time 81 Seconds
(without alignments)
1985.599 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 1207
Sequence: 1 MAPPTAGPLPGLPPLPDPG.....ALYPMHCLRGLLPMWLACGP 1207

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	82.5	1239	23	Human lipid metabo
2	613	50.8	621	23	Human lipid metabo
3	371	30.7	1619	23	Human lipid metabo
4	83	6.9	178	23	Human DITHP polype
5	23	1.9	466	22	Human protein sequ
6	23	1.9	787	22	Novel human diago
7	23	1.9	787	22	Human phosphatidyl
8	23	1.9	1014	23	Human lipid metabo
9	22	1.8	682	22	Novel human diago
10	14	1.2	1054	23	P. patens signal t

11	13	1.1	119	22	AAU87634	Novel central nerv
12	13	1.1	119	22	ABBI7239	Human nervous syst
13	13	1.1	119	22	AAU17072	Novel signal trans
14	13	1.1	119	22	AAU43643	Human polypeptide
15	13	1.1	214	22	AAU87352	Novel central nerv
16	13	1.1	214	22	AAU43569	Human polypeptide
17	12	1.0	102	22	AAEI3105	Human PLC 1636 pr
18	12	1.0	306	22	AAE94419	Human protein sequ
19	12	1.0	340	22	AAEI1930	Human CG121 (or C5
20	12	1.0	567	22	AAEI1925	Human protein sequ
21	12	1.0	639	22	AAE94695	Novel human diago
22	12	1.0	666	22	ABG12052	Novel lipid metabo
23	12	1.0	731	23	ABE07492	Human phospholip
24	12	1.0	759	23	AAE14270	Novel human phosph
25	12	1.0	762	22	AAE10440	Human phospholip
26	12	1.0	762	23	AAU76816	Human phospholip
27	12	1.0	762	23	AAE14268	Human phospholip
28	12	1.0	785	23	AAE14269	Human phospholip
29	12	1.0	828	23	ABE08008	Human lipid metabo
30	12	1.0	1058	23	AAE80177	Human protein sequ
31	12	1.0	1216	22	AAU79193	Human lipid metabo
32	12	1.0	1216	22	ABE08204	Novel central nerv
33	11	0.9	237	22	AAU87515	Novel central nerv
34	11	0.9	237	22	AAU23567	Novel human enzyme
35	11	0.9	254	22	ABBI1181	Human pancreas pho
36	11	0.9	541	22	AAU67205	Novel central nerv
37	11	0.9	595	23	ABE04337	Human phosphoester
38	11	0.9	806	22	AAE94052	Human protein sequ
39	11	0.9	1579	23	ABE6735	Human novel polype
40	11	0.9	1809	22	AAE13101	Human phospholip
41	11	0.9	1898	23	AAE07352	Human acid sequenc
42	11	0.9	156	22	AAE05974	Rat phospholip
43	10	0.8	229	23	ABE67416	Human novel polype
44	10	0.8	229	23	ABE67416	Human novel polype
45	10	0.8	332	22	ABBI1342	Human phospholip

ALIGNMENTS

RESULT 1	ABE08205	Human lipid metabolism enzyme-5 (LME-5).
ID	ABE08205	standard; Protein: 1239 AA.
XX	ABE08205;	
AC	XX	
XX	XX	
DT	XX	
DE	XX	
XX	XX	
XX	XX	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
KW	Human; LME-5; lipid metabolism enzyme-5 (LME-5).	
OS	Homo sapiens.	
XX	XX	
PN	WO200185956-A2.	
XX	XX	
PD	15-NOV-2001.	
XX	XX	
PF	11-MAY-2001; 2001WO-US15210.	
XX	XX	
PR	11-MAY-2000; 2000US-203511P.	
PR	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	
XX	XX	
PA	(INCYT) INCYTE GENOMICS INC.	
XX	XX	
PI	Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;	
PI	Khan FA, Gandhi AR, Au-Yang J, Lal P, Kearney L, Elliott VS;	
PI	Ding L, Thornton M;	

XX WPI: 2002-089794/12.
 DR N-PSDB; ABA96005.
 XX
 PT New lipid metabolism enzymes useful for diagnosing, treating and
 disorders, and cardiovascular disorders
 XX
 PS Claim 1; Page 114-116; 122pp; English.
 XX
 CC The sequence represents a novel human lipid metabolism enzyme (LME-5) of
 CC the invention. The invention relates to novel human LME's, and the
 CC polynucleotides which identify and encode them. The enzymes of the
 CC invention have cytosolic, neuroprotective, immunosuppressive,
 CC anti-inflammatory, and cardiovascular activity. The polypeptides and
 CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
 CC metabolism enzymes are useful in the diagnosis, treatment and prevention
 CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
 CC cardiovascular disorders, and in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
 CC for compounds that modulate the activity of LME. Polynucleotides encoding
 CC LME may be used for somatic or germline gene therapy, to detect and
 CC quantify gene expression in biopsied tissues in which expression of LME
 CC may be correlated with disease, to generate a transcript image of a
 CC tissue or cell type, to generate hybridization probes useful in mapping
 CC the naturally occurring genomic sequence, and for screening libraries of
 CC compounds in drug screening techniques. The polypeptide sequences may be
 CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
 CC primers derived from polynucleotide sequences encoding LME may be used to
 CC detect single nucleotide polymorphisms.
 CC
 XX Sequence 1239 AA:
 SQ
 Query Match 82.5%; Score 96; DB 23; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 212 EADTDHOGTGFEEFCATYKMASTRDLYLLMLTYSNKHDLDAASLQFLOVEQKMG 271
 DB 244 EADTDHOGTGFEEFCATYKMASTRDLYLLMLTYSNKHDLDAASLQFLOVEQKMG 303
 QY 272 VTLESQDITEQPEPCENKSKGLGIDGFTNTSPADIDFPHNNHNDOMTQPLSHY 331
 DB 304 VTLESQDITEQPEPCENKSKGLGIDGFTNTSPADIDFPHNNHNDOMTQPLSHY 363
 QY 332 FITSHNTYLVGDOLMSQSRVDMYAWYLQAGRCVEVDCWDGDEPRYIHHGTTLTKIL 391
 DB 364 FITSHNTYLVGDOLMSQSRVDMYAWYLQAGRCVEVDCWDGDEPRYIHHGTTLTKIL 423
 QY 392 FKQVITIKYAFIKNEYPIYILSIENHGSYIOQKMAQYLTDLIGDKDLLSSVSEDAT 451
 DB 424 FKQVITIKYAFIKNEYPIYILSIENHGSYIOQKMAQYLTDLIGDKDLLSSVSEDAT 483
 QY 452 LPSQMLKGIKLVKGGKLLPANISEDAEGBVSDESDADIDDDCKILNGDASTNKRVEN 511
 DB 484 LPSQMLKGIKLVKGGKLLPANISEDAEGBVSDESDADIDDDCKILNGDASTNKRVEN 543
 QY 512 TAKRKIDSLIKESKTRDCEDPNNSVSTLSPSGKLGKRSKAEDEVSDEGASRRNGRL 571
 DB 544 TAKRKIDSLIKESKTRDCEDPNNSVSTLSPSGKLGKRSKAEDEVSDEGASRRNGRL 603
 QY 572 VVGSFRRKKKSKLKKASVEGEGDQSPGQSGRATROKTKMLKSLSDLYKTKS 631
 DB 604 VVGSFRRKKKSKLKKASVEGEGDQSPGQSGRATROKTKMLKSLSDLYKTKS 663
 QY 632 VATHDIEEAAASWQVSSSEFKAHQILQOKPAQYLRFNOOOLSTRPSSYVDSNNP 691
 DB 664 VATHDIEEAAASWQVSSSEFKAHQILQOKPAQYLRFNOOOLSTRPSSYVDSNNP 723
 QY 692 QPFWNAGCOMVALNTQSEGRMLQLNRAKFSANGGCGYVLKPGCMQGVFNPNSEDPRLQ 751
 DB 724 QPFWNAGCOMVALNTQSEGRMLQLNRAKFSANGGCGYVLKPGCMQGVFNPNSEDPRLQ 783

QY 752 LKQVLRTISGOQLPKPRDSMLGDRGETIDPFVEVEITGLPYDCSRQRTFVVDNGFNP 811
 DB 784 LKQVLRTISGOQLPKPRDSMLGDRGETIDPFVEVEITGLPYDCSRQRTFVVDNGFNP 843
 QY 812 TWEETLVFWVHMPETALVFLVMDHDPDPIGRDFTGORTAFSSMPGYRHYVLEGEAS 871
 DB 844 TWEETLVFWVHMPETALVFLVMDHDPDPIGRDFTGORTAFSSMPGYRHYVLEGEAS 903
 QY 872 FVHVAVSDISGVKQALGLKGLFRLGPKRGSLDHAAGRPAPRSQRLIRTAAPTK 931
 DB 904 FVHVAVSDISGVKQALGLKGLFRLGPKRGSLDHAAGRPAPRSQRLIRTAAPTK 963
 QY 932 SQKPRGRPELVLTTRDPSKGVADVDVPPGPPAPAPAOEGSGSSPPGKAPAAVAE 991
 DB 964 SQKPRGRPELVLTTRDPSKGVADVDVPPGPPAPAPAOEGSGSSPPGKAPAAVAE 1033
 QY 992 KSPVRRPRLVLDGPGPAGMATCKKCVGSCAGVNTGTLQREPRPSPGPASRQAIRQ 1051
 DB 1024 KSPVRRPRLVLDGPGPAGMATCKKCVGSCAGVNTGTLQREPRPSPGPASRQAIRQ 1083
 QY 1052 PARADSLGAPCCGIDPHAIRSRKAPKPGAMRQGGSGSSSDSSPDSFGTEPRS 1111
 DB 1084 PARADSLGAPCCGIDPHAIRSRKAPKPGAMRQGGSGSGSSSDSSPDSFGTEPRS 1143
 QY 1112 PWWPGACROPALQGENSALFAOKLEIRSKSPWFSAGKFLPCVYLPHAPGMAAGPSP 1171
 DB 1144 PWWPGACROPALQGENSALFAOKLEIRSKSPWFSAGKFLPCVYLPHAPGMAAGPSP 1203
 QY 1172 AASAWTVSPRYLVLYALVPMHCLRGTLPLWLACGP 1207
 DB 1204 AASAWTVSPRYLVLYALVPMHCLRGTLPLWLACGP 1239
 RESULT 2
 ABB07493
 ID ABB07493 standard; Protein; 621 AA.
 XX
 AC ABB07493;
 DT 23-APR-2002 (first entry)
 XX
 DE Human lipid metabolism molecule (LMM) polypeptide (ID: 2965233CD1).
 KW Lipid metabolism molecule; LMM; cytosolic; neurotropic; neuroprotective;
 KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;
 KW cardiovascular; anti-HIV; antileptic; anti-angiogenic; hypertensive; human;
 KW cancer; gene therapy; protein therapy.
 XX
 OS Homo sapiens.
 OS
 XX
 FN WC020024490-A2.
 PD 17-JAN-2002.
 XX
 PE 06-JUL-2001; 2001WO-US21432.
 XX
 PR 07-JUL-2000; 2000US-216801P.
 PR 07-JUL-2000; 2000US-216803P.
 PR 14-JUL-2000; 2000US-218233P.
 PR 21-JUL-2000; 2000US-220046P.
 PR 26-JUL-2000; 2000US-220739P.
 PR 04-AUG-2000; 2000US-222824P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Tang YT, Azimzai Y, Das D, Thornton M, Lu DM, Tribouley CM,
 PI Yue H, Gandhi AR, Wala N, Khan FA, Lu Y, Yao MG, Hafalia AJA,
 PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugm KR;
 XX
 DR WPI: 2002-164631/21.
 DR N-PSDB; ABA94696.
 XX

PT Lipid metabolism molecules useful in diagnosing, treating or preventing
 PT cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
 PT skin and cardiovascular disorders -

PS Claim 1; Page 112-113; 128pp; English.

CC The invention provides human lipid metabolism molecule (LMM) polypeptides
 CC and polynucleotides. The LMM polypeptides can be expressed by standard
 CC recombinant methodology. The LMM polypeptides are useful for diagnosing
 CC or treating a condition or disease associated with the expression of LMM,
 CC or screening for compounds that specifically bind to or modulate the
 CC activity or expression of LMM. They are also used to generate antibodies
 CC and assess the toxicity of test compounds. The LMM polypeptides,
 CC modulators and antibodies are specifically useful for diagnosing,
 CC treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
 CC melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
 CC cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/
 CC inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
 CC or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
 CC esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
 CC disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
 CC disorders (e.g. hypertension, arterial dissections, vascular tumours, or
 CC thrombolysis). The present sequence represents a human LMM polypeptide
 CC sequence.

XX Sequence 621 AA:

Query Match 50.8%; Score 613; DB 23; Length 621;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPTAGRLPGLPPEDEGPPESRWLFLSANILPYVERCMAGOMKRLGSGK 60
 DB 2 MAPPTAGRLPGLPPEDEGPPESRWLFLSANILPYVERCMAGOMKRLGSGK 61
 QY 61 LVFVYLDHRSCTIRWRPRKNEKAKISIDISOEVSQSGSEVFORPPGSPFNCCFSI 120
 DB 62 LVFVYLDHRSCTIRWRPRKNEKAKISIDISOEVSQSGSEVFORPPGSPFNCCFSI 121
 QY 121 YHGSRESIDLVSSTSEVARTWYGLRYLMAGISDEDSARRKORTKOTFEADKN 180
 DB 122 YHGSRESIDLVSSTSEVARTWYGLRYLMAGISDEDSARRKORTKOTFEADKN 181
 QY 181 GDGSLSTGEVLDLHKLNVLNLRORVKOMPREADTDHGTGFEFECAFYKMSSTRDL 240
 DB 182 GDGSLSTGEVLDLHKLNVLNLRORVKOMPREADTDHGTGFEFECAFYKMSSTRDL 241
 QY 241 YILMLTYSNHKKHLDAAASLORFLQVROKMAVYTESCODIIEFEPCKENSKGLIGIDG 300
 DB 242 YILMLTYSNHKKHLDAAASLORFLQVROKMAVYTESCODIIEFEPCKENSKGLIGIDG 301
 QY 301 FTYNTRSPADIDNPEHHVHODMTOPLSHYFTTSSHNTYLVGDOLMSGRDMMYAVIQ 360
 DB 302 FTYNTRSPADIDNPEHHVHODMTOPLSHYFTTSSHNTYLVGDOLMSGRDMMYAVIQ 361
 QY 361 AGRCVAVDQWDPDGRPYVHGYTLTSKLFYDEVETINKYAFINKEPVILISINHC 420
 DB 362 AGRCVAVDQWDPDGRPYVHGYTLTSKLFYDEVETINKYAFINKEPVILISINHC 421
 QY 421 VIOOKKMAQVLTPLDGLDKLDLSSVSEDAATTLPSPOLKGLIIVKSKLPANISEDABEG 480
 DB 422 VIOOKKMAQVLTPLDGLDKLDLSSVSEDAATTLPSPOLKGLIIVKSKLPANISEDABEG 481
 QY 481 EVSDESDADEIDDDCKLLNDASTNRRKVENTAKRKIDSLIKSKTRDCDPNNFVSYTL 540
 DB 482 EVSDESDADEIDDDCKLLNDASTNRRKVENTAKRKIDSLIKSKTRDCDPNNFVSYTL 541
 QY 541 SPSPKLGKKAEDVSGSDAGASRRNGRLVYVGSFRRKKGSKLKAASVEGDEGDD 600
 DB 542 SPSPKLGKKAEDVSGSDAGASRRNGRLVYVGSFRRKKGSKLKAASVEGDEGDD 601
 QY 601 SPGQSGKATROK 613
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DB 602 SPGQSGKATROK 614

RESULT 3

ID AAU77498 standard; Protein; 1619 AA.

AAU77498;

05-JUN-2002 (first entry)

Human lipid metabolism enzyme, LMM-6.

Human lipid metabolism enzyme; LMM-6; immune system disorder;
 neurologic disorder; developmental disorder; cancer; neoplastic;
 cell proliferative disorder; immunomodulator; neuroprotective;
 cytosolic; enzyme.

Homo sapiens.

WO200216597-A2.

28-FEB-2002.

22-AUG-2001; 2001WO-0526365.

23-AUG-2000; 2000US-227429P.

08-SEP-2000; 2000US-231370P.

15-SEP-2000; 2000US-231212P.

29-SEP-2000; 2000US-236885P.

(INCY-) INCYTE GENOMICS INC.

Griffin JR, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;

Walla NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M;

Lal P;

WPI: 2002-280936/32.

N-PSDB: ABK12390.

Claim 50; Page 113-117; 122pp; English.

CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the
 CC polynucleotide sequences encoding them. The LMM polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LMM, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LMM-6.

XX Sequence 1619 AA:

Query Match 30.7%; Score 371; DB 23; Length 1619;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 550 SRAEDVESGSDAGASRRNGRLVYVGSFRRKKGSKLKAASVEGDEGDDSGQSGCA 609
 DB 1154 SRAEDVESGSDAGASRRNGRLVYVGSFRRKKGSKLKAASVEGDEGDDSGQSGCA 1213
 QY 610 TROKKTMTLSRLSDLVYKTTKVAATHDIMEAASMOVSSPSETAHOITLOOKPAOYLR 669
 DB 1214 TROKKTMTLSRLSDLVYKTTKVAATHDIMEAASMOVSSPSETAHOITLOOKPAOYLR 1273
 ||||||||||||


```

QY 670 NQOOLSRIPSSYRDSSNYPQPFNNAGCOMVALNYSQSEGRMTOLNRAKFSANGGGYV 729
DQ 1274 NQOOLSRIPSSYRDSSNYPQPFNNAGCOMVALNYSQSEGRMTOLNRAKFSANGGGYV 1333
QY 730 LKPGCMQGVFNPNSEDPDLPGOLKQOLVLRISGQOLPKPRDSMLGDRGELIIPFEVEI 789
DQ 1334 LKPGCMQGVFNPNSEDPDLPGOLKQOLVLRISGQOLPKPRDSMLGDRGELIIPFEVEI 1393
QY 790 IGLPVDSRQETRVVDNGFNPTWEELVPMVHMPETALVFLVMDHPDPIGRDFIGQRTL 849
DQ 1394 IGLPVDSRQETRVVDNGFNPTWEELVPMVHMPETALVFLVMDHPDPIGRDFIGQRTL 1453
QY 850 AFSSMMPGYRHVYLEGMEASIFVHVAVSDISGRVKQALGLKGLFLRGPKPSLDSHAAG 909
DQ 1454 AFSSMMPGYRHVYLEGMEASIFVHVAVSDISGRVKQALGLKGLFLRGPKPSLDSHAAG 1513
QY 910 RPPARPSVSR 920
DQ 1514 RPPARPSVSR 1524

RESULT 4
ID ABG59980 standard; Protein; 178 AA.
AC ABG59980;
XX
XX
DT 30-JUL-2002 (first entry)
DE
XX
XX
KW Human DITHP polypeptide #38.
KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infections; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW thymus.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200220754-A2.
XX
XX
PD 14-MAR-2002.
XX
XX
PF 29-AUG-2001; 2001WO-US27127.
XX
XX
PR 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230583P.
PR 06-SEP-2000; 2000US-230585P.
PR 06-SEP-2000; 2000US-230514P.
PR 06-SEP-2000; 2000US-230515P.
PR 06-SEP-2000; 2000US-230517P.
PR 06-SEP-2000; 2000US-230518P.
PR 06-SEP-2000; 2000US-230519P.
PR 06-SEP-2000; 2000US-230595P.
PR 06-SEP-2000; 2000US-230597P.
PR 06-SEP-2000; 2000US-230598P.
PR 06-SEP-2000; 2000US-230599P.
PR 06-SEP-2000; 2000US-230610P.
PR 06-SEP-2000; 2000US-230656P.
PR 06-SEP-2000; 2000US-230988P.
PR 07-SEP-2000; 2000US-230989P.
PR 07-SEP-2000; 2000US-231163P.
PR 07-SEP-2000; 2000US-231167P.
XX
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PA (INCY-) INCYTE GENOMICS INC.

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XX
PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
DR WPI: 2002-383054/41.
DR N-PSDB: ABR71572.
XX
XX
PT An isolated polynucleotide useful in diagnostics and therapeutics -
XX
XX
PS Claim 29; Page 554; 686pp; English.
PS
XX
XX
CC The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
XX
XX
SQ Sequence 178 AA:
XX
XX
Query Match 6.9%; Score 83; DB 23; Length 178;
Best Local Similarity 100.0%; Pred. No. 4.5e-76;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 320 VHDMTOPLSHYFTSSNNTYVGDOLMSGRVMTVMVLAQGRCEYVCMGPDPGEPT 379
DQ 96 VHDMTOPLSHYFTSSNNTYVGDOLMSGRVMTVMVLAQGRCEYVCMGPDPGEPT 155
XX
QY 360 VHGTYLTSKILFKDYIETINKY 402
DQ 156 VHGTYLTSKILFKDYIETINKY 178
XX
XX
RESULT 5
ID AAB95125 standard; Protein; 466 AA.
AC AAB95125;
XX
XX
DT 26-JUN-2001 (first entry)
DE
XX
XX
KW Human protein sequence SEQ ID NO:17124.
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
KW Homo sapiens.
XX
XX
OS Homo sapiens.
XX
XX
PN EP1074617-A2.
XX
XX
PD 07-FEB-2001.
XX
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX
PA (HELI-) HELIX RES INST.

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XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 DR
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length CDNA defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length CDNA -
 PS
 PS Claim 8; SEQ ID 17124; 2537bp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length CDNA defined in the specification, where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length CDNA. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length CDNA. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human CDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 466 AA;
 XX
 Query Match 1.9%; Score 23; DB 22; Length 466;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 821 VHMPEIALVFLVMDHPDPIGRDF 843
 DB 251 VHMPEIALVFLVMDHPDPIGRDF 273
 RESULT 6
 ABG13669 standard; Protein; 787 AA.
 XX
 AC ABG13669;
 XX
 DT 18-FEB-2002 (first entry)
 DE
 XX Novel human diagnostic protein #13660.
 XX
 KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS77856.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 PS Claim 20; SEQ ID No 44028; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 787 AA;
 XX
 Query Match 1.9%; Score 23; DB 22; Length 787;
 Best Local Similarity 100.0%; Pred. No. 6.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 821 VHMPEIALVFLVMDHPDPIGRDF 843
 DB 584 VHMPEIALVFLVMDHPDPIGRDF 606
 RESULT 7
 AAE14673
 ID AAE14673 standard; Protein; 787 AA.
 XX
 AC AAE14673;
 XX
 DT 26-JUL-2002 (first entry)
 DE
 XX Human phosphatidylinositol-specific phospholipase C-11-like enzyme.
 XX
 KM Human: phosphatidylinositol-specific phospholipase C-like enzyme;
 KM PI-PKC-like enzyme; chromosome 3; asthma; cancer; central nervous system;
 KM CNS disorder; Parkinson's disease; dementia; COPD; protein therapy;
 KM chronic obstructive pulmonary disease; gene therapy; vaccine.
 OS Homo sapiens.
 XX
 PN WO200226996-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 24-SEP-2001; 2001WO-EP11012.
 XX
 PR 27-SEP-2000; 2000US-235552P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Zhu Z;

XX WPI: 2002-372128/40.
 DR N-PSDB; AAD31081.
 XX
 PT Isolated polynucleotides encoding human phosphatidylinositol-specific
 phospholipase C-like enzymes, useful for preventing, diagnosing and
 treating e.g. asthma, cancer, a CNS disorder or chronic obstructive
 PT pulmonary disease -
 XX
 PS Claim 25; Fig 2; 125pp; English.
 XX
 CC The invention relates to polynucleotide encoding human
 CC phosphatidylinositol-specific phospholipase C-like enzyme
 CC (PI-PLC-like enzyme). Human PI-PLC-like enzyme gene is located on
 CC chromosome 3. The PI-PLC-like enzyme polypeptide and
 CC polynucleotide may be used in the prevention, diagnosis and
 CC treatment of diseases associated with enzyme dysfunction,
 CC e.g. asthma, cancer, central nervous system (CNS) disorder (e.g.
 CC Parkinson's disease, dementia) and chronic obstructive pulmonary disease
 CC (COPD). The polynucleotide and polypeptide may be used to treat
 CC disorders associated with decreased PI-PLC-like enzyme expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of PI-PLC-like enzymes, by expressing inactive proteins or to
 CC supplement the patient's own production of PI-PLC-like enzymes.
 CC The polynucleotide and its complements may also be used
 CC as DNA probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acids in samples. The PI-PLC-like enzymes
 CC may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of PI-PLC-like enzyme
 CC expression and activity. The anti-PI-PLC-like enzyme antibodies and
 CC antagonists may be used to down-regulate expression and activity of
 CC the enzyme and as diagnostic agents for detecting the presence of
 CC PI-PLC-like enzyme in samples. The present sequence is human
 CC phosphatidylinositol-specific phospholipase C-like enzyme.
 SQ Sequence 787 AA;

Query Match 1.9%; Score 23; DB 23; Length 787;
 Best Local Similarity 100.0%; Pred. No. 6.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VHMPEIALVRFVWMDHPDPIGRDF 843
 ||||||||||||||||||
 DB 584 VHMPEIALVRFVWMDHPDPIGRDF 606

RESULT 8
 ABB08001
 ID ABB08001 standard; Protein: 1014 AA.
 XX
 AC ABB08001;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme (LME)-1 (Id: 7472210CD1).
 XX
 KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective;
 KW nootropic; cerebroprotective; antiparkinsonian; antialzheimer's; vaccine;
 KW antileukemic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;
 KW gene therapy; protein therapy; enzyme.
 XX
 OS Homo sapiens.
 XX
 MO200229036-A2.
 XX
 PN 11-APR-2002.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31302.
 XX
 PR 06-OCT-2000; 2000US-238388P.
 PR 13-OCT-2000; 2000US-240616P.
 PR 02-NOV-2000; 2000US-245719P.
 PR 08-NOV-2000; 2000US-247503P.
 PT

PR 17-NOV-2000; 2000US-249503P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Harald L, Arvitu C, Das D, Griffin JA, Baughn MR, Ding L,
 PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J,
 PI Lal PG, Tribouley CM;
 XX
 DR WPI: 2002-315862/35.
 DR N-PSDB; ABL60537.
 XX
 PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and
 PT Creutzfeldt-Jakob disease -
 XX
 PS Claim 1; Page 110-113; 127pp; English.
 XX
 CC The invention relates to human lipid metabolism enzymes (LMEs) and
 CC encoding polynucleotides. The LMEs can be expressed by standard
 CC recombinant technology. The LME polypeptides, polynucleotides and
 CC modulators may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate LME expression such as cancer
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
 CC (e.g. Creutzfeldt-Jakob disease and Acquired Immune deficiency syndrome
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
 CC pectoris and mitral valve prolapse). The present sequence represents
 CC the human LME-1 polypeptide.
 XX
 SQ Sequence 1014 AA;

Query Match 1.9%; Score 23; DB 23; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 7.7e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VHMPEIALVRFVWMDHPDPIGRDF 843
 ||||||||||||||||||
 DB 811 VHMPEIALVRFVWMDHPDPIGRDF 833

RESULT 9
 ABG13670
 ID ABG13670 standard; Protein: 682 AA.
 XX
 AC ABG13670;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13661.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 MO200175067-A2.
 XX
 PN 11-OCT-2001.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS77857.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 44029; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantifying a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. Abg00010-Abg30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 682 AA:
 Query Match 1.8%; Score 22; DB 22; Length 682;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 775 GDRGEITDPVEVEITGLPYDC 796
 DB 64 GDRGEITDPVEVEITGLPYDC 85
 RESULT 10
 ID AAU11619 standard; Protein: 1054 AA.
 AC AAU11619;
 XX 12-MAR-2002 (first entry)
 DE P. patens signal transduction stress-related protein PLC-1.
 KW Signal transduction stress-related protein; STSRP; PLC-1; PLC-2;
 KW 14-3-3p-1; 14-3-3p-2; CBP-1; Phospholipase C; Ca2+ binding protein;
 KW transgenic plant; environmental stress; salinity; drought;
 KW low temperature.
 XX Physcomitrella patens.
 OS
 XX Key Location/Qualifiers
 FH MISC-difference 126 /note= "Encoded by CAG"
 FT MISC-difference 420..1054 /note= "Region not encoded by the cDNA sequence
 FT /note= "Region not encoded by the cDNA sequence
 FT appearing as AAS17965"
 PN WO200177355-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-US11398.
 PE 07-APR-2000; 2000US-196001P.
 PR (BADI) BASF PLANT SCI GMBH.
 PA
 XX Costa Silva EO, Bohnert HJ, Van Thieleen N, Chen R, Ishitani M;
 PI

XX WPI; 2002-049152/06.
 DR N-PSDB; AAS17965.
 XX
 PT New polypeptide, useful for increasing tolerance to environmental
 PT stress, comprises a Signal Transduction Stress-Related Protein selected
 PT from phospholipases, 14-3-3 proteins and calcium binding proteins -
 PS Claim 3; Fig 3A; 101pp; English.
 CC The invention relates to a Signal Transduction Stress-Related Protein
 CC (STSRP) isolated from Physcomitrella patens, and selected from
 CC Phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein
 CC (14-3-3p-1, 14-3-3p-2 and Ca2+-Binding Protein (CBP)-1, or their
 CC orthologues. Also include are a transgenic plant transformed with
 CC an STSRP coding nucleic acid, where the expression of the nucleic acid in
 CC the plant cell results in increased tolerance to an environmental stress
 CC as compared to a wild type variety of the plant cell, a nucleic
 CC acid encoding an STSRP, and an expression vector comprising the nucleic
 CC acid. The STSRP and nucleic acids are useful for increasing tolerance to
 CC environmental stress selected from salinity, drought and low temperature,
 CC in transgenic plants including monocot and dicot selected from maize,
 CC wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
 CC rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous
 CC plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa,
 CC coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and
 CC forage crops. The nucleic acid is also useful for identifying organisms
 CC e.g. Physcomitrella patens in a mixed population of microorganisms,
 CC for evolutionary and protein structural studies and are useful as markers
 CC for specific regions of the genome. The present sequence represents
 CC PLC-1.
 SO Sequence 1054 AA:
 Query Match 1.2%; Score 14; DB 23; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 320 VHODMTOPLSHYFI 333
 DB 104 VHODMTOPLSHYFI 117
 RESULT 11
 ID AAU87634 standard; Protein: 119 AA.
 AC AAU87634;
 XX 05-JUN-2002 (first entry)
 DE Novel central nervous system protein #544.
 KW Central nervous system protein
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysgenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200155318-A2.
 PN 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US01332.
 PF 31-JAN-2000; 2000US-0179065.
 PR

PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217486.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231245.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233403.
PR 14-SEP-2000; 2000US-0233404.
PR 14-SEP-2000; 2000US-0233405.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
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PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236370.
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PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246533.
PR 08-NOV-2000; 2000US-0246534.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249287.
PR 17-NOV-2000; 2000US-0249289.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251038.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI
XX
PI
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-581633/65.
DR
N-PSDB; ABK43964.
XX
XX
PT
PT
PT
New isolated nucleic acid encoding a protein for diagnosing,
preventing, treating or ameliorating medical conditions and used as
food additives or preservatives -

XX Claim 9; SEQ ID NO 1152; 837pp; English.

PS The invention describes an isolated nucleic acid molecule (I) encoding a
XX novel nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiosclerosis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 1.1%; Score 13; DB 22; Length 119;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YIMAGISDEDSIA 160

DB 53 YIMAGISDEDSIA 65

RESULT 12

ABBI7239 standard; Protein; 119 AA.

AC ABBI7239;

DT 23-JAN-2002 (first entry)

DE Human nervous system related polypeptide SEQ ID NO 5896.

XX Human; neurotrophic; neuroprotective; cytoskeletal; dermatological; virucide;
XX immunosuppressive; anti-HIV; antibacterial; vulnery;
XX antiparkinsonian; antischistosomal; antianemic; antithrombotic; cancer;
XX antineuritic; hepatotropic; cerebroprotective; antineuroinflammatory;
XX antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotoxic; gene therapy; vaccine.

XX Homo sapiens.

OS WO200159063-A2.

PN 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0188874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

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PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

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PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

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PR 06-SEP-2000; 2000US-0230437.

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PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

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PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.

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PR 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.

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PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.

PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239335.

PR 13-OCT-2000; 2000US-0239337.

PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.

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PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
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 PR 08-NOV-2000; 2000US-0246477.
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 PR 17-NOV-2000; 2000US-0249245.
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 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PR XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR N-PSDB; ABA13565.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Claim 11; SEQ ID NO 5896; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone

CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC XX
 SQ Sequence 119 AA;
 QY Query Match 1.1%; Score 13; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 148 YLMAGISDEDSLA 160
 53 YLMAGISDEDSLA 65
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 RESULT 13
 AAU17072
 ID AAU17072 standard; Protein: 119 AA.
 AC
 XX AAU17072;
 DT 07-NOV-2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, Seq ID 637.
 XX
 KW Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; Down syndrome; ischaemia; renal disorder;
 KW reproductive system; wound healing; endocrine; Addison's disease;
 KW acquired immune deficiency syndrome.
 KW
 OS Homo sapiens.
 OS
 PN MO200154733-A1.
 PN
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01312.
 PE
 XX 31-JAN-2000; 2000US-0179065.
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 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
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 PR 17-MAR-2000; 2000US-0190076.
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 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
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 PR 20-OCT-2000; 2000US-0241786.
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 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0246417.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
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 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI: 2001-465460/50.
 DR N-PSDB; AAS26989.
 XX
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders
 XX
 PS
 PS
 XX
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), Chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),

CC as stimulators of B-cell responsiveness to pathogens, activators of
CC T-cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AAU17059-AAU17663 represent novel signal transduction
CC pathway protein, amino acid sequences of the invention.
XX

Query Match 1.1%; Score 13; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 0 00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 148 YLMAGISDESLA 160
DB 53 YLMAGISDESLA 65

RESULT 14
AAM43643
ID AAM43643 standard; Protein; 119 AA.
XX
AC AAM43643;
XX
DT 22-OCT-2001 (first entry)
XX

DE Human polypeptide SEQ ID NO 321.
XX

KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiatherogenic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; anticonvulsant; antibacterial;
KW antiparasitic; cardiatic; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN MO200155308-A2.
XX
PD 02-AUG-2001.
XX

PF 17-JAN-2001; 2001MO-US01309.
XX

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 19-MAY-2000; 2000US-0205515.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0244676.
PR 08-NOV-2000; 2000US-0244677.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.

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PR	17-NOV-2000	2000US-0249218
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PR	17-NOV-2000	2000US-0249245
PR	17-NOV-2000	2000US-0249265
PR	17-NOV-2000	2000US-0249284
PR	17-NOV-2000	2000US-0249297
PR	17-NOV-2000	2000US-0249299
PR	17-NOV-2000	2000US-0249300
PR	01-DEC-2000	2000US-0250160
PR	01-DEC-2000	2000US-0250186
PR	01-DEC-2000	2000US-0250391
PR	05-DEC-2000	2000US-0251030
PR	05-DEC-2000	2000US-0251198
PR	05-DEC-2000	2000US-0256719
PR	06-DEC-2000	2000US-0251479
PR	08-DEC-2000	2000US-0251856
PR	08-DEC-2000	2000US-0251868
PR	08-DEC-2000	2000US-0251869
PR	08-DEC-2000	2000US-0251989
PR	08-DEC-2000	2000US-0251990
PR	11-DEC-2000	2000US-0254097
PR	05-JAN-2001	2001US-0239678

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.

N-PSDB; ABK43682

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 9; SEQ ID No 870; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysplasia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

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query Match      1.1%; Score 13; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 148 YLMAGISDEDSLA 160
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Db 89 YLMAGISDEDSLA 101
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Search completed: March 28, 2003, 14:02:24
Job time : 88 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 14:00:21 ; Search time 54 Seconds
(without alignments)
2148.782 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 1207
Sequence: 1 MAPPTAGPLPGPALPEDPG.....ALYPWHLRGLTLPLACGP 1207

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	12	1.0	764	1	1-phosphatidylinos
2	12	1.0	764	1	1-phosphatidylinos
3	12	1.0	764	1	1-phosphatidylinos
4	12	1.0	764	1	1-phosphatidylinos
5	12	1.0	764	1	1-phosphatidylinos
6	12	1.0	764	1	1-phosphatidylinos
7	12	1.0	764	1	1-phosphatidylinos
8	12	1.0	764	1	1-phosphatidylinos
9	12	1.0	764	1	1-phosphatidylinos
10	12	1.0	764	1	1-phosphatidylinos
11	12	1.0	764	1	1-phosphatidylinos
12	12	1.0	764	1	1-phosphatidylinos
13	12	1.0	764	1	1-phosphatidylinos
14	12	1.0	764	1	1-phosphatidylinos
15	12	1.0	764	1	1-phosphatidylinos
16	12	1.0	764	1	1-phosphatidylinos
17	12	1.0	764	1	1-phosphatidylinos
18	12	1.0	764	1	1-phosphatidylinos
19	12	1.0	764	1	1-phosphatidylinos
20	12	1.0	764	1	1-phosphatidylinos
21	12	1.0	764	1	1-phosphatidylinos
22	12	1.0	764	1	1-phosphatidylinos
23	12	1.0	764	1	1-phosphatidylinos
24	12	1.0	764	1	1-phosphatidylinos
25	12	1.0	764	1	1-phosphatidylinos
26	12	1.0	764	1	1-phosphatidylinos
27	12	1.0	764	1	1-phosphatidylinos
28	12	1.0	764	1	1-phosphatidylinos
29	12	1.0	764	1	1-phosphatidylinos

30	8	0.7	243	2	A40394	spec-related prote
31	8	0.7	264	2	D71037	hypothetical prote
32	8	0.7	317	1	A31797	Spec-related prote
33	8	0.7	318	2	G95255	tim-barrel protein
34	8	0.7	332	2	A82688	octaprenyl-dihosp
35	8	0.7	336	2	G98120	conserved hypothet
36	8	0.7	337	2	S42416	probable membrane
37	8	0.7	338	2	B82128	conserved hypothet
38	8	0.7	357	2	D83017	probable transcript
39	8	0.7	382	2	T06639	hypothetical prote
40	8	0.7	413	2	D86920	probable UDP-galac
41	8	0.7	441	2	E72579	hypothetical prote
42	8	0.7	465	2	B82558	IMP dehydrogenase
43	8	0.7	513	2	T45658	1-phosphatidylinos
44	8	0.7	531	1	S54098	1-phosphatidylinos
45	8	0.7	543	2	AB0460	ubiquinone biosynt

ALIGNMENTS

RESULT 1

514113

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-2 - boy

N:Alternate names: phosphoinositidase C; phospholipase C-delta-2; triphosphoinositide

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Jun-2000

R:Meldrum, E.; Kriz, R.W.; Totty, N.; Parker, P.J.

Eur. J. Biochem. 196, 159-165, 1991.

A:Title: A second gene product of the inositol-phospholipid-specific phospholipase C-

A:Reference number: 514113; MUID:91160548; PMID:1848183

A:Accession: 514113

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1764 <ME2>

A:Experimental source: brain

R:Meldrum, E.; Katan, M.; Parker, P.

Eur. J. Biochem. 182, 673-677, 1989

A:Title: A novel inositol-phospholipid-specific phospholipase C. Rapid purification a

A:Reference number: 504944; MUID:89325315; PMID:2753038

A:Accession: 504944

A:Status: preliminary

A:Molecule type: protein

A:Residues: 528-541, 'X', '543-553, 659-669 <ME2>

A:Experimental source: brain

C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triph

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p

C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; sl

F:134-122/Domain: pleckstrin repeat homology <PLK>

F:170-202/Domain: calmodulin repeat homology <EF1>

F:292-435/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

F:611-723/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match 1.0%; Score 12; DB 1; Length 764;

Best local similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346

DB 303 SSHNTYLVGDQL 314

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Submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23037

A:Accession: T46339

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-913 <A>

A:Cross-references: EMBL:AL137267

A:Experimental source: adult testis; clone DKFZp434A0814

C:Genetics:

A:Note: DKFZp434A0814.1

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidyl-
odiestererase domain y homology

F:58-207/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 1.0%; Score 12; DB 2; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

Db 354 FNNAGCOMVALN 365

RESULT 3

A:Accession: A43346

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) beta-2 - human

N:Alternate names: phospholipase C beta-2; triphosphoinositide phosphodiesterase

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999

R:Accession: A43346

R:Par: D.; Jhon, D.Y.; Kriz, R.; Knopf, J.; Rhee, S.G.

J. Biol. Chem. 267, 16048-16055, 1992

A:Title: Cloning, sequencing, expression, and Gq-independent activation of phospholipase

A:Reference number: A43346; MUID:9235553; PMID:1644792

A:Accession: A43346

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1181 <PAR>

A:Cross-references: GB:M95678; NID:q190039; PIDN:AAA36453.1; PID:q190040

A:Note: sequence extracted from NCBI backbone (NCBI:110494)

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidyl-
odiestererase domain y homology

C:Keywords: phosphoric diester hydrolase

F:314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

F:541-661/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom

Query Match 1.0%; Score 12; DB 2; Length 1181;
Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

Db 616 FNNAGCOMVALN 627

RESULT 4

A:Accession: A48001

phospholipase C (EC 3.1.4.3) beta, oocyte - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 22-Jun-1999

R:Accession: A48001

R:Ma, H.W.; Blitzer, R.D.; Healy, E.C.; Premont, R.T.; Landau, E.M.; Iyengar, R.

J. Biol. Chem. 268, 19915-19918, 1993

A:Title: Receptor-evoked Cl(-) current in Xenopus oocytes is mediated through a beta-tyr

A:Reference number: A48001; MUID:9338545; PMID:8397190

A:Accession: A48001

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1210 <MA>

A:Cross-references: GB:L20816; NID:q405589; PIDN:AAA03065.1; PID:q405590

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidyl-
odiestererase domain y homology

C:Keywords: phosphoric diester hydrolase

F:319-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x
F:575-695/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match 1.0%; Score 12; DB 2; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

Db 650 FNNAGCOMVALN 661

RESULT 5

A:Accession: S68251

phospholipase C, inositol-1lipid specific (EC 3.1.4.-) isoform beta - turkey

C:Species: Meleagris gallopavo (common turkey)

C>Date: 05-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 22-Jun-1999

R:Accession: S68251; S72374; A61270

R:Waldo, G.L.; Paterson, A.; Boyer, J.L.; Nicholas, R.A.; Harden, T.K.

Biochem. J. 316, 559-568, 1996

A:Title: Molecular cloning, expression and regulatory activity of G-alpha(11) - and be

A:Reference number: S68251; MUID:96257751; PMID:8667401

A:Accession: S68251

A:Molecule type: mRNA

A:Residues: 1-1211 <MAL>

A:Cross-references: GB:U49431; NID:q1223919; PIDN:AAC60011.1; PID:q1223920

A:Experimental source: erythrocyte

A:Accession: S72374

A:Molecule type: protein

A:Residues: 210-216, 'M', 218-231, 244-248, 284-291, 345-353, 'S', 355-360, 453-461, 661-679 <

A:Experimental source: erythrocyte

R:Waldo, G.L.; Morris, A.J.; Klapper, D.G.; Harden, T.K.

Mol. Pharmacol. 40, 480-489, 1991

A:Title: Receptor- and G-protein-regulated 150-kDa avian phospholipase C: inhibition

ished by immunoreactivity and peptide sequence.

A:Reference number: A61270; MUID:9201673; PMID:1656188

A:Accession: A61270

A>Status: preliminary

A:Molecule type: protein

A:Residues: 284-292, 'X', 294-296, 'R', 568-577, 751-753, 'L', 755-759, 765-776, 'T', 778-780, 8

A:Experimental source: erythrocyte

A:Note: 885-His was also found

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phospha

odiestererase domain y homology

C:Keywords: phosphoric diester hydrolase

F:314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

F:543-663/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match 1.0%; Score 12; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 QDMTQPLSHYFI 333

Db 312 QDMTQPLSHYFI 323

RESULT 6

A:Accession: A28822

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - bovine

N:Alternate names: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta; ph

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 22-Jun-1999

R:Accession: A28822; A39236

R:Katan, M.; Kriz, R.W.; Totty, N.; Philp, R.; Meldrum, E.; Aldape, R.A.; Knopf, J.L.

Cell 54, 171-177, 1988

A:Title: Determination of the primary structure of PLC-154 demonstrates diversity of

A:Reference number: A28822; MUID:88270496; PMID:2455601

A:Accession: A28822

A:Molecule type: mRNA

A:Residues: 1-1216 <KAT>

A:Cross-references: GB:J03137; NID:q163521; PIDN:AAA30702.1; PID:q163522

R:Ryu, S.H.; Kim, U.H.; Wahl, M.I.; Brown, A.B.; Carpenter, G.; Huang, K.P.; Rhee, S.

J. Biol. Chem. 265, 17941-17945, 1990
 A:Title: Feedback regulation of phospholipase C-beta by protein kinase C.
 A:Reference number: A39236; MUID:91009263; PMID:2211670
 A:Accession: A39236
 A:Molecule type: protein
 A:Residues: 879-889 <RTU>
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology
 C:Keywords: phosphoprotein; phosphoric diester hydrolase
 F:318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:518-659/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom
 F:887/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental

Query Match 1.0%; Score 12; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 7
 A28821
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - rat
 N:Alternate names: triphosphoinositide phosphodiesterase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 22-Jun-1999
 C:Accession: A28821
 R:Sun, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A:Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MUID:88270495; PMID:3390863
 A:Accession: A28821
 A:Molecule type: mRNA
 A:Residues: 1-1216 <SUH>
 A:Cross-references: GB:M20636; GB:J03136; NID:9206217; PIDN:AAA41885.1; PID:9206218
 A:Experimental source: brain
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology
 C:Keywords: phosphoprotein; phosphoric diester hydrolase
 F:318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:518-659/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom

Query Match 1.0%; Score 12; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 8
 T42440
 phospholipase C homolog - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence-revision 03-Dec-1999 #text-change 02-Sep-2000
 C:Accession: T42440
 R:Shibamoto, M.; Kariya, K.; Liao, Y.; Hu, C.D.; Watari, Y.; Goshima, M.; Shima, F.; Ka
 J. Biol. Chem. 273, 6218-6222, 1998
 A:Title: Identification of PLC210, a Caenorhabditis elegans phospholipase C, as a putati
 A:Reference number: 222164; MUID:98165800; PMID:9497345
 A:Accession: T42440
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1839 <SHI>
 A:Cross-references: EMBL:AF044576; NID:92957269; PIDN:AC38963.1; PID:92957270
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homolo
 F:912-1058/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x ho

Query Match 0.9%; Score 11; DB 2; Length 1898;
 Best Local Similarity 100.0%; Pred. No. 0.085;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 410 PVILSTENHCS 420
 DB 998 PVILSTENHCS 1008

RESULT 9
 T21581
 hypothetical protein F31B12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 02-Sep-2000
 C:Accession: T21581
 R:Kershaw, J.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z19444
 A:Accession: T21581
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1922 <WTL>
 A:Cross-references: EMBL:Z50740; PIDN:CAA90606.1; GSPDB:GN00028; CESP:F31B12.1
 A:Experimental source: clone F31B12
 C:Genetics:
 A:Gene: CESP:F31B12.1
 A:Map position: X
 A:Introns: 44/1; 137/3; 207/3; 305/1; 347/1; 425/3; 486/3; 536/3; 593/1; 619/2; 708/1
 3; 1724/3; 1847/3
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:940-1066/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

Query Match 0.9%; Score 11; DB 2; Length 1922;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 PVILSTENHCS 420
 DB 1026 PVILSTENHCS 1036

RESULT 10
 B28821
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 - rat
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 02-Jun-2000
 C:Accession: B28821; I55942
 R:Sun, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A:Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MUID:88270495; PMID:3390863
 A:Accession: B28821
 A:Residues: 1-756 <SUH>
 A:Molecule type: mRNA
 A:Cross-references: GB:M20637; GB:J03136; NID:9206219; PIDN:AAA41886.1; PID:9206220
 A:Experimental source: brain
 R:Tagiawa, H.; Tanase, H.; Nojima, H.
 J. Hypertens. 9, 997-1004, 1991
 A:Title: Phospholipase C-delta gene of the spontaneously hypertensive rat harbors pol
 A:Reference number: I55942; MUID:92098966; PMID:1684614
 A:Accession: I55942
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411, 'M', 'A13-422', 'S', '424-462', 'D', '464-626', 'A', '628', 'K', '630-667', 'A', '669-756
 A:Cross-references: GB:S74591; NID:9241276
 A:Note: this translation is not annotated in Genbank entry S74591, release 113.0
 A:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-tripho
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homolo
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:176-208/Domain: calmodulin repeat homology <EF2>

F:296-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 0.8%; Score 10; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGCGGYLKP 732
DB 596 NGCGGYLKP 605

RESULT 11

A44165

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - slime mold (D)
N:Alternate names: phosphoinositide-specific phospholipase C
C:Species: Dictyostelium discoideum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C:Accession: A44165

R:Drayer, A.L.; Van Haastert, P.J.
J. Biol. Chem. 267, 18387-18392, 1992
A:Title: Molecular cloning and expression of a phosphoinositide-specific phospholipase C
A:Reference number: A44165; MID:92406741; PMID:1326523

A:Accession: A44165
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-801 <DRA>

A:Cross-references: GB:M95783; NID:q167846; PIDN:AAA33235.1; PID:167847
A:Node: sequence extracted from NCBI backbone (NCBI:113302)
C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat homol
C:Keywords: EF hand; phosphoprotein; phosphoric diester hydrolase
F:324-465/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:538-656/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:658-769/Domain: protein kinase C C2 region homology <KC2>

Query Match 0.8%; Score 10; DB 1; Length 801;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGCGGYLKP 732
DB 640 NGCGGYLKP 649

RESULT 12
T32374
hypothetical protein K10F12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
C:Accession: T32374

R:Wohlmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid K10F12.
A:Reference number: Z21157
A:Accession: T32374

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-895 <WOB>

A:Cross-references: EMBL:AF025462; PIDN:AA71005.1; GSPDB:GN00021; CESP:K10F12.3
A:Experimental source: strain Bristol N2; clone K10F12
C:Genetics:

A:Gene: CESP:K10F12.3
A:Map position: 3
A:Intons: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 62
C:Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
sphodiesterase domain Y homology
F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 0.8%; Score 10; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTOPLSHY 331
DB 300 QDMTOPLSHY 309

RESULT 13
T27376
hypothetical protein Y75B12B.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T27376

R:White, S.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20360
A:Accession: T27376
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-896 <WIT>

A:Cross-references: EMBL:AL032663; PIDN:CAA21765.1; GSPDB:GN00023; CESP:Y75B12B.6
A:Experimental source: clone Y75B12B
C:Genetics:
A:Gene: CESP:Y75B12B.6
A:Map position: 5
A:Intons: 21/3; 54/3; 115/3; 163/2; 189/3; 223/2; 273/1; 325/1; 642/2; 674/3; 783/1;
C:Superfamily: squid 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phos
phodiesterase domain Y homology
F:306-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

QY 723 NGCGGYLKP 732
DB 631 NGCGGYLKP 640

RESULT 14
I54390
phosphoinositide-specific phospholipase C (EC 3.1.4.-) epsilon - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I54390

R:Kohn, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota,
Hum. Mol. Genet. 4, 667-674, 1995
A:Title: Identification of a novel phospholipase C family gene at chromosome 2q33 th
A:Reference number: I54390; MID:95359933; PMID:7633416
A:Accession: I54390

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <RES>

A:Cross-references: GB:042108; NID:9780121; PIDN:BA07688.1; PID:9780122
C:Genetics:

A:Gene: GDB:PLCE; PLC-L
A:Cross-references: GDB:699207; OMIM:600597
A:Map position: 2q33-2q33
C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinosito
domain Y homology
C:Keywords: phosphoric diester hydrolase
F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

Query Match 0.8%; Score 10; DB 2; Length 896;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 YPVLISINH 418
DB 401 YPVLISINH 410

RESULT 15
I54390
phosphoinositide-specific phospholipase C (EC 3.1.4.-) epsilon - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I54390

R:Kohn, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota,
Hum. Mol. Genet. 4, 667-674, 1995
A:Title: Identification of a novel phospholipase C family gene at chromosome 2q33 th
A:Reference number: I54390; MID:95359933; PMID:7633416
A:Accession: I54390

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <RES>

A:Cross-references: GB:042108; NID:9780121; PIDN:BA07688.1; PID:9780122
C:Genetics:

A:Gene: GDB:PLCE; PLC-L
A:Cross-references: GDB:699207; OMIM:600597
A:Map position: 2q33-2q33
C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinosito
domain Y homology
C:Keywords: phosphoric diester hydrolase
F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

Query Match 0.8%; Score 10; DB 1; Length 997;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTOPLSHY 331
DB 300 QDMTOPLSHY 309

RESULT 15
I54390
phosphoinositide-specific phospholipase C (EC 3.1.4.-) epsilon - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I54390

R:Kohn, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota,
Hum. Mol. Genet. 4, 667-674, 1995
A:Title: Identification of a novel phospholipase C family gene at chromosome 2q33 th
A:Reference number: I54390; MID:95359933; PMID:7633416
A:Accession: I54390

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <RES>

A:Cross-references: GB:042108; NID:9780121; PIDN:BA07688.1; PID:9780122
C:Genetics:

A:Gene: GDB:PLCE; PLC-L
A:Cross-references: GDB:699207; OMIM:600597
A:Map position: 2q33-2q33
C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinosito
domain Y homology
C:Keywords: phosphoric diester hydrolase
F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

S62358
 Inositol 1,4,5-trisphosphate-binding protein, 130K - rat
 N:Alternate names: phospholipase C delta 1 homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: S62358; S69328
 R:Kanematsu, T.; Misumi, Y.; Watanabe, Y.; Ozaki, S.; Koga, T.; Iwanaga, S.; Ikehara, Y.
 Biochem. J. 313, 319-325, 1996
 A:Title: A new inositol 1,4,5-trisphosphate binding protein similar to phospholipase C- δ
 A:Reference number: S62358; MUID:96132642; PMID:8546702
 A:Accession: S62358
 A:Molecule type: mRNA
 A:Residues: 1-1096 <KAN1>
 A:Cross-references: EMBL:D45920; NID:q1183843; PIDN:BAA08351.1; PID:q1183844
 A:Accession: S69328
 A:Molecule type: protein
 A:Residues: 172-191; 228-242; 1024-1034 <KAN2>
 C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinositol-4-
 domain X homology
 F:401-543/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F:585-705/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom

Query Match 0.8%; Score 10; DB 1; Length 1096;
 Best Local Similarity 100.0%; Pred. NO. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTQPLSHY 331
 |||||
 DB 399 QDMTQPLSHY 408

Search completed: March 28, 2003, 14:06:00
 Job time : 60 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:53:20 / Search time 29 Seconds
(without alignments)
1726.273 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPPTAGPLPGPALPPEDPG.....ALYPHCLRGTLPLWLAGCP 1207

Scoring table: OLIGO
Gapop 60.0, Gapept 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Length	ID	Description
1	324	26.8	Y450_HUMAN	075038 homo sapien
2	12	1.0	PIB2_HUMAN	000722 homo sapien
3	12	1.0	PIB1_BOVIN	P10894 bos taurus
4	12	1.0	PIB1_HUMAN	Q9nq66 homo sapien
5	12	1.0	PIB1_RAT	P10687 ratius norv
6	10	0.8	PIB1_RAT	P10688 ratius norv
7	10	0.8	PIB1_RAT	Q02158 dictyosteli
8	9	0.7	PIB1_DROME	P13217 drosophila
9	9	0.7	PIB1_DROME	Q15147 homo sapien
10	9	0.7	PIB1_RAT	Q9nq07 ratius norv
11	9	0.7	PIB1_HUMAN	P19174 homo sapien
12	9	0.7	PIB1_BOVIN	P10686 ratius norv
13	9	0.7	PIB1_BOVIN	P08487 bos taurus
14	9	0.7	DPOX_MOUSE	Q61493 mus musculu
15	8	0.7	PIB1_HUMAN	Q03975 lytechinus
16	8	0.7	LPSB_LYTP1	P09485 lytechinus
17	8	0.7	UBIR_YERPE	Q8zaml yersinia pe
18	8	0.7	UBIR_YERPE	Q9kxg4 vibrio chol
19	8	0.7	HEM1_STRCO	Q9xw15 streptomyce
20	8	0.7	PIB1_BOVIN	P10895 bos taurus
21	8	0.7	YJ76_YEAST	P47144 saccharomyc
22	8	0.7	PIB1_HUMAN	P51178 homo sapien
23	8	0.7	YK03_YEAST	P36097 saccharomyc
24	8	0.7	PIB3_HUMAN	P51432 mus musculu
25	8	0.7	PIB3_MOUSE	P16885 homo sapien
26	8	0.7	PIB2_HUMAN	P24135 ratius norv
27	8	0.7	PIB2_RAT	Q9j104 mus musculu
28	8	0.7	FMN2_MOUSE	Q9x1f5 thermotoga
29	7	0.6	YE42_THEMA	Q52106 actinobact
30	7	0.6	MERT_ACTICA	Q51769 pseudomonas
31	7	0.6	MERT_PSEFL	P04336 salmonella
32	7	0.6	MERT_SALTI	P41482 autographa
33	7	0.6	Y102_NPVAC	

34	7	0.6	137	1	HOLD_ECOLI	P28632 escherichia
35	7	0.6	141	1	GLBI_PHESE	P11740 pheretima s
36	7	0.6	146	1	RBFA_RHIO	Q98B17 rhizobium 1
37	7	0.6	163	1	PFDS_YEAST	Q04493 saccharomyc
38	7	0.6	170	1	ING_SIGHI	Q9qxx2 sigmondon hl
39	7	0.6	207	1	PIG1_MOUSE	Q62077 mus musculu
40	7	0.6	212	1	RERC_ARATH	Q9xw17 arabidopsis
41	7	0.6	250	1	PSA2_YEAST	P23639 saccharomyc
42	7	0.6	259	1	YCB0_YEAST	P25594 saccharomyc
43	7	0.6	264	1	YCB0_ANAPL	Q42296 anas platyr
44	7	0.6	264	1	APAL_CHICK	P08250 gallus gall
45	7	0.6	264	1	APAL_CORUA	P32918 coturnix co

ALIGNMENTS

RESULT 1
Y450_HUMAN STANDARD; PRT; 425 AA.

AC 075038;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical Protein KIAA0450.
GN KIAA0450.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
RX MEDLINE=98116662; PubMed=945484;
RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
RA Nakajima D., Nomura N., Ohara O.;
RT Characterization of cDNA clones in size-fractionated cDNA libraries
RT from human brain.";

RL DNA Res. 4:345-349(1997).
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CC or send an email to license@sib-sib.ch).

CC EMBL; AB007919; BAA32295.1; -;
DR Hypothetical protein.
SQ SEQUENCE 425 AA; 43842 MW; 2A6D733CA149E665 CRC64;

Query Match 26.8%; Score 324; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	884	YKQALGLKLFTRPGSLDSHAAGRPAPRSVSQRLRTASAPTSQKGRGPEL	943
DB	102	VKQALGLKLFTRPGSLDSHAAGRPAPRSVSQRLRTASAPTSQKGRGPEL	161
QY	944	VIGTRDTGSKGVADVVPPGPGAPAPAOBEGSGSPGKPAVAEKSPPRVPPRYL	1003
DB	162	VIGTRDTGSKGVADVVPPGPGAPAPAOBEGSGSPGKPAVAEKSPPRVPPRYL	221
QY	1004	DGPGPMATCKKCVGSCAGVNTGGLRERPPSPGASROAIFROPARADSIGAPC	1063
DB	222	DGPGPMATCKKCVGSCAGVNTGGLRERPPSPGASROAIFROPARADSIGAPC	281
QY	1064	CGIDPFAITGRSREARPGAGAMROGPGSGSSSDSSPSDPSGIPERSRPMEGACROPG	1123
DB	282	CGIDPFAITGRSREARPGAGAMROGPGSGSSSDSSPSDPSGIPERSRPMEGACROPG	341
QY	1124	ALQGENSALFAQKLEIRSKSPMFSAGKPLPCVUIPLPAFGMAGPGSPAAASAMTVSPRV	1183

DB 342 ALGEMSALEFQAKLEIRKSPMSACKPLPCVVLPHAPGMAGPGSPAASAMTVSPRV 401
 QY 1184 LVVALYPMHCRGTLLPWLACGP 1207
 DB 402 LVVALYPMHCRGTLLPWLACGP 425

RESULT 2
 PIB2_HUMAN
 ID PIB2_HUMAN STANDARD; PRT; 1181 AA.
 AC 000722:

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 2
 DE (EC 3.1.4.11) (PLC-beta-2) (phospholipase C-beta-2).
 GN PLCB2.

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP MEDLINE=92355553; PubMed=1644792;
 RX Park D., Jhon D.-Y., Kriz R., Knopf J., Rhee S.G.;

RT Cloning, sequencing, expression, and Gq-independent activation of
 phospholipase C-beta 2.
 RL J. Biol. Chem. 267:16048-16055 (1992).

CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS.

CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.

CC -1- COFACTOR: Calcium.

CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA-2 IS
 CC MOST EFFECTIVELY MEDIATED BY ONE G-PROTEIN ALPHA SUBUNIT,

CC ALPHA-16.

CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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DR EMBL: M95678; AAA36453.1; -
 DR PIR: A43346; A43346.
 DR HSSP: P10688; IDJX.

DR Genew: HGNC:9055; PLCB2.
 DR MIM: 604114; -

DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.

DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.

DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.

DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.

DR SMART: SM00239; C2; 1.
 DR SMART: SM00148; PLCX; 1.

DR SMART: SM00149; PLCY; 1.
 DR PROSITE: PS50004; C2 DOMAIN 2; 1.

DR PROSITE: PS50007; PIPLC_X DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.

FT DOMAIN 312 463 DOMAIN X (BY SIMILARITY).
 FT DOMAIN 542 658 DOMAIN Y (BY SIMILARITY).
 FT ACT_SITE 665 763 C2 DOMAIN.
 FT ACT_SITE 327 327 BY SIMILARITY.
 FT ACT_SITE 374 374 BY SIMILARITY.
 SQ SEQUENCE 1181 AA; 133679 MW; 7A6889E204D17FNA CRC64;

Query Match 1.0%; Score 12; DB 1; Length 1181;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FNNACQWVALN 705
 DB 616 FNNACQWVALN 627

RESULT 3

PIB1_BOVIN
 ID PIB1_BOVIN STANDARD; PRT; 1216 AA.
 AC P10894;

DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (phospholipase C-beta-1) (PLC-154).

GN PLCB1.
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]

RP MEDLINE=88270496; PubMed=2455601;
 RX Katan M., Kriz R.W., Totty N., Philip R., Meldrum E., Aldape R.A.,

RT Knopf J.L., Parker P.J.;
 RT "Determination of the primary structure of PLC-154 demonstrates

RT diversity of phospholipase C activities."
 RL Cell 54:171-177 (1988).

CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS.

CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.

CC -1- COFACTOR: Calcium.

CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.

CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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DR EMBL: J03137; AAA30702.1; -
 DR PIR: A28822; A28822.

DR HSSP: P10688; IDJX.
 DR InterPro: IPR000008; C2.

DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.

DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.

DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.

DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.

DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2.DOMAIN.2; 1.
 DR PROSITE; PS50007; PIP2C_X.DOMAIN; 1.
 DR PROSITE; PS50008; PIP2C_Y.DOMAIN; 1.
 DR Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467 DOMAIN X.
 FT DOMAIN 540 656 DOMAIN Y.
 FT ACT_SITE 663 761 C2 DOMAIN.
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT MOD_RES 378 378 BY SIMILARITY.
 FT SEQUENCE 1216 AA; 138714 MW; BEF809177F1B7AB8 CRC64;
 Query Match 1.0%; Score 12; DB 1; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 694 FNNAGCONVALN 705
 Db 614 FNNAGCONVALN 625
 RESULT 4
 ID P1BL_HUMAN STANDARD; PRT; 1216 AA.
 AC Q9N066; Q9N065; Q9N089; Q9NTH4; O60325; Q9H4H2; Q9H0W2; Q9UJP6;
 AC Q9UW26;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).
 GN PLCB1 OR KIA0581.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE-Brain;
 RA Carlasole A., Sala C., Roncarati R., Formenti E., Terstappen G.C.;
 RT Cloning and characterization of the human phosphoinositide-specific
 RT phospholipase C-beta 1 (PLCBeta1).
 RL Biochim. Biophys. Acta 1517:63-72(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE-2025428; PubMed-10760467;
 RA Peruzzi D., Calabrese G., Faenza I., Manzoli L., Matteucci A.,
 RA Giannarino F., Billi A.M., Stupia L., Palca G., Cocco L.;
 RT Identification and chromosomal localisation by fluorescence in situ
 RT hybridisation of human gene of phosphoinositide-specific phospholipase
 RT C beta 1.
 RL Biochim. Biophys. Acta 1484:175-182(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21638749; PubMed-11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagdaley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jackson K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lavelle S.,

RA Lehtsaialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McNurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulton J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT The DNA sequence and comparative analysis of human chromosome 20.;
 RL Nature 414:865-871(2001).
 RN [4]
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).
 RC TISSUE-Testis;
 RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE-98290545; PubMed-9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.;
 RL DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DICYCLIGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYME.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy]-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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 DR EMBL: AJ278313; CAB98142.1;
 DR EMBL: AJ278314; CAB98143.1;
 DR EMBL: AY004175; AAF6613.1;
 DR EMBL: AL031683; CAC16181.1;
 DR EMBL: AL031683; CAC3166.1;
 DR EMBL: AL050315; CAB56498.1;
 DR EMBL: AL049632; CAB46663.1;
 DR EMBL: AL137267; CAB70666.1;
 DR EMBL: AB011153; BAA25507.1;
 DR HSP; P10688; IDX.
 DR Gene; HGNC:15917; PLCB1.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR01711; PI_PLC_Y.
 DR Pfam: PF00168; C2.2
 DR Pfam: PF00387; PI_PLC_Y; 3.
 DR Pfam: PF00388; PI_PLC-X; 2.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.

DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PSS0004; C2 DOMAIN 2; 1.
 DR PROSITE; PSS0007; PIPIC_X DOMAIN; 1.
 DR PROSITE; PSS0008; PIPIC_Y DOMAIN; 1.
 DR Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 316 467
 FT DOMAIN 540 656
 FT DOMAIN 663 761
 FT ACT_SITE 331 331
 FT ACT_SITE 378 378
 FT MOD_RES 887 887
 FT VARSPLOT 1142 1216

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 5
 PDBL_RAT STANDARD; PRT; 1216 AA.
 AC P10687;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC-154).
 GN PLCB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86270495; PubMed=3390863;
 RA Suh P.-G., Ryu S.-H., Moon K.-H., Suh H.-W., Rhee S.-G.;
 RA Rhon D.-Y., Lee H.-R., Park D., Lee C.-W., Lee K.-H., Yoo O.-J.,
 RA Rhee S.-G.;
 RT "Cloning, sequencing, purification, and Gq-dependent activation of
 RT phospholipase C-beta 3";
 RT J. Biol. Chem. 268:6654-6661(1993).
 RL 1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE

CC C ENZYMES.
 CC -1 CATALYTIC ACTIVITY: 1-phosphatidy1-ID-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1 COFACTOR: Calcium.
 CC -1 SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
 CC -1 TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
 CC parotid gland, liver, uterus, lung, heart, adrenal gland and
 CC ovary. Not detected in spleen, pancreas, intestine, thymus or
 CC kidney.
 CC -1 MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
 CC -1 SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1 SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 CC EMBL: M20636; AAA41885.1; -.
 CC PIR: A28821; A28821.
 CC HSP: P10688; IDTX.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR001192; PI-PLC.
 CC InterPro: IPR000909; PI-PLC_Xdom.
 CC InterPro: IPR001711; PI-PLC_Y.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00387; PI-PLC-Y; 1.
 CC Pfam: PF00388; PI-PLC-X; 1.
 CC PRINTS: PR00390; PPHPLIPASEC.
 CC PRODOM: PD001202; PI-PLC_Y; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00148; PLCYC; 1.
 CC SMART: SM00149; PLCYC; 1.
 CC PROSITE: PSS0004; C2 DOMAIN 2; 1.
 CC PROSITE: PSS0007; PIPIC_X DOMAIN; 1.
 CC PROSITE: PSS0008; PIPIC_Y DOMAIN; 1.
 CC Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467
 FT DOMAIN 540 656
 FT DOMAIN 663 761
 FT ACT_SITE 331 331
 FT ACT_SITE 378 378
 FT MOD_RES 887 887
 FT SEQUENCE 1216 AA; 138344 MW; 92F23691781F788B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 6
 PDBL_RAT STANDARD; PRT; 756 AA.
 AC P10688; O9QVD3; O9QVD4; O9QVD5;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-II).
 GN PLCD1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=101116;
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=68270495; PubMed=3390863;
 RA Suh P., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.,"
 RL Cell 54:161-169(1988).
 RN [2]
 RP SEQUENCE OF 50-57; 128-140 AND 728-738.
 RC TISSUE=Brain;
 RX MEDLINE=92202192; PubMed=1313009;
 RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
 RA Iwanaga S., Hirata M.;
 RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
 cytosol.,"
 RL J Biol. Chem. 267:6518-6525(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 12-130.
 RX MEDLINE=96107342; PubMed=8521504;
 RA Ferguson K.M., Lemmon M.A., Schlessinger J., Sigler P.B.;
 RT "Structure of the high affinity complex of inositol trisphosphate
 with a phospholipase C pleckstrin homology domain.,"
 RL Cell 83:1037-1046(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 205-756.
 RX MEDLINE=96378790; PubMed=8784353;
 RA Grobler J.A., Essen L.-O., Williams R.L., Hurley J.H.;
 RT "C2 domain conformational changes in phospholipase C-delta 1.,"
 RL Nat. Struct. Biol. 3:788-795(1996).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 133-756.
 RX MEDLINE=96186808; PubMed=8602259;
 RA Essen L.-O., Persic O., Cheung R., Katan M., Williams R.L.;
 RT "Crystal structure of a mammalian phosphoinositide-specific
 phospholipase C delta.,"
 RL Nature 380:595-602(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 133-756.
 RX MEDLINE=92215812; PubMed=9062102;
 RA Essen L.-O., Persic O., Lynch D.E., Katan M., Williams R.L.;
 RT "A ternary metal binding site in the C2 domain of phosphoinositide-
 specific phospholipase C-delta 1.,"
 RL Biochemistry 36:2753-2762(1997).
 RL [7]
 RP FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYMES.
 CC [1]
 CC CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC [2]
 CC COFACTOR: Calcium.
 CC [3]
 CC SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC [4]
 CC SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC [5]
 CC SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC [6]
 CC SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC [7]
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 CC [8]
 CC EMBL, M20637; AAA41886.1; -.
 DR PIR, B28821; B28821.
 DR PDB, IDJG; 07-JUL-97.
 DR PDB, IDJH; 07-JUL-97.
 DR PDB, IDJI; 07-JUL-97.
 DR PDB, IDJW; 23-JUL-97.
 DR PDB, IDJX; 07-JUL-97.
 DR PDB; IDJY; 07-JUL-97.

CC		MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC	-1-	DICINGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
RT	J. Biol. Chem.	267:18387-18392(1992).
RT	phospholipase C of Dictyostelium discoideum."	
RT	"Molecular cloning and expression of a phosphoinositide-specific	
RA	Drazner A.L., van Haastert P.J.:"	
RP	MEDLINE=92406741; PubMed=1326523;	
RP	STRAIN-NC-4;	
RN	[1]	
OX	NCBI_Taxid=44689;	
OC	Eukaryota; Mycelozoa; Dictyostellida; Dictyostelium.	
GN	Ptara or PtC.	
OS	Dictyostelium discoideum (Slime mold).	
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	
DE	(EC 3.1.4.11) (PLC) (Phosphoinositide-specific phospholipase C).	
CY	723 NCGCGYVLPK 732	
DB	596 NCGCGYVLPK 605	
SO	SEQUENCE	756 AA; 85962 MW; E33F2313AC81E9F9 CRC64;
FT	CA_BIND	153 164 EF-HAND 1 (POTENTIAL).
FT	CA_BIND	189 200 EF-HAND 2 (POTENTIAL).
FT	DOMAIN	296 440 DOMAIN X.
FT	DOMAIN	492 609 DOMAIN Y.
FT	DOMAIN	630 720 C2 DOMAIN.
FT	ACT_SITE	311 311
FT	ACT_SITE	356 356
QI	Query Match	0.8%; Score 10; DB 1; Length 756;
Matches	10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
PIPA.DICDI		
ID	PIPA.DICDI	STANDARD; PRT; 801 AA.
AC	002158;	
DT	01-OCT-1993 (Rel. 27, Created)	
DT	01-OCT-1993 (Rel. 27, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	
DE	(EC 3.1.4.11) (PLC) (Phosphoinositide-specific phospholipase C).	
CC		

CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES; INCREASE IN
 CC EXPRESSION IN THE CULMINATING FRUITING BODY AND DURING
 CC STARVATION.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M95783; AAA33235.1; -
 CC PIR; A44165; A44165.
 CC HSSP; P10688; 1DJX.
 CC Dictydb; DD05034; Pipa.
 CC Interpro; IPR000008; C2.
 CC Interpro; IPR002048; EF-hand.
 CC Interpro; IPR001192; PI_PLC.
 CC Interpro; IPR000909; PI_PLC_Xdom.
 CC Interpro; IPR001711; PI_PLC_Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00387; PI_PLC-Y; 1.
 CC Pfam; PF00388; PI_PLC-X; 1.
 CC PRINTS; PR00360; C2DOMAIN.
 CC PRODOM; PD001202; PI_PLC_Y; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCYC; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS00018; EF_HAND; 1.
 CC PROSITE; PS50004; C2_DOMAIN; 1.
 CC PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
 CC KMW Hydrolyase; lipid degradation; Transducer; Calcium-binding;
 CC Phosphorylation.
 CC FT DOMAIN 322 464 DOMAIN X.
 CC FT DOMAIN 542 652 DOMAIN Y.
 CC FT DOMAIN 661 765 C2 DOMAIN.
 CC FT CA_BIND 490 501 EF-HAND (POTENTIAL).
 CC FT ACT_SITE 337 337 BY SIMILARITY.
 CC FT ACT_SITE 382 382 BY SIMILARITY.
 CC FT MOD_RES 524 524 PHOSPHORYLATION (POTENTIAL).
 CC FT MOD_RES 531 531 PHOSPHORYLATION (BY PKA AND PKG)
 CC (POTENTIAL).
 CC SQ SEQUENCE 801 AA; 91280 MW; DB4FA8C829812DD9 CRC64;
 CC
 CC Query Match 0.8%; Score 10; DB 1; Length 801;
 CC Best Local Similarity 100.0%; Pred. No. 0.21;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGCGYVLRP 732
 DB 640 NGCGYVLRP 649

RESULT 8
 ID PIPA_DROME STANDARD; PRT; 1095 AA.
 AC P13217;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase

DE (EC 3.1.4.11) (Phosphoinositide-specific phospholipase C).
 GN NORPA.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88311074; PubMed=2457447;
 RA Bloomquist B.T., Shortridge R.D., Schneuwly S., Perdev M.H.,
 RA Montell C., Steller H., Rubin G., Pak W.L.;
 RT "Isolation of a putative phospholipase C gene of Drosophila, norpa,
 RT cell 54.723-733(1988)."
 CC
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J03138; AAA28724.1; -
 CC PIR; A31225; A31225.
 CC HSSP; P10688; 1QAS.
 CC FlyBase; FBgn0004625; norpa.
 CC Interpro; IPR000008; C2.
 CC Interpro; IPR001192; PI_PLC.
 CC Interpro; IPR000909; PI_PLC_Xdom.
 CC Interpro; IPR001711; PI_PLC_Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00387; PI_PLC-Y; 1.
 CC Pfam; PF00388; PI_PLC-X; 1.
 CC PRINTS; PR00390; PPHPLIPASEC.
 CC PRODOM; PD001202; PI_PLC_Y; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCYC; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS50004; C2_DOMAIN; 1.
 CC PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
 CC KMW Hydrolyase; lipid degradation; Vision; Transducer.
 CC FT DOMAIN 320 469 DOMAIN X.
 CC FT DOMAIN 550 666 DOMAIN Y.
 CC FT DOMAIN 673 771 C2 DOMAIN.
 CC FT ACT_SITE 334 334 BY SIMILARITY.
 CC FT ACT_SITE 381 381 BY SIMILARITY.
 CC SQ SEQUENCE 1095 AA; 124822 MW; 2D9455EF0ACBE6983 CRC64;
 CC
 CC Query Match 0.7%; Score 9; DB 1; Length 1095;
 CC Best Local Similarity 100.0%; Pred. No. 2.9;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGQWV 702
 DB 624 FWNAGQWV 632

RESULT 9
 ID PIB4_HUMAN STANDARD; PRT; 1175 AA.
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase

CC 015147: 09U002: 09B0M5: 09B0M6: 09B0M8:
CC 15-0CT-2001 (Rel. 4.0, Created)
CC 15-JUN-2002 (Rel. 4.1, Last sequence update)
CC 15-JUN-2002 (Rel. 4.1, Last annotation update)
CC 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
CC DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
CC PLCB4.
CC OS Homo sapiens (Human).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI TaxID=9606:
CC [1]
CC RN SEQUENCE FROM N.A. (ISOFORM 1).
CC RP TISSUE=Retina;
CC RX MEDLINE=96079091: Pubmed=8530101:
CC RA Alvarez R.A., Chalyalyn A.J., Xu P., Hardcastle A., Bhattacharya S.,
CC Rao P.N., Pettenati M.J., Anderson R.E., Baehr W.,
CC "cDNA sequence and gene locus of the human retinal phosphoinositide-
CC specific phospholipase-C beta 4 (PLCB4).";
CC Genomics 29:53-61(1995).
CC [2]
CC RN SEQUENCE FROM N.A. (ISOFORMS 1: 2 AND 3).
CC RP MEDLINE=21638749: Pubmed=11780052:
CC RX Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
CC Jones M., Stavridis G., Almeida J.P., Babage A.K., Baguley C.L.,
CC Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
CC Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
CC Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
CC Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
CC Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
CC Coulson A., Coville G.J., Deadman R., Dham P.D., Dunn M.,
CC Ellington A.G., Griffiths J.A., Fraser A., French L., Garner P.,
CC Ellington A.G., Griffiths J.A., Fraser A., French L., Garner P.,
CC Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
CC Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
CC Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
CC Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
CC Levasiallo M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
CC Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
CC Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
CC Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
CC Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
CC Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
CC Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
CC Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
CC Tracey A., Tromans A.C., Yaudin M., Wall M., Wallis J.M.,
CC Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
CC Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
CC Rogers J.;
CC RT *The DNA sequence and comparative analysis of human chromosome 20.";
CC RL Nature 414:865-871(2001).
CC CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DICYCLYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
CC CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC CC -1- COFACTOR: Calcium.
CC CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1, 2 (shown here) and
CC 3; are produced by alternative splicing.
CC CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
CC CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN
CC CC
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DR	EMBL; AL0231652; CAA21068.1; -
DR	EMBL; AL023805; CAC34525.1; -
DR	EMBL; AL023805; CAC34527.1; -
DR	EMBL; AL023805; CAC34528.1; -
DR	EMBL; LA1349; AAB02027.1; -
DR	HSSP; P10688; IDJX.
DR	Gnew; HGNC:9059; PLCB4.
DR	MIM; 600810; -
DR	InterPro; IPR000008; C2.
DR	InterPro; IPR001192; PI_PLC.
DR	InterPro; IPR000909; PI_PLC_Xdom.
DR	InterPro; IPR001711; PI_PLC_Y.
DR	Pfam; PF00168; C2; 1.
DR	Pfam; PF00387; PI-PLC-Y; 1.
DR	Pfam; PF00388; PI-PLC-X; 3.
DR	PRINTS; PR00390; PHPLIPASEC.
DR	Prodrom; PD001202; PI_PLC_Y; 1.
DR	SMART; SM00239; C2; 1.
DR	SMART; SM00148; PLCCG; 1.
DR	SMART; SM00149; PLCYC; 1.
DR	PROSITE; PS50004; C2_DOMAIN_2; 1.
DR	PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR	PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW	Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium;
KW	Alternative splicing.
KM	DOMAIN 313 463
FT	DOMAIN 565 681
FT	DOMAIN 688 786
FT	ACT_SITE 328 328
FT	ACT_SITE 375 375
FT	VARSPLIC 1 153
FT	VARSPLIC 154 167
FT	VARSPLIC 1 268
FT	CONFLICT 447 447
FT	CONFLICT 757 757
FT	CONFLICT 787 787
FT	CONFLICT 840 840
FT	CONFLICT 902 902
SQ	SEQUENCE 1175 AA; 134463 MW; AB2CBEB9EF57357 CRC64;
Query Match	
Best Local Similarity 100.0%; Score 9; DB 1; Length 1175;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	. 694 FNNAGCOMV 702
DB	639 FNNAGCOMV 647
RESULT 10	
ID	PIB4_RAT STANDARD; PRT; 1175 AA.
DC	Q9OW07; Q9Z0G6; O88356;
DT	16-OCT-2001 (Rel. 40; Created)
DT	16-OCT-2001 (Rel. 40; Last sequence update)
DT	15-JUN-2002 (Rel. 41; Last annotation update)
DE	1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 4 (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
GN	PLCB4.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM A).
RC	STRAIN-Sprague-Dawley; TISSUE-Brain;
RC	MEDLINE=94012687; PUBMED=8407970;
RA	Lee C.-W., Park D.J., Lee K.-H., Kim C.G., Rhee S.G.;
RT	"Purification, molecular cloning, and sequencing of phospholipase C-
RT	beta 4";
RL	J. Biol. Chem. 268: 21318-21327(1993).
RN	[2]

RP SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN-Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=93343926; PubMed=7688223;
 RA Kim M.J., Bahk Y.Y., Min D.S., Lee S.J., Ryu S.H., Suh P.G.;
 RT "Cloning of cDNA encoding rat phospholipase C-beta 4, a new member of
 RL the phospholipase C.";
 RN Biochem. Biophys. Res. Commun. 194:706-712(1993).
 RP [3]
 RP SEQUENCE OF 447-1175 FROM N.A. (ISOFORM C).
 RC TISSUE=Brain;
 RX MEDLINE=99132015; PubMed=9931434;
 RA Adamski F.M., Timms K.M., Shieh B.H.;
 RT "A unique isoform of phospholipase Cbeta4 highly expressed in the
 RL cerebellum and eye.";
 CC Biochim. Biophys. Acta 1444:55-60(1999).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L15556; AAK13557.1; -
 DR EMBL: U57836; AAD10403.1; -
 DR EMBL: AF031370; AAC98145.1; -
 DR EMBL: AF027571; AAC24984.1; -
 DR HSSP: P10688; IDJX.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; PPHPLIPASFC.
 DR Prodom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00238; C2; 1.
 DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCY; 1.
 DR PROSITE: PS50004; C2 DOMAIN 2; 1.
 DR PROSITE: PS50007; PIPLC_X DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 313 463
 FT DOMAIN 565 681
 FT ACT_SITE 688 786
 FT ACT_SITE 328 328
 FT ACT_SITE 375 375
 FT VAASPLIC 1013 1022
 FT VAASPLIC 1023 1075
 FT VAASPLIC 1154 1175
 FT CONFLICT 255 255
 FT CONFLICT 308 308
 FT CONFLICT 417 417
 C) L -> M (IN REF. 2).
 R -> A (IN REF. 2).
 Q -> E (IN REF. 2).

FT CONFLICT 470 470 E -> K (IN REF. 2).
 FT CONFLICT 504 504 A -> AA (IN REF. 1).
 FT CONFLICT 545 546 EQ -> DE (IN REF. 2).
 FT CONFLICT 734 734 I -> L (IN REF. 2).
 FT CONFLICT 741 741 R -> H (IN REF. 2).
 FT CONFLICT 764 764 L -> M (IN REF. 2).
 FT CONFLICT 776 776 D -> N (IN REF. 2).
 FT CONFLICT 828 828 F -> L (IN REF. 1).
 FT CONFLICT 843 843 S -> Y (IN REF. 2).
 FT CONFLICT 852 852 L -> M (IN REF. 3).
 FT CONFLICT 916 916 Q -> T (IN REF. 2).
 FT CONFLICT 1024 1024 W -> C (IN REF. 3).
 FT CONFLICT 1043 1043 L -> M (IN REF. 3).
 FT CONFLICT 1057 1057 A -> V (IN REF. 3).
 FT CONFLICT 1067 1067 L -> V (IN REF. 3).
 FT CONFLICT 1084 1084 S -> C (IN REF. 3).
 SQ SEQUENCE 1175 AA; 134496 MW; 7379C6BB95B8CED CRC64;
 Query Match 0.7%; Score 9; DB 1; Length 1175;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 694 FWNACQMV 702
 Db 639 FWNACQMV 647
 DB 639 FWNACQMV 647
 RESULT 11
 PIGL HUMAN STANDARD; PRT; 1290 AA.
 AC P19174;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II)
 DE DE
 GN PLCG1 OR PLCI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vein, and Brain;
 RX MEDLINE=90355993; PubMed=2167438;
 RA Burgess W.H., Dionne C.A., Kaplow J.M., Mudd R., Friesel R.,
 RA Zilberstein A., Schlesinger J., Jaffe M.;
 RT "Characterization and cDNA cloning of phospholipase C-gamma, a major
 RT substrate for heparin-binding growth factor 1 (acidic fibroblast
 RT growth factor)-activated tyrosine kinase.";
 RL Mol. Cell. Biol. 10:4770-4777(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA DeJonckheere P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babaei A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates R.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammon S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Latrod G.K., Lawlor S.,
 RA Levenslaiho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachle L.J., McIay K., McKerrry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.D.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin R., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [3]
 RP STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=93208890; PubMed=7681365;
 RA Kohda D., Hatanaka H., Ooka M., Mandiyan V., Ullrich A.,
 RA Schlessinger J., Inagaki F.;
 RT "Solution structure of the SH3 domain of phospholipase C-gamma.";
 RL Cell 72:953-960(1993).
 CC -1- FUNCTION: PLC-GAMMA IS A MAJOR SUBSTRATE FOR HEPARIN-BINDING
 CC GROWTH FACTOR 1 (ACIDIC FIBROBLAST GROWTH FACTOR)-ACTIVATED
 CC TYROSINE KINASE.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL: M34667; AAA36452.1; -;
 DR EMBL: AL022394; CAAL8537.1; -;
 DR PIR: A36466; A36466.
 DR PDB: 2HSF; 31-AUG-94.
 DR PDB: 1HSO; 31-AUG-94.
 DR Genew; HGNC:9065; PLCG1.
 DR MIM; 172420; -;
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PL_PLC.
 DR InterPro: IPR000909; PL_PLC_xdom.
 DR InterPro: IPR001711; PL_PLC_Y.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 2.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00169; PH; 2.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRODOM: PD000066; SH3; 1.
 DR PRODOM: PD000093; SH2; 2.
 DR PRODOM: PD001202; PL_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00233; PH; 2.

DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCY; 1.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS50001; SH2; 2.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PROSITE: PS50004; C2_DOMAIN; 2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 DR HydroLase; Lipid degradation; Phosphorylation; 3D-structure; Polymorphism.
 KW Repeat: Calcium-binding; Phosphorylation; SH2 domain; SH3 domain;
 FT DOMAIN 27 142
 FT CA_BIND 165 176 EF-HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT DOMAIN 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 813 813 I -> T (IN DBSNP:753381).
 FT /FTID-VAR_011908.
 SQ SEQUENCE 1290 AA; 148531 MW; AE05ABE2A18EDDAC CRC64;
 Query Match 0.7%; Score 9; DB 1; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 3; 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 408 EYVILSTE 416
 DB 406 EYVILSTE 414
 ID PIGL_RAT STANDARD; PRT; 1290 AA.
 AC P10586;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (phospholipase C-gamma-1) (PLC-11)
 DE (PLC-148).
 GN PLCG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289733; PubMed=2840660;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Inositol phospholipid-specific phospholipase C: complete cDNA and
 RT protein sequences and sequence homology to tyrosine kinase-related
 RT oncogene products.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5419-5423(1988).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2

CC diacylglycerol.
 CC -1- CORFACTOR: Calcium.
 CC -1- PTA: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
 CC -----
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 CC -----
 CC EMBL: Y00301; CAA68406.1; -.
 CC PIR: S00666; S00666.
 CC PDB: 2PLD; 26-JAN-95.
 CC PDB: 2PLE; 26-JAN-95.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001849; PH.
 CC InterPro: IPR001192; PL-PLC.
 CC InterPro: IPR000909; PL-PLC_Xdom.
 CC InterPro: IPR001711; PL-PLC_X.
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR001452; SH3.
 CC Pfam: PF00017; SH2; 2.
 CC Pfam: PF00018; SH3; 1.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00169; PH; 2.
 CC Pfam: PF00387; PI-PLC-X; 1.
 CC Pfam: PF00388; PI-PLC-X; 1.
 CC PRINTS: PR00401; SH2DOMAIN.
 CC PRINTS: PR00452; SH3DOMAIN.
 CC ProDom: PD000066; SH3; 1.
 CC ProDom: PD000093; SH2; 2.
 CC ProDom: PD001202; PL-PLC_Y; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00233; PH; 2.
 CC SMART: SM00148; PLCYC; 1.
 CC SMART: SM00149; PLCYC; 1.
 CC SMART: SM00252; SH2; 2.
 CC SMART: SM00326; SH3; 1.
 CC PROSITE: PS00018; EF_HAND; 1.
 CC PROSITE: PS0001; SH2; 2.
 CC PROSITE: PS0002; SH3; 1.
 CC PROSITE: PS0003; PH_DOMAIN; 2.
 CC PROSITE: PS0004; C2_DOMAIN; 2; 1.
 CC PROSITE: PS0007; PIPLC_X_DOMAIN; 1.
 CC PROSITE: PS0008; PIPLC_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 CC Repeat; Calcium-binding; Phosphorylation; 3D-structure.
 CC FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 CC FT DOMAIN 27 142 DOMAIN X.
 CC FT DOMAIN 320 464 PH 2 (FIRST PART).
 CC FT DOMAIN 489 523 SH2 1.
 CC FT DOMAIN 550 657 SH2 2.
 CC FT DOMAIN 668 756 SH3.
 CC FT DOMAIN 791 851 PH 2 (SECOND PART).
 CC FT DOMAIN 895 931 DOMAIN Y.
 CC FT DOMAIN 953 1070 C2_DOMAIN.
 CC FT DOMAIN 1075 1177 BY SIMILARITY.
 CC ACT_SITE 335 335

FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION.
 FT MOD_RES 783 783 PHOSPHORYLATION.
 FT MOD_RES 1254 1254 PHOSPHORYLATION.
 SO SEQUENCE 1291 AA; 148312 MM; 9F31CTDAA3FEBA77 CMC64;
 Query Match 0.78; Score 9; DB 1; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 408 EXPYLISTE 416
 Db 406 EXPYLISTE 414
 RESULT 14
 ID DPOZ_MOUSE STANDARD; PRT; 3122 AA.
 AC 061493; 09QWX6; 09JMD6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase zeta catalytic subunit (Ec 2.7.7.7) (Seizure related
 DE protein 4).
 GN REV3L OR POLZ OR SEZ4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/Ola; TISSUE-Testis;
 RX MEDLINE-99202265; PubMed-10102037;
 RA Van Sloun P.P.H., Romeijn R.J., Eeken J.C.J.;
 RT "Molecular cloning, expression and chromosomal localisation of the
 RT mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
 RL Mutat. Res. 433:109-116(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kajiwara K.;
 RT "Molecular analyses of Sex4 encoding murine homologue of yeast REV3 in
 RT brain neurons.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2368-3122 FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-Embryonic brain;
 RX MEDLINE-96216731; PubMed-8645260;
 RA Kajiwara K., Nagawawa H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
 RA Sugaya E.;
 RT "Molecular characterization of seizure-related genes isolated by
 RT differential screening.";
 RL Biochem. Biophys. Res. Commun. 219:795-799(1996).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + [DNA](N).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF083464; AAC98785.1; -.
 CC EMBL: AB031049; BAA90768.1; -.
 CC EMBL: D78644; BAA11461.1; -.
 CC MGD: MGI:1337131; Rev3l.
 CC InterPro: IPR002064; DNA_POL_B.
 CC InterPro: IPR004578; POL2.
 CC Pfam: PF00136; DNA_POL_B; 2.
 CC Pfam: PF0104; DNA_POL_B_exo; 2.

PRINTS; PRO0106; DNAPOLB.
 DR SMART; SM00486; POLB; 1.
 DR TIGRFAMS; TIGR00592; POL2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
 FT ZN_FING 3034 3049
 FT ZN_FING 3078 3096
 FT CONFLICT 92 92
 FT CONFLICT 294 294
 FT CONFLICT 578 578
 FT CONFLICT 609 609
 FT CONFLICT 1278 1278
 FT CONFLICT 1298 1298
 FT CONFLICT 1416 1416
 FT CONFLICT 1848 1848
 FT CONFLICT 2368 2368
 SQ SEQUENCE 3122 AA; 350654 MW; A39846CA7365B48 CRC64;

Query Match 0.7%; Score 9; DB 1; Length 3122;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1100 SSPDSPGIP 1108
 DB 2109 SSPDSPGIP 2117

RESULT 15
 LPSB_LYTP1
 ID LPSB_LYTP1 STANDARD; PRT; 243 AA.
 AC 603975;

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calcium-binding protein LPS1-beta (fragment).
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Echinozoa; Echinodermata; Toxopneustidae;
 OC Lytechinus.
 OC NCBI_TaxID=7653;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Sperm;
 RX MEDLINE=91244831; Pubmed=2037596;
 RA Xiang M., Ge T., Tomlinson C.R., Klein W.H.;
 RT Structure and promoter activity of the LPS1 genes of Lytechinus
 RT pictus. Duplicated exons account for LPS1 proteins with eight calcium
 RT binding domains.";
 RL J. Biol. Chem. 266:10524-10533(1991).
 CC 1- FUNCTION: CALCIUM-BINDING PROTEIN INVOLVED IN LARVAL DEVELOPMENT
 CC AND METAMORPHOSIS. LIKELY TO FUNCTION AS CALCIUM BUFFERS
 CC MEDIATING THE TRANSPORT OF CALCIUM FROM THE SEA WATER TO THE
 CC BLASTOCOEL WHERE CALCIUM IS REQUIRED FOR SKELETON FORMATION.
 CC 1- TISSUE SPECIFICITY: ABORAL ECTODERM, A SQUAMOUS EPITHELIUM
 CC COVERING THE SURFACE OF THE LATE STAGE EMBRYO AND LARVA.
 CC 1- DEVELOPMENTAL STAGE: ACTIVATED EARLY IN DEVELOPMENT IN ABORAL
 CC ECTODERM CELLS.
 CC 1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO SPECS.

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DR EMBL; M62848; AAA30004.1; ALT_SEQ.
 DR HSSP; P02593; ICMG.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 6.

DR PRODOM; PD000012; EF-hand; 3.
 DR SMART; SM00054; EFH; 5.
 DR PROSITE; PS00018; EF_HAND; 6.
 DR Calcium-binding; Repeat.
 FT REPEAT 1 150
 FT REPEAT 151 >243
 FT CA_BIND 29 40
 FT CA_BIND 60 71
 FT CA_BIND 98 109
 FT CA_BIND 134 145
 FT CA_BIND 167 178
 FT CA_BIND 204 215
 FT NON_TER 243
 SQ SEQUENCE 243 AA; 27504 MW; 505B2BB070F7ED62 CRC64;

Query Match 0.7%; Score 8; DB 1; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 DKNDGSL 185
 DB 167 DKNDGSL 174

Search completed: March 28, 2003, 14:02:59
 Job time : 35 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:59:00 ; Search time 112 Seconds

(without alignments)
2220.526 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPPTAGLPGLPPEDPG.....ALYPWHCLRGTLPLWLAGCP 1207

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SPTRMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	45.6	656	4	Q8TEH5
2	286	23.7	716	4	Q8WUS6
3	23	1.9	466	4	Q9H9U2
4	23	1.9	787	4	Q9UP73
5	12	1.0	447	11	Q9CUC1
6	12	1.0	639	4	Q9H8H5
7	12	1.0	738	5	Q97037
8	12	1.0	762	4	Q9BRC7
9	12	1.0	772	6	Q8SPR7
10	12	1.0	1012	5	Q97035
11	12	1.0	1183	11	Q89040
12	12	1.0	1210	13	Q92137
13	12	1.0	1211	13	Q92137
14	11	0.9	32	3	P78708
15	11	0.9	632	11	Q9JXM2
16	11	0.9	806	4	Q9H9X8

17	11	0.9	1103	4	Q9UHV3
18	11	0.9	1355	5	Q97033
19	11	0.9	1609	4	Q9P212
20	11	0.9	1895	5	Q9TVI2
21	11	0.9	1898	5	Q9TVI2
22	11	0.9	1994	4	Q9HC53
23	11	0.9	2281	11	Q99P84
24	11	0.9	2303	4	Q9H8X6
25	10	0.8	756	11	Q921B4
26	10	0.8	756	11	Q921B4
27	10	0.8	771	11	Q963E3
28	10	0.8	772	11	Q62711
29	10	0.8	895	5	Q17232
30	10	0.8	896	5	Q9XWB7
31	10	0.8	997	4	Q15111
32	10	0.8	1096	11	Q62688
33	10	0.7	118	6	Q951V4
34	9	0.7	427	17	Q9H166
35	9	0.7	505	5	Q97337
36	9	0.7	596	10	Q49950
37	9	0.7	613	4	Q96FL6
38	9	0.7	673	6	Q95LH9
39	9	0.7	725	5	Q96101
40	9	0.7	725	5	Q9TZN8
41	9	0.7	757	4	Q8TE37
42	9	0.7	779	5	Q9U121
43	9	0.7	789	4	Q8TEC1
44	9	0.7	884	2	Q9X2W8
45	9	0.7	1010	13	Q9YHU7

ALIGNMENTS

RESULT 1	Q8TEH5	PRELIMINARY:	PRT:	656 AA.
AC	Q8TEH5	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	FLJ00222 protein (Fragment).			
GN	FLJ00222.			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Jikuya H., Takano T., Nomura N., Kikuno R., Nagase T., Ohara O.;			
RT	"The nucleotide sequence of a long cDNA clone isolated from human spleen."			
RL	Submitted (Jan-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AK074149; BAB84975.1; ..			
FT	NON_TER			
SQ	SEQUENCE	656 AA;	70138 MW;	1E65D386AB07F1DA CRC64;
Query Match	Best Local Similarity	45.6%;	Score 550;	DB 4;
Matches 650;	Conservative	99.8%;	Pred. No. 0;	Length 656;
			Mismatches 1;	Indels 0;
				Gaps 0;
QY	557	ESGEDAGASRRNGRLVVGSSFSRRKKGSLKKAASVEEGDEGDSPGGOSRGATROKRTM	616	Q9UHV3 homo sapien
DB	6	ESGEDAGASRRNGRLVVGSSFSRRKKGSLKKAASVEEGDEGDSPGGOSRGATROKRTM	65	Q97033 ephydactia f
QY	617	KLSRALSDLVKTKTSVATDIEEAASSWQVSSFSSTRAHQLOOQPAQYLRFNQOQLSR	676	Q9P212 homo sapien
DB	66	KLSRALSDLVKTKTSVATDIEEAASSWQVSSFSSTRAHQLOOQPAQYLRFNQOQLSR	125	Q9TVI2 caenorhabd1
QY	677	ITYSSTRVDSNNYPOPFNNAGCOMVALNYOSEGRMLQINRAKFSANGCGVLRPGCMC	736	Q9H533 homo sapien
DB	126	ITYSSTRVDSNNYPOPFNNAGCOMVALNYOSEGRMLQINRAKFSANGCGVLRPGCMC	185	Q99P84 homo sapien

QY 737 QGVNPNSEDELPGOLKKOVLRIISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDC 796
 DB 186 QGVNPNSEDELPGOLKKOVLRIISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDC 245
 QY 797 SREOTRVVDNGFNPTWEETLVFMVHMPETALVRELVMDHDPIDGRDIFGORTLAFSSMMP 856
 DB 246 SREOTRVVDNGFNPTWEETLVFMVHMPETALVRELVMDHDPIDGRDIFGORTLAFSSMMP 305
 QY 857 GYRHVYLEGMEEASIFVHVAVSDISGVKQALGLKGLFNGPKRGSIDSHAAGRPPARPS 916
 DB 306 GYRHVYLEGMEEASIFVHVAVSDISGVKQALGLKGLFNGPKRGSIDSHAAGRPPARPS 365
 QY 917 VSQRLRTASAPTKSKQPKRKGPELVLTGRDTSKGVADVPPGPGAPAPAOEGP 976
 DB 366 VSQRLRTASAPTKSKQPKRKGPELVLTGRDTSKGVADVPPGPGAPAPAOEGP 425
 QY 977 GSGSPRKAAPAAVAEKSPVVRPRVLIDGPGPAGMAATCKKCVVSCAGVNTGLOREPR 1036
 DB 426 GSGSPRKAAPAAVAEKSPVVRPRVLIDGPGPAGMAATCKKCVVSCAGVNTGLOREPR 485
 QY 1037 PSEGPASQAIRQOPARADSLGAPCCGLDPRAIPGRSREAKPGAGMROGSGSGSMS 1096
 DB 486 PSEGPASQAIRQOPARADSLGAPCCGLDPRAIPGRSREAKPGAGMROGSGSGSMS 545
 QY 1097 SDSSSPSPGIPERSPPWPGACRQPGALOGEMSALFAQKLEIRSKSPMFSAGKPLPC 1156
 DB 546 SDSSSPSPGIPERSPPWPGACRQPGALOGEMSALFAQKLEIRSKSPMFSAGKPLPC 605
 QY 1157 VVLPFHAGMAGPGSPAASAMTVSPRYLVYALYPWHNCRGTLTLPWLACGP 1207
 DB 606 VVLPFHAGMAGPGSPAASAMTVSPRYLVYALYPWHNCRGTLTLPWLACGP 656

RESULT 2
 Q8WUS6 PRELIMINARY: PRT: 716 AA.
 ID Q8WUS6: O8WUS6:
 AC O8WUS6:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Hypothetical 75.7 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-BRAIN;
 *RA Strausberg R.;
 RL Submitted (DCC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019679; AAH19679.1; -
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00387; PI_PLC_Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 716 AA: 75724 MW: 148244B142852AB0 CRC64;

Query Match 23.7%; Score 286; DB 4; Length 716;
 Best Local Similarity 100.0%; Pred. No. 5.2e-292;
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 697 ACCGWAALYQSEGRMLQINRAKFSANGCGVYLPKGCWCGVFNPNSEDELPGOLKKOL 756
 DB 1 ACCGWAALYQSEGRMLQINRAKFSANGCGVYLPKGCWCGVFNPNSEDELPGOLKKOL 60

QY 757 VLRITSGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDCSREOTRVVDNGFNPTWEET 816
 DB 61 VLRITSGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDCSREOTRVVDNGFNPTWEET 120
 QY 817 LVFMVHMPETALVRLVMDHDPIDGRDIFGORTLAFSSMMPGYRHVYLEGMEEASIFVHVA 876
 DB 121 LVFMVHMPETALVRLVMDHDPIDGRDIFGORTLAFSSMMPGYRHVYLEGMEEASIFVHVA 180
 QY 877 VSDISGVKQALGLKGLFNGPKRGSIDSHAAGRPPARPSVQRLRTASAPTKSKQPG 936
 DB 181 VSDISGVKQALGLKGLFNGPKRGSIDSHAAGRPPARPSVQRLRTASAPTKSKQPG 240
 QY 937 RRGPELVLTGRDTSKGVADVPPGPGAPAPAOEGP 982
 DB 241 RRGPELVLTGRDTSKGVADVPPGPGAPAPAOEGP 286

RESULT 3
 Q9H9U2 PRELIMINARY: PRT: 466 AA.
 ID Q9H9U2: O9H9U2:
 AC Q9H9U2:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CDNA FLJ12548 fls, clone NT2RM4000657, weakly similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1 (EC 3.1.4.11).
 DE (EC 3.1.4.11).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isoqal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.;
 *NEBO human cDNA sequencing project.
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK022610; BAB14129.1; -
 DR HSP; P10688; 1D3H.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00387; PI_PLC_Y; 1.
 DR PRINTS; PR00390; PPHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 466 AA: 52711 MW: 070CD43363C772ED CRC64;

Query Match 1.9%; Score 23; DB 4; Length 466;
 Best Local Similarity 100.0%; Pred. No. 8e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VFMPEIALVRLVMDHDPIDGRDIF 843
 DB 251 VFMPEIALVRLVMDHDPIDGRDIF 273

RESULT 4
 Q9UPU3 PRELIMINARY: PRT: 787 AA.
 ID Q9UPU3:
 AC Q9UPU3:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE KIAA1069 protein (Fragment).
 GN KIAA1069.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRN;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB028992; BAA83021.1;
 DR HSSP: P10688; IDH.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 FT NON-TER 1
 SQ SEQUENCE 787 AA; 89169 MW; 2EFC0355E4CFC8D CRC64;
 Query Match 1.9%; Score 23; DB 4; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 821 VHMPEALVRLVMDHPDGRGP 843
 DB 584 VHMPEALVRLVMDHPDGRGP 606
 RESULT 5
 O99CUC1 PRELIMINARY; PRT; 447 AA.
 AC O99CUC1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 DE clone:4933427D11, full insert sequence (fragment).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fetschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Guslincich S., Hill D., Hornmann M., Hume D.A., Kamaya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.
 RL Nature 409:685-690(2001).
 DR EMBL: AK016945; BAB30513.1;
 DR HSSP: P10688; 10AS
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR Pfam: PF00036; EFhand; 3.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR SMART: SM0054; EFh; 3.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 FT NON-TER 447
 SQ SEQUENCE 447 AA; 51990 MW; 7B81156D3DCEFA1C CRC64;
 Query Match 1.0%; Score 12; DB 11; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 335 SSSNTYLVGDQL 346
 DB 303 SSSNTYLVGDQL 314
 RESULT 6
 Q9H8H5 PRELIMINARY; PRT; 639 AA.
 AC Q9H8H5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE cDNA FLJ13627 f1s, clone PLACE1011046, highly similar to
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 1
 DE (EC 3.1.4.11) (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Ito T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 Tanase T., Nomura Y., Jogiya S., Komai F., Hara K., Takeuchi K.,
 RA Arima M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.,
 RT NEDO human cDNA sequencing project.
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK021689; BAB16641.1;
 DR HSSP: P10688; IDH.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS50007; PIPIC_X DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y DOMAIN; 1.
 FT NON TER 639 639
 SO SEQUENCE 639 AA; 72530 MW; 23EEFE24EAE1A185 CRC64;

Query Match 1.0%; Score 12; DB 4; Length 639;
 Best Local Similarity 100.0%; Pred. No. 0.0042;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWMAGCCQVVALN 705
 DB 191 FWMAGCCQVVALN 202

RESULT 7

ID 097037 PRELIMINARY; PRT; 738 AA.

AC 097037; 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE PIC-del-tah.
 OS Hydra magnipapillata (Hydra).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
 OC Hydridae; Hydra.
 OX NCBI_TaxID=6085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=105;
 RA Koyanagi M., Ono K., Suga H., Iwabe N., Miyata T.;
 RT "Phospholipase C cDNAs from sponge and hydra: Antiquity of genes
 involved in the inositol phospholipid signaling pathway."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017513; BAA76278.1; -
 DR HSP; P10688; 10AS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00036; efhand; 2.
 DR Pfam; PF00388; PI_PLC-X; 1.
 DR Pfam; PF00387; PI_PLC-Y; 1.
 DR PRINTS; PR00390; PPHILIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00149; PLCXG; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
 SO SEQUENCE 738 AA; 84469 MW; 058120C26A618A6 CRC64;

Query Match 1.0%; Score 12; DB 5; Length 738;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 TLTSKILFKDVI 396
 DB 361 TLTSKILFKDVI 372

RESULT 8

ID 098RC7 PRELIMINARY; PRT; 762 AA.

AC 098RC7; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 87.6 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006355; AAH06355.1; -

DR HSP; P10688; 10AS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00036; efhand; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00388; PI_PLC-X; 1.
 DR Pfam; PF00387; PI_PLC-Y; 1.
 DR PRINTS; PR00390; PPHILIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00054; EFh; 3.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00149; PLCXG; 1.
 DR SMART; SM00148; PLCXG; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50018; EF_HAND; UNKNOWN_2.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
 KW Hypothetical protein.
 SO SEQUENCE 762 AA; 87585 MW; 544ABE5CE2AE3EF CRC64;

Query Match 1.0%; Score 12; DB 4; Length 762;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
 DB 303 SSHNTYLVGDQL 314

RESULT 9

ID 08SPR7 PRELIMINARY; PRT; 772 AA.

AC 08SPR7; 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Phospholipase C delta 4.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith T.P.L.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF498759; AAM18122.1; -
 SO SEQUENCE 772 AA; 88075 MW; 86E5706A74247548 CRC64;

Query Match 1.0%; Score 12; DB 6; Length 772;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
 DB 310 SSHNTYLVGDQL 321

RESULT 10

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097035 ID 097035 PRELIMINARY; PRT; 1012 AA.
AC 097035:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE PLC-beta1.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Koyanagi M., Ono K., Suga H., Iwabe N., Miyata T.;
RT "Phospholipase C cDNAs from sponge and hydra: Antiquity of genes
involved in the inositol phospholipid signaling pathway.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017511; BAA/6276.1; -.
DR HSSP; P10688; 1DX.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1012 AA; 116186 MW; BD7CF51F96A23118 CRC64;

Query Match 1.0%; Score 12; DB 5; Length 1012;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWMAGCOMVALN 705
DB 609 FWMAGCOMVALN 620

RESULT 11
ID 089040 PRELIMINARY; PRT; 1183 AA.
AC 089040:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Phospholipase C beta 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GUSTATORY;
RA Roessler P., Kroner C., Freitag J., Noe J., Breer H.;
RT "Identification of a phospholipase C beta subtype in rat taste
cells.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011035; CAA09465.1; -.
DR HSSP; P10688; 1OAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.

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DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1183 AA; 134882 MW; BA3AD63FE074A18C CRC64;

Query Match 1.0%; Score 12; DB 11; Length 1183;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWMAGCOMVALN 705
DB 624 FWMAGCOMVALN 635

RESULT 12
ID 092137 PRELIMINARY; PRT; 1210 AA.
AC 092137:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE (lecithinase C) (Clostridium welchii alpha-toxin) (Clostridium
DE OIDEUMATENS beta- and gamma-toxins).
CN PLC1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9338545; PubMed-8397190;
RA Ma H.W., Biltzer R.D., Healy E., Premont R.T., Landau E.M.,
RA Iyengar R.;
RT "Receptor-evoked Cl- current in Xenopus oocytes is mediated through a
RT beta-type phospholipase C. Cloning of a new form of the enzyme.";
RL J. Biol. Chem. 268:19915-19918(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Rawlings N.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = 1,2-
CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.
CC -1- COFACTOR: ZINC.
DR EMBL; L20816; AAA03065.1; -.
DR EMBL; Y15901; CAA75861.1; -.
DR HSSP; P10688; 1OAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase.
SQ SEQUENCE 1210 AA; 138649 MW; E414CF70EC0F56DC CRC64;

Query Match 1.0%; Score 12; DB 13; Length 1210;

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Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FMNAGCOMVALN 705
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DB 650 FMNAGCOMVALN 661

RESULT 13

ID 091086 PRELIMINARY; PRT: 1211 AA.

AC 091086;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phospholipase C beta.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_Taxid=9103;
RN [1]

SEQUENCE FROM N.A.

RA MEDLINE=96257751; PubMed=8687401;
RT Waldo G.L., Paterson A., Boyer J.L., Nicholas R.A., Harden T.K.;
RT "Molecular cloning, expression and regulatory activity of G alpha 11-
RT erythrocytes.";
RT Biochem. J. 316:559-568(1996).
DR EMBL: U94431; AAC60011.1; -
DR HSSP: P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00388; PI_PLC-X; 1.
DR PRINTS: PR00390; PHPLIPASEC.
DR PRODOM: PD001202; PI_PLC_Y.1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00149; PLCYC; 1.
DR SMART: PS0004; C2_DOMAIN_2; 1.
DR PROSITE: PS50007; PIPIC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.
SQ SEQUENCE 1211 AA; 139061 MW; 4E96A10C6AFDB5A CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTQPLSHYFI 333
|||||
DB 312 QDMTQPLSHYFI 323

RESULT 14

ID P78708 PRELIMINARY; PRT: 32 AA.

AC P78708;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phospholipase C (Fragment).
GN NCPLC-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=MYCELIAL;
RX MEDLINE=97306430; PubMed=9163731;

RA Jung O.J., Lee E.J., Kim J.W., Chung Y.R., Lee C.-W.;
RT "Identification of putative phospholipase C
RT genes in filamentous fungi.";
RL Mol. Cells 7:192-199(1997).
DR EMBL: U65687; AAB39567.1; -
DR HSSP: P10688; 10X.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR Pfam: PF00388; PI_PLC-X; 1.
DR PROSITE: PS50007; PIPIC_X_DOMAIN; 1.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3570 MW; 18FA4E795CCA2PD9 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GRCYEVDCMD 372
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DB 22 GRCYEVDCMD 32

RESULT 15

ID 09JMK2 PRELIMINARY; PRT: 622 AA.

AC 09JMK2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phospholipase C-like protein (Fragment).
GN PCEI OR 4933403A2IRK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]

SEQUENCE FROM N.A.

RA MEDLINE=20581708; PubMed=11146508;
RT Tidhar A., Reichenstein M., Cohen D., Faerman A., Copeland N.G.,
RT Gilbert D.J., Jenkins N.A., Shani M.;
RT "A novel transgenic marker for migrating limb muscle precursors and
RT for vascular smooth muscle cells.";
RL Dev. Dyn. 220:60-73(2001).
DR EMBL: AF233885; AAF40208.1; -
DR HSSP: P10688; 10X.
DR MGD: MGI:1921305; Pcel.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR001711; PI_PLC_Y.
DR InterPro: IPR000159; RA_domain.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00387; PI_PLC-Y; 1.
DR Pfam: PF00788; RA; 1.
DR PRINTS: PR00390; PHPLIPASEC.
DR PRODOM: PD001202; PI_PLC_Y.1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00149; PLCYC; 1.
DR SMART: SM00314; RA; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 622 AA; 69951 MW; 523525661DFED363 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 ANGCGGYLKP 732
|||||
DB 152 ANGCGGYLKP 162

Search completed: March 28, 2003, 14:04:58

Mon Mar 31 11:07:15 2003

us-09-927-112-2.oligo.rspt

Page 7

Job time : 118 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 14:02:31 ; Search time 31 Seconds
(without alignments)
1145.596 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPPRAGPLPGLPPEDPG.....ALYWHCLRGTLPLWLAQGP 1207

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	0.8	744	US-09-738-884-5	Sequence 5, Appl1
2	9	0.7	736	US-09-738-884-2	Sequence 2, Appl1
3	9	0.7	1230	US-08-138-641-2	Sequence 2, Appl1
4	9	0.7	1230	US-08-138-133-2	Sequence 2, Appl1
5	8	0.7	177	US-08-850-910A-18	Sequence 18, Appl1
6	8	0.7	335	US-09-222-938A-4	Sequence 4, Appl1
7	8	0.7	744	US-09-738-884-4	Sequence 4, Appl1
8	7	0.6	131	US-08-664-596B-18	Sequence 18, Appl1
9	7	0.6	137	US-08-279-058B-38	Sequence 38, Appl1
10	7	0.6	137	US-08-828-323-38	Sequence 38, Appl1
11	7	0.6	171	PCT-US95-04910-12	Sequence 12, Appl1
12	7	0.6	180	US-08-924-759-24	Sequence 24, Appl1
13	7	0.6	180	US-09-248-335-24	Sequence 24, Appl1
14	7	0.6	224	US-09-228-986-130	Sequence 130, Appl1
15	7	0.6	237	US-08-750-532-18	Sequence 18, Appl1
16	7	0.6	244	US-08-936-165A-379	Sequence 379, Appl1
17	7	0.6	267	US-08-818-112-142	Sequence 142, Appl1
18	7	0.6	267	US-08-818-111-137	Sequence 137, Appl1
19	7	0.6	267	US-09-056-556-142	Sequence 142, Appl1
20	7	0.6	267	US-09-072-596-137	Sequence 137, Appl1
21	7	0.6	272	US-09-189-637A-311	Sequence 311, Appl1
22	7	0.6	285	US-09-327-681-6	Sequence 6, Appl1
23	7	0.6	293	US-09-069-023-20	Sequence 20, Appl1
24	7	0.6	325	US-09-108-020-49	Sequence 49, Appl1
25	7	0.6	357	US-08-638-911A-37	Sequence 37, Appl1
26	7	0.6	357	US-09-149-476-755	Sequence 755, Appl1
27	7	0.6	376	US-08-279-590A-2	Sequence 2, Appl1

28	7	0.6	376	2	US-08-910-092-2	Sequence 2, Appl1
29	7	0.6	394	4	US-09-218-197-2	Sequence 2, Appl1
30	7	0.6	399	4	US-09-120-772-2	Sequence 2, Appl1
31	7	0.6	412	4	US-09-445-472-1	Sequence 1, Appl1
32	7	0.6	425	4	US-09-247-155-99	Sequence 99, Appl1
33	7	0.6	448	1	US-08-570-157-3	Sequence 3, Appl1
34	7	0.6	448	4	US-08-076-510-3	Sequence 3, Appl1
35	7	0.6	455	4	US-09-240-639-10	Sequence 10, Appl1
36	7	0.6	462	4	US-08-165-241-1	Sequence 1, Appl1
37	7	0.6	485	1	US-08-068-395A-1	Sequence 1, Appl1
38	7	0.6	485	1	US-08-464-365-1	Sequence 1, Appl1
39	7	0.6	505	1	US-08-068-395A-3	Sequence 3, Appl1
40	7	0.6	505	1	US-08-464-365-3	Sequence 3, Appl1
41	7	0.6	505	4	US-09-509-902A-11	Sequence 11, Appl1
42	7	0.6	522	4	US-08-894-818B-3	Sequence 3, Appl1
43	7	0.6	522	4	US-09-445-472-4	Sequence 4, Appl1
44	7	0.6	543	4	US-09-535-008-63	Sequence 63, Appl1
45	7	0.6	577	2	US-08-852-153-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-738-884-5
; Sequence 5, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GIEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-738-884-5

Query Match 0.8%; Score 10; DB 4; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGGCGVLPK 732
DB 585 NGGCGVLPK 594

RESULT 2
US-09-738-884-2
; Sequence 2, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GIEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human
US-09-738-884-2

Query Match 0.7%; Score 9; DB 4; Length 736;

Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 LVKGGKLP 471
|||||||
Db 425 LVKGGKLP 433

RESULT 3

US-08-138-641-2
Sequence 2, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:
APPLICANT: Koblán, Kenneth S.
APPLICANT: Pompliano, David L.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-138-641-2

Query Match 0.7%; Score 9; DB 1; Length 1290;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 408 EYVILSIE 416
|||||||
Db 406 EYVILSIE 414

RESULT 4

US-08-138-133-2
Sequence 2, Application US/08138133
Patent No. 5519163
GENERAL INFORMATION:

APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MERCHANT, KEVIN J.
TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
TITLE OF INVENTION: PHOSPHOLIPASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MUTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-138-133-2

Query Match 0.7%; Score 9; DB 1; Length 1290;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 408 EYVILSIE 416
|||||||
Db 406 EYVILSIE 414

RESULT 5

US-08-850-910A-18
Sequence 18, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:

APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENT PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROESTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988

APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-850-910A-18

Query Match 0.7%; Score 8; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 SORPGRG 939
DB 152 SORPGRG 159

RESULT 6
US-09-222-938A-4
Sequence 4, Application US/09222938A
Patent No. 6437108
GENERAL INFORMATION:
APPLICANT: Youngman, Phillip
APPLICANT: Filtz, Christian
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222,938A
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 335
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-222-938A-4

Query Match 0.7%; Score 8; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 SDEDSLAR 161
DB 90 SDEDSLAR 97

RESULT 7
US-09-738-884-4
Sequence 4, Application US/09738884
Patent No. 6391606
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4
LENGTH: 744
TYPE: PRT
ORGANISM: Citicellus griseus
US-09-738-884-4

Query Match 0.7%; Score 8; DB 4; Length 744;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ISGQQLPK 768
DB 625 ISGQQLPK 632

RESULT 8
US-08-664-596B-18
Sequence 18, Application US/08664596B
Patent No. 5807703
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-664-596B-18

Query Match 0.6%; Score 7; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 SSDSSP 1102
DB 119 SSDSSP 125

RESULT 9

US-08-279-058B-38
; Sequence 38, Application US/08279058B
; Patent No. 5668004
; GENERAL INFORMATION:
; APPLICANT: Michael E. O'Donnell
; TITLE OF INVENTION: DNA POLYMERASE III
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,058B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yamwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: CRF D-1056CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-279-058B-38

Query Match 0.6%; Score 7; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1122 PGALOG 1128
Db 22 PGALOG 28

RESULT 10
US-08-828-323-38
; Sequence 38, Application US/08828323A
; Patent No. 6413753
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael
; TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
; FILE REFERENCE: 19603/10214
; CURRENT APPLICATION NUMBER: US/08/828,323A
; CURRENT FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-828-323-38

Query Match 0.6%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1122 PGALOG 1128
Db 22 PGALOG 28

RESULT 11
PCT-US95-04910-12
; Sequence 12, Application PC/TUS9504910
; GENERAL INFORMATION:
; APPLICANT: The Government of the United
; APPLICANT: States of America as represented
; APPLICANT: by the Secretary, Department of
; APPLICANT: Health and Human Services
; TITLE OF INVENTION: ISOLATION AND
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL PRIMATE T-CELL
; TITLE OF INVENTION: LYMPHOTROPIC VIRUS AND THE USE OF THIS VIRUS
; TITLE OF INVENTION: OR COMPONENTS THEREOF IN DIAGNOSTIC ASSAYS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04910
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/231,526
; FILING DATE: 22-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAM S. FEILER
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4125PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acids
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
PCT-US95-04910-12

Query Match 0.6%; Score 7; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 ARROTR 166
Db 4 ARROTR 10

RESULT 12
US-08-924-759-24
; Sequence 24, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET

CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,759
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1128
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: MAIZE
IMMEDIATE SOURCE:
LIBRARY: CSL.PK0059.E2
US-08-924-759-24

Query Match 0.6%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 887 ALGKGL 893
|||||
DB 24 ALGKGL 30

RESULT 13
US-09-248-335-24
Sequence 24, Application US/09248335
Patent No. 6096504
GENERAL INFORMATION:
APPLICANT: MCCONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 24
LENGTH: 180
TYPE: PRT
ORGANISM: maize
US-09-248-335-24

Query Match 0.6%; Score 7; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 887 ALGKGL 893
|||||
DB 24 ALGKGL 30

RESULT 14

US-09-228-986-130
Sequence 130, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and their use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 130
LENGTH: 224
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-228-986-130

Query Match 0.6%; Score 7; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1096 SSDSSP 1102
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DB 202 SSDSSP 208

RESULT 15
US-08-750-532-18
Sequence 18, Application US/08750532
Patent No. 5736339
GENERAL INFORMATION:
APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozi
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,532
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/130236
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITTA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 18;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 237 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-750-532-18

Query Match 0.6%; Score 7; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1169 GSPAAAS 1175
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 Db 133 GSPAAAS 139

Search completed: March 28, 2003, 14:12:10
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: March 28, 2003, 14:05:06 ; Search time 38 Seconds

(without alignments)
1865.249 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 1207
Sequence: 1 MAPPTAGPLPGPALPPEDPC.....ALYPMHICRTLLPWLAGCP 1207

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Gapop 60.0 , Gapext 60.0

Searched: 237916 seqs, 58723674 residues

Word size : 0

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA*

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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1207	100.0	1207	US-09-927-112-2	Sequence 2, Appli
2	324	26.8	325	US-09-927-112-10	Sequence 10, Appl
3	14	1.2	1054	US-09-828-447-11	Sequence 11, Appl
4	13	1.1	119	US-09-764-868-637	Sequence 637, App
5	13	1.1	119	US-09-955-999-84	Sequence 84, Appl
6	12	1.0	102	US-09-822-635-7	Sequence 7, Appli
7	12	1.0	119	US-09-800-971-9	Sequence 9, Appli
8	12	1.0	128	US-09-800-971-8	Sequence 8, Appli
9	12	1.0	128	US-09-927-112-8	Sequence 8, Appli
10	12	1.0	128	US-09-908-664-11	Sequence 11, Appl
11	12	1.0	128	US-09-908-664-20	Sequence 20, Appl
12	12	1.0	340	US-09-835-996A-19	Sequence 19, Appl
13	12	1.0	567	US-09-835-996A-8	Sequence 8, Appli
14	12	1.0	762	US-09-804-969-15	Sequence 15, Appl
15	12	1.0	762	US-09-908-664-2	Sequence 2, Appli
16	11	0.9	119	US-09-908-664-15	Sequence 15, Appl
17	11	0.9	128	US-09-908-664-23	Sequence 23, Appl
18	11	0.9	1809	US-09-822-635-2	Sequence 2, Appli
19	10	0.8	92	US-09-927-112-16	Sequence 16, Appl

20	10	0.8	182	10	US-09-800-971-7	Sequence 7, Appli
21	10	0.8	201	10	US-09-867-550-1334	Sequence 1334, Ap
22	10	0.8	628	10	US-09-828-447-12	Sequence 12, Appl
23	10	0.8	744	9	US-10-096-961-5	Sequence 5, Appli
24	9	0.7	736	9	US-10-096-961-2	Sequence 2, Appli
25	9	0.7	736	10	US-09-800-971-2	Sequence 2, Appli
26	8	0.7	48	10	US-09-864-761-42929	Sequence 42929, A
27	8	0.7	63	10	US-09-908-664-17	Sequence 17, Appl
28	8	0.7	158	10	US-09-764-870-377	Sequence 377, App
29	8	0.7	158	10	US-09-764-860-342	Sequence 342, App
30	8	0.7	158	10	US-09-927-112-11	Sequence 11, Appl
31	8	0.7	170	10	US-09-908-664-11	Sequence 13, Appl
32	8	0.7	191	10	US-09-908-664-22	Sequence 22, Appl
33	8	0.7	335	10	US-09-815-242-13433	Sequence 13433, A
34	8	0.7	335	10	US-09-815-242-13658	Sequence 13658, A
35	8	0.7	384	9	US-09-738-626-6924	Sequence 6924, Ap
36	8	0.7	608	10	US-09-908-664-5	Sequence 5, Appli
37	8	0.7	744	9	US-10-096-961-4	Sequence 4, Appli
38	8	0.7	875	9	US-09-548-933-15	Sequence 15, Appl
39	8	0.7	1567	10	US-09-835-232-2	Sequence 2, Appli
40	7	0.6	51	10	US-09-864-761-48515	Sequence 48515, A
41	7	0.6	71	10	US-09-764-877-1515	Sequence 1515, Ap
42	7	0.6	83	10	US-09-050-010-7	Sequence 7, Appli
43	7	0.6	93	10	US-09-764-864-676	Sequence 676, App
44	7	0.6	104	10	US-09-864-761-39244	Sequence 39244, A
45	7	0.6	113	9	US-09-738-626-4430	Sequence 4430, Ap

ALIGNMENTS

RESULT 1
US-09-927-112-2
Sequence 2, Application US/09927112
Patent No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32544, a novel human phospholipase C and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 38155-20048.00
CURRENT APPLICATION NUMBER: US/09/927,112
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/246,808
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1207
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-112-2

Query Match 100.0%; Score 1207; DB 10; Length 1207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPTAGPLPGPALPPEDPCPESRRLFLSANILPVVERKGMAGOMQVYKLRGSGK 60
DB 1 MAPPTAGPLPGPALPPEDPCPESRRLFLSANILPVVERKGMAGOMQVYKLRGSGK 60
QY 1 VRFYTLDEHRSCTIWRSRKNEKAKISIDTQEVSEGRSEVORVYDGSFDDNCFST 120
DB 1 VRFYTLDEHRSCTIWRSRKNEKAKISIDTQEVSEGRSEVORVYDGSFDDNCFST 120
QY 61 LVRFYTLDEHRSCTIWRSRKNEKAKISIDTQEVSEGRSEVORVYDGSFDDNCFST 120
DB 61 LVRFYTLDEHRSCTIWRSRKNEKAKISIDTQEVSEGRSEVORVYDGSFDDNCFST 120
QY 121 YHGSRESIDLVSTSEVARTWTGLRYLMAGISDEDSLARRQTRDQWLKOTFDEADKN 180
DB 121 YHGSRESIDLVSTSEVARTWTGLRYLMAGISDEDSLARRQTRDQWLKOTFDEADKN 180
QY 181 GGSLSIGEVYDOLHLKLVNLPKRVYKQMFREADTDHOGTLGFEFCATFKKMSSTRDL 240
DB 181 GGSLSIGEVYDOLHLKLVNLPKRVYKQMFREADTDHOGTLGFEFCATFKKMSSTRDL 240

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QY 241 YLLMLTYSNKHDLDAASLORFLOVEOKMAGVLESCODILEQEPCEPKSKGLGIDG 300
D 241 YLLMLTYSNKHDLDAASLORFLOVEOKMAGVLESCODILEQEPCEPKSKGLGIDG 300
QY 301 FTNTRSPADIDFPEHHNHODMTOPLSHYFTTSSNTLYVDQMSOSRDMYAMVLO 360
D 301 FTNTRSPADIDFPEHHNHODMTOPLSHYFTTSSNTLYVDQMSOSRDMYAMVLO 360
QY 361 AGRCVCEVDCWDGDPHEPIVHNGYTLRSKILPFQVJETINKYAFINKEPVILSIENHCS 420
D 361 AGRCVCEVDCWDGDPHEPIVHNGYTLRSKILPFQVJETINKYAFINKEPVILSIENHCS 420
QY 421 VIOOKMAOYLTDILGDKLDLSVSSSEDAATLPSPOLMKGRILYKGRKLPANISEDABEG 480
D 421 VIOOKMAOYLTDILGDKLDLSVSSSEDAATLPSPOLMKGRILYKGRKLPANISEDABEG 480
QY 481 EVSEDESDADIEDDCKLINDASTNKRREVENTAKRKLDLSIKRSKIRDCEDPNEVSSTL 540
D 481 EVSEDESDADIEDDCKLINDASTNKRREVENTAKRKLDLSIKRSKIRDCEDPNEVSSTL 540
QY 541 SPGSKLGRSKAEDEYSEGDAGASRRNGRLVYGSFSRRKKKSKLKKAAYEEGDEGOD 600
D 541 SPGSKLGRSKAEDEYSEGDAGASRRNGRLVYGSFSRRKKKSKLKKAAYEEGDEGOD 600
QY 601 SPGSGRGATROKTKTKLSALSDLYKTKSVATHDIEEPAASSWQVSSFSETKAHQIIO 660
D 601 SPGSGRGATROKTKTKLSALSDLYKTKSVATHDIEEPAASSWQVSSFSETKAHQIIO 660
QY 661 OKRAQILRFNOQOLSRITSSSYRVDSNTNPOEFMAGCOMALNOSGRLQOLNRAF 720
D 661 OKRAQILRFNOQOLSRITSSSYRVDSNTNPOEFMAGCOMALNOSGRLQOLNRAF 720
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D 721 SANGCGGYVLKPGCMQGYVFNPNSEDPPLPGOLKKOLVLRILISGOOLPKPRDMLGDRGI 780
QY 781 IDPFEVEIILGLPVDCSRQOTRYVDNGFNPMWETLVYMHMPELALRYFLVMDHDPIC 840
D 781 IDPFEVEIILGLPVDCSRQOTRYVDNGFNPMWETLVYMHMPELALRYFLVMDHDPIC 840
QY 841 RDEIGORTLAFSSMPGYRHYVLEGEAEASIFVHAVASDISGKVOALGKGLFLRGPP 900
D 841 RDEIGORTLAFSSMPGYRHYVLEGEAEASIFVHAVASDISGKVOALGKGLFLRGPP 900
QY 901 GSIDSHAAARRPARPSVSRILRTASAPTKSQKPGRGFPPELVLTGRTDTSKGVADVV 960
D 901 GSIDSHAAARRPARPSVSRILRTASAPTKSQKPGRGFPPELVLTGRTDTSKGVADVV 960
QY 961 PPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPTVRPRVLDGPGPAGMAATCMKCV 1020
D 961 PPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPTVRPRVLDGPGPAGMAATCMKCV 1020
QY 1021 GSCAGVNTGGLQREPRPSPGPASROAARQOPRARADSLGAPCCGLDHPHAIIGRSREAPK 1080
D 1021 GSCAGVNTGGLQREPRPSPGPASROAARQOPRARADSLGAPCCGLDHPHAIIGRSREAPK 1080
QY 1081 GPGAMROBPSSGSSSSSPDSCPIEPRSRMPREGACROGALQEMSALEPAOKLEET 1140
D 1081 GPGAMROBPSSGSSSSSPDSCPIEPRSRMPREGACROGALQEMSALEPAOKLEET 1140
QY 1141 RSKSPMSAGRPILPCVYLPHAPGAGGSPAAASAMTVSRVLVALVYWHCLRGTL 1200
D 1141 RSKSPMSAGRPILPCVYLPHAPGAGGSPAAASAMTVSRVLVALVYWHCLRGTL 1200
QY 1201 PWLAGCP 1207
D 1201 PWLAGCP 1207

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RESULT 2
US-09-927-112-10
Sequence 10, Application US/09927112

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; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR APPLICATION NUMBER: 2001-08-10
; PRIOR FILING DATE: 2000/246,808
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-10

Query Match 26.8%; Score 324; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.2e-310;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 884 VKOALGKGLRKPSPKSLDASHAAGRPAPRSYORILKRTASAPTKSQKPGRGFPPEL 943
D 2 VKOALGKGLRKPSPKSLDASHAAGRPAPRSYORILKRTASAPTKSQKPGRGFPPEL 943
QY 944 VLGRDTSKGVADVYPPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPTVRPRV 1003
D 62 VLGRDTSKGVADVYPPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPTVRPRV 1003
QY 1004 DGPBGAAATCMKCVGSCAGVNTGGLQREPRPSPGPASROAARQOPRARADSLGAPC 1063
D 122 DGPBGAAATCMKCVGSCAGVNTGGLQREPRPSPGPASROAARQOPRARADSLGAPC 1063
QY 1064 GCLDPHAIIGRSREAPKPGPAGMROGPGSSGSSSPDSCPIEPRSRMPREGACROG 1123
D 182 GCLDPHAIIGRSREAPKPGPAGMROGPGSSGSSSPDSCPIEPRSRMPREGACROG 1123
QY 1124 ALQEMSALEPAOKLEETIRSKSPMSAGRPILPCVYLPHAPGAGGSPAAASAMTVSPRY 1183
D 242 ALQEMSALEPAOKLEETIRSKSPMSAGRPILPCVYLPHAPGAGGSPAAASAMTVSPRY 1183
QY 1184 LVVALVYWHCLRGTLPWLAGCP 1207
D 302 LVVALVYWHCLRGTLPWLAGCP 325

RESULT 3
US-09-828-447-11
; Sequence 11, Application US/09828447
; Patent No. US20020069432A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
; FILE REFERENCE: 16313-0037
; CURRENT APPLICATION NUMBER: US/09/828,447
; PRIOR APPLICATION NUMBER: 2001-08-20
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1054
; TYPE: PRT

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; ORGANISM: Physcomitrella patens
US-09-828-447-11

Query Match
Best Local Similarity 1.2%; Score 14; DB 10; Length 1054;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 VHODMTQPLSHYFI 333
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DB 104 VHODMTQPLSHYFI 117

RESULT 4
US-09-764-868-637
; Sequence 637, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-637

Query Match
Best Local Similarity 1.1%; Score 13; DB 9; Length 119;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YLMAGISDEDSLA 160
|||||
DB 53 YLMAGISDEDSLA 65

RESULT 5
US-09-955-999-84
; Sequence 84, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; FILE REFERENCE: PT086P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-955-999-84

Query Match
Best Local Similarity 1.1%; Score 13; DB 9; Length 119;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YLMAGISDEDSLA 160
|||||
DB 53 YLMAGISDEDSLA 65

RESULT 6
US-09-822-635-7
; Sequence 7, Application US/09822635
; Patent No. US20010039331A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND
; FILE REFERENCE: 10448-035001
; CURRENT APPLICATION NUMBER: US/09/822,635
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,921
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-822-635-7

Query Match
Best Local Similarity 1.0%; Score 12; DB 10; Length 102;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
|||||
DB 53 FWNAGCOMVALN 64

RESULT 7
US-09-800-971-9
; Sequence 9, Application US/09800971
; Patent No. US20020098577A1
; GENERAL INFORMATION:
; APPLICANT: Rachel A. Meyers
; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
; FILE REFERENCE: 10448-023001
; CURRENT APPLICATION NUMBER: US/09/800,971
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,453
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/188,032
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
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US-09-800-971-9

Query Match 1.0%; Score 12; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 77 FWNAGCOMVALN 88

RESULT 8

US-09-800-971-8
; Sequence 8, Application US/09800971
; Patent No. US20020098577A1
; GENERAL INFORMATION:
; APPLICANT: Rachel A. Meyers
; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
; FILE REFERENCE: 10448-023001
; CURRENT APPLICATION NUMBER: US/09/800,971
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,453
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/188,032
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-800-971-8

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 9

US-09-927-112-8
; Sequence 8, Application US/09927112
; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Sllios-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-8

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 10

US-09-908-664-11
; Sequence 11, Application US/09908664
; Patent No. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-908-664-11

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 11

US-09-908-664-20
; Sequence 20, Application US/09908664
; Patent No. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-908-664-20

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

Db 79 FNNAGCOMVALN 90

RESULT 12

US-09-835-996A-19
Sequence 19, Application US/09835996A
Patent No. US20020142953A1

GENERAL INFORMATION:

APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiahong
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835,996A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-19

Query Match 1.0%; Score 12; DB 10; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
|||||
Db 303 SSHNTYLVGDQL 314

RESULT 13

US-09-835-996A-8
Sequence 8, Application US/09835996A
Patent No. US20020142953A1

GENERAL INFORMATION:

APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiahong
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM

FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835,996A
CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-8

Query Match 1.0%; Score 12; DB 10; Length 567;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
|||||
Db 303 SSHNTYLVGDQL 314

RESULT 14

US-09-804-969-15
Sequence 15, Application US/09804969
Patent No. US20020081595A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi
APPLICANT: Nepomniachtch, Boris
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuln, Alejandro
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides
FILE REFERENCE: LEX-0148-USA
CURRENT APPLICATION NUMBER: US/09/804,969
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/188,885
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 60/189,693
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 762
TYPE: PRT
ORGANISM: homo sapiens
US-09-804-969-15

Query Match 1.0%; Score 12; DB 10; Length 762;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
|||||
Db 303 SSHNTYLVGDQL 314

RESULT 15

US-09-908-664-2
Sequence 2, Application US/09908664
Patent No. US20020115178A1

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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-908-664-2

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Query Match          1.0%; Score 12; DB 10; Length 762;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 335 SSHTYLVGDQL 346
   |||||
Db 303 SSHTYLVGDQL 314

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Job time : 41 secs